

Mon Nov 1 10:45:58 2004

us-10-044-692-1.rni

VP 6,261,836 (various 3-8-10)
Signature 324-10070
on 6,261,836
Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 16:25:00 : Search time 310 Seconds
(without alignments)
9205.862 Million cell updates/sec

Title: US-10-044-692-1

Perfect score: 4015

Sequence: 1 GCAGGCGCGCGCTGCTGC.....TTTTCAGTTTGAAAAA 4015

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	4015	100.0	US-08-851-843A-224	Sequence 224, App
2	4015	100.0	US-08-974-549A-1	Sequence 1, App1
3	4015	100.0	US-08-854-050-224	Sequence 224, App
4	4015	100.0	US-09-430-323-224	Sequence 224, App
5	4015	100.0	US-09-572-423B-3	Sequence 3, App1
6	4015	100.0	US-09-128-354-1	Sequence 1, App1
7	4015	100.0	US-09-675-321-1	Sequence 1, App1
8	4015	100.0	US-09-052-919-1	Sequence 1, App1
9	4015	100.0	US-08-912-951-1	Sequence 1, App1
10	4015	100.0	US-09-733-294A-3	Sequence 3, App1
11	4015	100.0	US-09-402-181B-1	Sequence 1, App1
12	4015	100.0	US-09-402-181B-1	Sequence 1, App1
13	4015	100.0	US-09-953-052-1	Sequence 1, App1
14	4015	100.0	US-09-465-491-1	Sequence 1, App1
15	4015	100.0	US-09-974-549A-343	Sequence 343, App
16	4008.6	99.8	US-09-402-181B-343	Sequence 343, App
17	4008.6	99.8	US-09-721-456-343	Sequence 343, App
18	3849.2	95.9	US-08-851-843A-173	Sequence 173, App
19	3849.2	95.9	US-08-974-549A-292	Sequence 292, App
20	3849.2	95.9	US-08-854-050-173	Sequence 173, App
21	3849.2	95.9	US-09-430-323-173	Sequence 173, App
22	3849.2	95.9	US-09-402-181B-292	Sequence 292, App
23	3849.2	95.9	US-09-721-456-292	Sequence 292, App
24	3641	90.7	US-08-851-843A-4	Sequence 4, App1
25	3641	90.7	US-08-912-951-4	Sequence 4, App1
26	3641	90.7	US-09-402-181B-4	Sequence 4, App1
27	3641	90.7	US-09-721-456-4	Sequence 4, App1

28	2205.2	54.9	3451	3	US-08-974-549A-721	Sequence 721, App
29	2205.2	54.9	3451	3	US-09-721-456-721	Sequence 721, App
30	2200.8	54.8	3396	3	US-08-974-549A-639	Sequence 639, App
31	2200.8	54.8	3396	4	US-09-721-456-639	Sequence 639, App
32	2196.6	54.7	3396	3	US-08-974-549A-638	Sequence 638, App
33	2196.6	54.7	3396	4	US-09-721-456-638	Sequence 638, App
34	1960.4	48.8	2176	3	US-08-974-549A-3	Sequence 3, App1
35	1960.4	48.8	2176	4	US-08-912-951-3	Sequence 3, App1
36	1960.4	48.8	2176	4	US-09-402-181B-3	Sequence 3, App1
37	1960.4	48.8	2176	4	US-09-721-456-3	Sequence 3, App1
38	1877.2	46.8	2171	3	US-08-851-843A-100	Sequence 100, App
39	1877.2	46.8	2171	3	US-08-974-549A-266	Sequence 266, App
40	1877.2	46.8	2171	3	US-08-854-050-100	Sequence 100, App
41	1877.2	46.8	2171	3	US-09-430-323-100	Sequence 100, App
42	1877.2	46.8	2171	4	US-09-402-181B-266	Sequence 266, App
43	1877.2	46.8	2171	4	US-09-721-456-266	Sequence 266, App
44	1862.2	46.4	3396	3	US-08-974-549A-642	Sequence 642, App
45	1862.2	46.4	3396	4	US-09-721-456-642	Sequence 642, App

ALIGNMENTS

RESULT 1
Sequence 224, Application US/08851843A
Patent No. 6093809

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Langner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hprt"
OTHER INFORMATION: /note= "human telomerase reverse
transcriptase (hprt) catalytic protein
OTHER INFORMATION: component"
US-08-851-843A-224

Query Match 100.0%; Score 4015; DB 3; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGCTCTCTCTGCGCACTGGGAAGCCCTGAGCCCGCCACCCCGCGATGCC 60
DB 1 GCAGCGCTGCTCTCTCTGCGCACTGGGAAGCCCTGAGCCCGCCACCCCGCGATGCC 60
QY 61 GCGGCTCCCCCGCGCGAGCGCGGCTCTCTGCTGCGAGCCACTACCGGAGGTGCT 120
DB 61 GCGGCTCCCCCGCGCGAGCGCGGCTCTCTGCTGCGAGCCACTACCGGAGGTGCT 120
QY 121 GCCCTGCGCACTTCTGTCGCGCGCTGAGGCGCCGAGGCTGCGCTGTCAGCGCG 180
DB 121 GCCCTGCGCACTTCTGTCGCGCGCTGAGGCGCCGAGGCTGCGCTGTCAGCGCG 180
QY 181 GGACCCCGCGCTTTCGCGCGCTGTCGCGCGCGCAAGTGTGCTGCTGCGCGCG 240
DB 181 GGACCCCGCGCTTTCGCGCGCTGTCGCGCGCGCAAGTGTGCTGCTGCGCGCG 240
QY 241 ACGGCGCGCGCGCGCGCGCGCGCTCTCTGCGCACTGCTGCTGAGGAGCTGTCG 300
DB 241 ACGGCGCGCGCGCGCGCGCGCGCTCTCTGCGCACTGCTGCTGAGGAGCTGTCG 300
QY 301 CGAGTGTCTGCAAGAGCTGTGTCGAGCGCGCGCGCGCAAGTGTGCTGCTGCG 360
DB 301 CGAGTGTCTGCAAGAGCTGTGTCGAGCGCGCGCGCGCAAGTGTGCTGCTGCG 360
QY 361 CGAGTGTCTGCAAGAGCTGTGTCGAGCGCGCGCGCGCAAGTGTGCTGCTGCG 420
DB 361 CGAGTGTCTGCAAGAGCTGTGTCGAGCGCGCGCGCGCGCAAGTGTGCTGCTGCG 420
QY 421 CTTGCGCAACAGTGTGTCGAGCGCGCGCGCGCGCGCGCTTTCACCAAGCTGCG 480
DB 421 CTTGCGCAACAGTGTGTCGAGCGCGCGCGCGCGCGCGCTTTCACCAAGCTGCG 480
QY 481 CCGCGTGGCGCAAGAGCTGTGTCGAGCGCGCGCGCGCGCGCTTTCACCAAGCT 540
DB 481 CCGCGTGGCGCAAGAGCTGTGTCGAGCGCGCGCGCGCGCGCTTTCACCAAGCT 540
QY 541 GCGTCCAGAGCTGCTTACAGTGTGTCGAGCGCGCGCGCGCGCGCTTTCACCAAG 600
DB 541 GCGTCCAGAGCTGCTTACAGTGTGTCGAGCGCGCGCGCGCGCGCTTTCACCAAG 600
QY 601 TGAAGCGCGCGCGCGCGCGCGCGCGCTTTCACCAAGAGCTTTCACCAAGAG 660
DB 601 TGAAGCGCGCGCGCGCGCGCGCGCGCTTTCACCAAGAGCTTTCACCAAGAG 660
QY 661 CTGGAACCTAAGGTGTCAGAGGAGCGCGCGCGCGCGCGCTTTCACCAAGAG 720
DB 661 CTGGAACCTAAGGTGTCAGAGGAGCGCGCGCGCGCGCGCTTTCACCAAGAG 720
QY 721 GAGGCGCGCGCGCGCGCGCGCGCGCGCTTTCACCAAGAGCGCGCGCGCGCG 780
DB 721 GAGGCGCGCGCGCGCGCGCGCGCGCGCTTTCACCAAGAGCGCGCGCGCGCG 780
QY 781 TGGCCCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840

DB 781 TGGCCCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 841 GCGTGAACCGAGTACCGTGTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 900
DB 841 GCGTGAACCGAGTACCGTGTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 901 CACCTCTTTGAGAGGTGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 960
DB 901 CACCTCTTTGAGAGGTGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 961 GCACCGAGCG 1020
DB 961 GCACCGAGCG 1020
QY 1021 CCGGTTGACCGCGAGACCAAGCACTTCTCTACTCTCTGAGCGCAAGAGCACTGCG 1080
DB 1021 CCGGTTGACCGCGAGACCAAGCACTTCTCTACTCTCTGAGCGCAAGAGCACTGCG 1080
QY 1081 GCGCTCTTCTACTGAGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1081 GCGCTCTTCTACTGAGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1141 GACCACTTTTCTGAGTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB 1141 GACCACTTTTCTGAGTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1201 GCCCAGCGCTACTGCAATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB 1201 GCCCAGCGCTACTGCAATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1261 GTGCCCCCTACCGAGGTGCTCTCAAGACGCACTGCGCGCGCGCGCGCG 1320
DB 1261 GTGCCCCCTACCGAGGTGCTCTCAAGACGCACTGCGCGCGCGCGCGCG 1320
QY 1321 AGCGGCTGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
DB 1321 AGCGGCTGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1381 CACAGACCG 1440
DB 1381 CACAGACCG 1440
QY 1441 CGGCTTCTGTCGAGAGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1500
DB 1441 CGGCTTCTGTCGAGAGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1500
QY 1501 CAAAGACCG 1560
DB 1501 CAAAGACCG 1560
QY 1561 GCTCTGCTGCAAGAGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1620
DB 1561 GCTCTGCTGCAAGAGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1620
QY 1621 GAGCCCAAGAGGTGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1680
DB 1621 GAGCCCAAGAGGTGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1680
QY 1681 CAAATTCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 CAAATTCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 TGTTCAGAGAGACCAAGCTTTCACCAAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 TGTTCAGAGAGACCAAGCTTTCACCAAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 CAAATTCAAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1801 CAAATTCAAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 GGAAGCAGAGGTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 GGAAGCAGAGGTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920

1921 CTTATCCCAAGCCTGAGCGGCTGCGCCGATTTGGAACATGACTACGTGCTGAGAC 1980
1921 CTTATCCCAAGCCTGAGCGGCTGCGCCGATTTGGAACATGACTACGTGCTGAGAC 1980
1981 CAGAACTTCCGAGAGAAAGAGGCGCCGAGCGCTCTACCTCGAGGCTGAAGCACTGTT 2040
1981 CAGAACTTCCGAGAGAAAGAGGCGCCGAGCGCTCTACCTCGAGGCTGAAGCACTGTT 2040
2041 CAGCGTGTCTCAACTAGAGCGGCGCGCGCCCGCCCTCTCGGCGCGCTCTGTGTGCG 2100
2041 CAGCGTGTCTCAACTAGAGCGGCGCGCGCCCGCCCTCTCGGCGCGCTCTGTGTGCG 2100
2101 CTTGAGAGCATATCCAGGCGCTGCGGCACTTTCGCTGCGGCTGCGGCGCCAGAGACC 2160
2101 CTTGAGAGCATATCCAGGCGCTGCGGCACTTTCGCTGCGGCTGCGGCGCCAGAGACC 2160
2161 GCGGCTGTGAGCTGTACTTGTCAAGGTGATGACGCGCGGCTGACACCATCCCA 2220
2161 GCGGCTGTGAGCTGTACTTGTCAAGGTGATGACGCGCGGCTGACACCATCCCA 2220
2221 GGAACAGCTCAGGAGGTCTATGCGCAGCATCATCAACCCAGAACAGTACTGCTGCG 2280
2221 GGAACAGCTCAGGAGGTCTATGCGCAGCATCATCAACCCAGAACAGTACTGCTGCG 2280
2281 TCGGATGCGCGGTGTCAGAAAGCGCGCCGATGGGCACTCCGCAAGGCGCTTGAAGGCA 2340
2281 TCGGATGCGCGGTGTCAGAAAGCGCGCCGATGGGCACTCCGCAAGGCGCTTGAAGGCA 2340
2341 CGTCTCTACTTGAAGAGACCTTCAGCGCTGATGACAGAGTTCGTGCTCAGCTGAGGA 2400
2341 CGTCTCTACTTGAAGAGACCTTCAGCGCTGATGACAGAGTTCGTGCTCAGCTGAGGA 2400
2401 GACCAAGCCGCTGAGAGGATGCGCTGCTCATGAGCAGAGCTCCTCTTAATGAGGCGCAG 2460
2401 GACCAAGCCGCTGAGAGGATGCGCTGCTCATGAGCAGAGCTCCTCTTAATGAGGCGCAG 2460
2461 CAGTGGGCGCTTGAAGAGCTTCTCAAGCTCATGAGGCGCAGAGGCGCTGAGGCG 2520
2461 CAGTGGGCGCTTGAAGAGCTTCTCAAGCTCATGAGGCGCAGAGGCGCTGAGGCG 2520
2521 CAGTCTCTACTGACAGTGCAGAGGAGATCCGCGAGGCTCTCTCTCAGCGCTGCTG 2580
2521 CAGTCTCTACTGACAGTGCAGAGGAGATCCGCGAGGCTCTCTCTCAGCGCTGCTG 2580
2581 CAGCTGTGCTACGCGGAGCATGAGAACAGGCTGTTGCGGAGATTCGCGGAGACGCGCT 2640
2581 CAGCTGTGCTACGCGGAGCATGAGAACAGGCTGTTGCGGAGATTCGCGGAGACGCGCT 2640
2641 GCTCTGCGGTTTGGGATGATTTCTGTTGGTGAACCTCACTCAACCGCGGAGAAC 2700
2641 GCTCTGCGGTTTGGGATGATTTCTGTTGGTGAACCTCACTCAACCGCGGAGAAC 2700
2701 CTTCTCAGAGACCTGCTGTCAGAGTGTCCCTGATGATGCTGCTGAGAACCTTGCGGA 2760
2701 CTTCTCAGAGACCTGCTGTCAGAGTGTCCCTGATGATGCTGCTGAGAACCTTGCGGA 2760
2761 GACAGTGTGGAATCTTCCCTGATGAGAACGAGGCGCTGCTGAGAACCTTGCTGAGAT 2820
2761 GACAGTGTGGAATCTTCCCTGATGAGAACGAGGCGCTGCTGAGAACCTTGCTGAGAT 2820
2821 GCGGCGCCCAAGGCTATTTCCCTGCTGCGGCGCTGCTGCTGAGAACCTTGAGAGT 2880
2821 GCGGCGCCCAAGGCTATTTCCCTGCTGCGGCGCTGCTGCTGAGAACCTTGAGAGT 2880
2881 GCGAGAGCACTACTCAGCTATGCGCGAGCTCTCATCAGAGCAGTCTCACTTCAACCG 2940
2881 GCGAGAGCACTACTCAGCTATGCGCGAGCTCTCATCAGAGCAGTCTCACTTCAACCG 2940
2941 CCGCTTCAAGGCTGAGAGAACATGCTGCTGCAAACTCTTGGGCTTTCGCGCTGAGATG 3000
2941 CCGCTTCAAGGCTGAGAGAACATGCTGCTGCAAACTCTTGGGCTTTCGCGCTGAGATG 3000

3001 TCACAGCCGTTTCTGATTTGACAGTGAACAGCCTTCAGACGCTGTGACCAACATCTA 3060
3001 TCACAGCCGTTTCTGATTTGACAGTGAACAGCCTTCAGACGCTGTGACCAACATCTA 3060
3061 CAAGTCTCTCTGCTGACAGCGGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTTC 3120
3061 CAAGTCTCTCTGCTGACAGCGGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTTC 3120
3121 TCAGAGATTTGGAAGAACCCCACTTTTCTGCGGCTGATCTGACAGGCGCTCCCT 3180
3121 TCAGAGATTTGGAAGAACCCCACTTTTCTGCGGCTGATCTGACAGGCGCTCCCT 3180
3181 CTGCTACTCTCACTCTGAAAGCCCAAGAGCAGAGGATGTGCTGCGGCGCCAGGCGCGC 3240
3181 CTGCTACTCTCACTCTGAAAGCCCAAGAGCAGAGGATGTGCTGCGGCGCCAGGCGCGC 3240
3241 CCGGCTCTGCTGCTGAGGCGGTGACAGTGTGCTGCAACAGCATTTCTGCTCAAGCT 3300
3241 CCGGCTCTGCTGCTGAGGCGGTGACAGTGTGCTGCAACAGCATTTCTGCTCAAGCT 3300
3301 GACTGACACCGTGTCTCACTTATGTCCTCTGCGGCTGCTCAGAGACGCGCAGCGA 3360
3301 GACTGACACCGTGTCTCACTTATGTCCTCTGCGGCTGCTCAGAGACGCGCAGCGA 3360
3361 GCTGAGTGGAGAGCTTCCGCGGAGCAGAGCTGACTGCTGAGGCGCGCAGCCAGC 3420
3361 GCTGAGTGGAGAGCTTCCGCGGAGCAGAGCTGACTGCTGAGGCGCGCAGCCAGC 3420
3421 ACTGCTCTGAGCTTCAAGACCATCTGAGCTGATGAGCCACCGCCCAAGCCTGAGCGCA 3480
3421 ACTGCTCTGAGCTTCAAGACCATCTGAGCTGATGAGCCACCGCCCAAGCCTGAGCGCA 3480
3481 GAGCAGACACCGAGAGCCCTGCTGACAGCGGCTGACAGGCGGAGGAGGAGGCGCGC 3540
3481 GAGCAGACACCGAGAGCCCTGCTGACAGCGGCTGACAGGCGGAGGAGGAGGCGCGC 3540
3541 CACACCCAGGCGCGAGCAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTG 3600
3541 CACACCCAGGCGCGAGCAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTG 3600
3601 CATGTCCGCTGAGAGCTGAGTGTCCGCTGAGGAGCTGAGGAGCTGAGGAGCTG 3660
3601 CATGTCCGCTGAGAGCTGAGTGTCCGCTGAGGAGCTGAGGAGCTGAGGAGCTG 3660
3661 GAGTGTCCAGACACCTGCTGCTTCACTTCCCAAGGCTGCTGCTGCTGCTGCTGCTG 3720
3661 GAGTGTCCAGACACCTGCTGCTTCACTTCCCAAGGCTGCTGCTGCTGCTGCTGCTG 3720
3721 GGGCAGCTTTTCTCAACAGGAGCCGCGCTTCACTCCCAATAGAAATAGTCATCC 3780
3721 GGGCAGCTTTTCTCAACAGGAGCCGCGCTTCACTCCCAATAGAAATAGTCATCC 3780
3781 CCAAGTTGCGCAATTTTCAACCCCTGCGCTGCTTCTTCTGCTTCAACCCCAATCC 3840
3781 CCAAGTTGCGCAATTTTCAACCCCTGCGCTGCTTCTTCTGCTTCAACCCCAATCC 3840
3841 AGTGGAGACCTTGAAGAGACCTTGGAGAGCTTGGAGATTTGGAGTACCAAGGTG 3900
3841 AGTGGAGACCTTGAAGAGACCTTGGAGAGCTTGGAGATTTGGAGTACCAAGGTG 3900
3901 CCGTGAACAGGCGAGAGCCCTGACCTGAGTGGGAGGCTCTGAGGCTCAATTTGGGG 3960
3901 CCGTGAACAGGCGAGAGCCCTGACCTGAGTGGGAGGCTCTGAGGCTCAATTTGGGG 3960
3961 GAGGTGCTGTGGAGTAAATCTGAATATAGATTTTTCAGTTTGAAGAAAA 4015
3961 GAGGTGCTGTGGAGTAAATCTGAATATAGATTTTTCAGTTTGAAGAAAA 4015

RESULT 2
US-08-974-549A-1
; Sequence 1, Application US/08974549A
; Patent No. 6166178

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Hatley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56..3454

OTHER INFORMATION: /product= "hTRT"
 OTHER INFORMATION: /note= "human telomerase reverse
 OTHER INFORMATION: transcriptase (hTRT) catalytic protein
 OTHER INFORMATION: component"
 US-08-974-549A-1
 Query Match 100.0%; Score 4015; DB 3; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GCAGCGCTGCGTCTGCTGCGAGTGGAGAGCCCTGCGCCACCCCGGAGTGC 60
 1 GCAGCGCTGCGTCTGCTGCGAGTGGAGAGCCCTGCGCCACCCCGGAGTGC 60
 61 GCGCGCTCCCGCTGCGAGCGAGCGTCCCTGCTGCGAGCCTACCGAGTGTCT 120
 61 GCGCGCTCCCGCTGCGAGCGAGCGTCCCTGCTGCGAGCCTACCGAGTGTCT 120
 121 GCGCTGCGCAGTTCGTGCGCGCGCTTGGAGCCCGAGGCTGCGGCTGTGCA 180
 121 GCGCTGCGCAGTTCGTGCGCGCGCTTGGAGCCCGAGGCTGCGGCTGTGCA 180
 181 GGAACCGCGCGCTTTCGCGCGCTGCGAGCGCGCGAGGAGCTGCTGCTGAG 240
 181 GGAACCGCGCGCTTTCGCGCGCTGCGAGCGCGCGAGGAGCTGCTGCTGAG 240
 241 AGGCG 300
 241 AGGCG 300
 301 CCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGAGGAGCTGCTGCTGCTGCG 360
 301 CCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGAGGAGCTGCTGCTGCTGCG 360
 361 GCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 361 GCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 421 CCG 480
 421 CCG 480
 481 CCG 540
 481 CCG 540
 541 GCGTCCAGCTGCGCTACAGAGTGTGCGAGCGCGCGCGCGCGCGCGCGCG 600
 541 GCGTCCAGCTGCGCTACAGAGTGTGCGAGCGCGCGCGCGCGCGCGCGCG 600
 601 TCAGGCG 660
 601 TCAGGCG 660
 661 CTGGAACCAATAGGCTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
 661 CTGGAACCAATAGGCTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
 721 GAGGCG 780
 721 GAGGCG 780
 781 TGCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
 781 TGCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
 841 GCGTGAACGAGTGAACGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 900
 841 GCGTGAACGAGTGAACGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 900
 901 CACCTCTTGGAGGAGGCGCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCA 960
 901 CACCTCTTGGAGGAGGCGCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCA 960

OY	961	GCACACGCGGGGGCCCCCATCCATCCATCGCGGGCCACACAGTCCCTGGGACAAGCCTTGCC	1020
Db	961	GCACACGCGGGGGCCCCCATCCATCCATCGCGGGCCACACAGTCCCTGGGACAAGCCTTGCC	1020
OY	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCACAGCGACAAGAGCACTGCG	1080
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCACAGCGACAAGAGCACTGCG	1080
OY	1081	GGCCTCTCTTCTACTACTCACTCTCTGAGGGCCCAAGCTGACCTGGGCGCTGGAGAGCTGTGGA	1140
Db	1081	GGCCTCTCTTCTACTACTCACTCTCTGAGGGCCCAAGCTGACCTGGGCGCTGGAGAGCTGTGGA	1140
OY	1141	GACCACTCTTCTGAGGTTCCAGGCGCTTGATGCCAGGGACCTCCCGCAGGTTGCCCGCT	1200
Db	1141	GACCACTCTTCTGAGGTTCCAGGCGCTTGATGCCAGGGACCTCCCGCAGGTTGCCCGCT	1200
OY	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTCTGTTCTGAGAGCTGTTGGGAACACAGCGCA	1260
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTCTGTTCTGAGAGCTGTTGGGAACACAGCGCA	1260
OY	1261	GTGCCCCCTACGGGGGGGTCTCAAGAGGCACTGGCCGGCTGGAGGTGGGCAACCCAGC	1320
Db	1261	GTGCCCCCTACGGGGGGGTCTCAAGAGGCACTGGCCGGCTGGAGGTGGGCAACCCAGC	1320
OY	1321	AGCCGGTGTCTGTGCTCCGCGAGAAAGCCCCAGGGCTCTGTGCGCGCCCCGAGAGAGAGA	1380
Db	1321	AGCCGGTGTCTGTGCTCCGCGAGAAAGCCCCAGGGCTCTGTGCGCGCCCCGAGAGAGAGA	1380
OY	1381	CACAGACCCCCGTGCGCTGTGTGTACAGTCTCCGCGACAGACAGACCCCTTGGCAGGTGA	1440
Db	1381	CACAGACCCCCGTGCGCTGTGTGTACAGTCTCCGCGACAGACAGACCCCTTGGCAGGTGA	1440
OY	1441	CGGCTCTGTGCGGGCGCTGCTGCGCGCGGCTGGTGCCCAAGCCCTCTGGGCTCCAGGCA	1500
Db	1441	CGGCTCTGTGCGGGCGCTGCTGCGCGCGGCTGGTGCCCAAGCCCTCTGGGCTCCAGGCA	1500
OY	1501	CAACGAACGCGGCTTCTCAGGAACACCAAGAACTTCCTCCGCGGAAGCATGCCAA	1560
Db	1501	CAACGAACGCGGCTTCTCAGGAACACCAAGAACTTCCTCCGCGGAAGCATGCCAA	1560
OY	1561	GCTCTGCGTCGACGAGAGCTGACGTGGAAATGAGCGTGGGGGACTGCGCTTGGCTGCGAG	1620
Db	1561	GCTCTCTGCGTCGACGAGAGCTGACGTGGAAATGAGCGTGGGGGACTGCGCTTGGCTGCGAG	1620
OY	1621	GAGCCCAAGGGGTGGCTGTGTTCCGCGCGCAGAGGACCGCTGCTGCGTGAAGAGATCTGGC	1680
Db	1621	GAGCCCAAGGGGTGGCTGTGTTCCGCGCGCAGAGGACCGCTGCTGCGTGAAGAGATCTGGC	1680
OY	1681	CAAGTTCTCTGCACTGGCGTGAATGAGTGTACGTGTCAGAGCTGTCAAGTCTTTCTTTTA	1740
Db	1681	CAAGTTCTCTGCACTGGCGTGAATGAGTGTACGTGTCAGAGCTGTCAAGTCTTTCTTTTA	1740
OY	1741	TGTCACGAGACCAAGTTCCTTCAAAAAGAGGCTCTTTTCTTCAACGGAGAGAGTCTGGAG	1800
Db	1741	TGTCACGAGACCAAGTTCCTTCAAAAAGAGGCTCTTTTCTTCAACGGAGAGAGTCTGGAG	1800
OY	1801	CAAGTTGCAAAAGCATTTGGATTCAGACAGCACTTGAAGAGGGTGCACTTGGCGAGCTGTC	1860
Db	1801	CAAGTTGCAAAAGCATTTGGATTCAGACAGCACTTGAAGAGGGTGCACTTGGCGAGCTGTC	1860
OY	1861	GGAACACAGAGGTCAAGGACAGATCCGGGAAAGCAGAGCGCGCCCTGCTGAAGTCCAGACTCG	1920
Db	1861	GGAACACAGAGGTCAAGGACAGATCCGGGAAAGCAGAGCGCGCCCTGCTGAAGTCCAGACTCG	1920
OY	1921	CTTCACTCCCAAGCCTGACGGGCTGCGGCGCATTTGGAACATGACCTACGTGTGGAGGC	1980
Db	1921	CTTCACTCCCAAGCCTGACGGGCTGCGGCGCATTTGGAACATGACCTACGTGTGGAGGC	1980
OY	1981	CAGAACCTTCCGACAGAAAGAGGGCCGAGGCTTCACTCTGAGAGGTGAAGAGCACTGTT	2040
Db	1981	CAGAACCTTCCGACAGAAAGAGGGCCGAGGCTTCACTCTGAGAGGTGAAGAGCACTGTT	2040

QY	2041	NAGGTCGTAACTACAGAGGAGGAGGAGCGCCCGGCGCTCCTGGAGCGCTCTGTCGTAGG	2100
Db	2041	CAGGTCGTCAACTACAGAGGAGGAGGAGCGCGCGCGCCCGGCGCTCTGGAGCGCTCTGTCGTAGG	2100
QY	2101	CCTGGACGATATATCCACAGAGGCGCTGGCGCACCTTCGTGTCGTGTGCGAGGCCAGAACCC	2160
Db	2101	CCTGGACGATATATCCACAGAGGCGCTGGCGCACCTTCGTGTCGTGTGCGAGGCCAGAACCC	2160
QY	2161	GCCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGCGTACGACACATATCCCA	2220
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGCGCGTACGACACATATCCCA	2220
QY	2221	GGACAGGCTACGGAGGCGATCGCAGATCATTAACCCACAGAACAGTATCTGCGTGGC	2280
Db	2221	GGACAGGCTACGGAGGCGATCGCAGATCATTAACCCACAGAACAGTATCTGCGTGGC	2280
QY	2281	TCGGTATCCCTGTGTCCAGAGGCGCGCCATGAGCACGTCGCGCAAGGCGTTTCAGAGACCA	2340
Db	2281	TCGGTATCCCTGTGTCCAGAGGCGCGCCATGAGCACGTCGCGCAAGGCGTTTCAGAGACCA	2340
QY	2341	CGTCTCTACCTTGTACAGACCTTCAGCCGTACATGCGACAGTTGCTGTCACTTCAGAGA	2400
Db	2341	CGTCTCTACCTTGTACAGACCTTCAGCCGTACATGCGACAGTTGCTGTCACTTCAGAGA	2400
QY	2401	GACCAAGCCCGCTGAGGGATGCGCGCTCATGACACAGACCTTCCTCGAATGAGGCGAG	2460
Db	2401	GACCAAGCCCGCTGAGGGATGCGCGCTCATGACACAGACCTTCCTCGAATGAGGCGAG	2460
QY	2461	CAGTGGACCTTCTCGACGCTTCCTACGCTTCATGTGCGACACGCGCGGCGSCATCAGAGG	2520
Db	2461	CAGTGGACCTTCTCGACGCTTCCTACGCTTCATGTGCGACACGCGCGGCGSCATCAGAGG	2520
QY	2521	CAAGTCTCTACGTCAGTGCAGAGGAGATCCGCGAGGCGTCCATCTCTTCACAGCTGTCTG	2580
Db	2521	CAAGTCTCTACGTCAGTGCAGAGGAGATCCGCGAGGCGTCCATCTCTTCACAGCTGTCTG	2580
QY	2581	CAGCTGTGCTACGCGCGCACATGAGAACACAGCTGTTTCCGGGAGATGCGCGGAGACGGCT	2640
Db	2581	CAGCTGTGCTACGCGCGCACATGAGAACACAGCTGTTTCCGGGAGATGCGCGGAGACGGCT	2640
QY	2641	GCTCTGTGCTTGTGAGTGAATTTCTTGTGTGTGACACCTCACTCAACCCACGCGAGAAC	2700
Db	2641	GCTCTGTGCTTGTGAGTGAATTTCTTGTGTGTGACACCTCACTCAACCCACGCGAGAAC	2700
QY	2701	CTTCTCTCAGAACCTGTGTCGAGGTGTCTCTGAGTATGGCTGCGGTGTGAACCTTTCGGAA	2760
Db	2701	CTTCTCTCAGAACCTGTGTCGAGGTGTCTCTGAGTATGGCTGCGGTGTGAACCTTTCGGAA	2760
QY	2761	GACAGTGTGTAACTTCCCTGTGTAAGAACAGAGCCCTGGGTGTGCAAGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGTAACTTCCCTGTGTAAGAACAGAGCCCTGGGTGTGCAAGGCTTTTGTTCAGAT	2820
QY	2821	GCCGCGCCACAGGCGCTATTCCTCTGTGTGAGGCTGTGCTGTGGAATACCGGACCTTCGAGGT	2880
Db	2821	GCCGCGCCACAGGCGCTATTCCTCTGTGTGAGGCTGTGCTGTGGAATACCGGACCTTCGAGGT	2880
QY	2881	GCAGAGCAGTACTTCCAGCTATGCCCCGAGCCTTCATCAGAGCAGCTCTCACTTTCACCG	2940
Db	2881	GCAGAGCAGTACTTCCAGCTATGCCCCGAGCCTTCATCAGAGCAGCTCTCACTTTCACCG	2940
QY	2941	CGGCTTCAAGGCTGGAGAGAACATGCGTCGCAAACTCTTTGGGGGTCTTGGCGCTGAAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGAGAGAACATGCGTCGCAAACTCTTTGGGGGTCTTGGCGCTGAAAGTG	3000
QY	3001	TCACAGCCTGTGTTCTGGAATTTGAGGTGAACAGGCTCCAGACGGGTGTGCAACAATCTA	3060
Db	3001	TCACAGCCTGTGTTCTGGAATTTGAGGTGAACAGGCTCCAGACGGGTGTGCAACAATCTA	3060
QY	3061	CAAGATCTCTCTGTGTCAGAGCGTACAGGTTTCAAGCATGTGTGTGTCAGCTGCCATTTCA	3120
Db	3061	CAAGATCTCTCTGTGTCAGAGCGTACAGGTTTCAAGCATGTGTGTGTCAGCTGCCATTTCA	3120
QY	3121	TCAGCAAGTTTGAAGAACCCCACTTTTCTGTGGCGGTCAATCTCTGACAGCGCTCCCT	3180

```

Db      3121 TCAGCAAGTTGGAGAAACCCCAATTTTCTGCGGCTGATCTCTGACACGGCTCTCT 3180
Qy      3181 CTGTACTTCATCTTGAAGCAAGAAAGCAAGGATGTCCTGCGGCGCAAGGCGCGC 3240
Db      3181 CTGTACTTCATCTTGAAGCAAGAAAGCAAGGATGTCCTGCGGCGCAAGGCGCGC 3240
Qy      3241 CGGCGCTCTGCGCTCCGAGGCGGTCAGTGGCTGTGTCACCAAGCATTCCTGCTCAAGCT 3300
Db      3241 CGGCGCTCTGCGCTCCGAGGCGGTCAGTGGCTGTGTCACCAAGCATTCCTGCTCAAGCT 3300
Qy      3301 GACTCGACACCGTGTCACTTACGTGCTCACTTGGGGTCACTGAGACAGCCGAGAGCA 3360
Db      3301 GACTCGACACCGTGTCACTTACGTGCTCACTTGGGGTCACTGAGACAGCCGAGAGCA 3360
Qy      3361 GCTGAGTCGGAAGTCCCGGCGAGAGAGCTGACCTGACCTGAGAGCGCGCAACCCGCGC 3420
Db      3421 ACTGCGCTCAGACTTCAAGACCAATCTGACTGATGAGCCACCGCGCCACAGCGCGCGA 3480
Qy      3421 ACTGCGCTCAGACTTCAAGACCAATCTGACTGATGAGCCACCGCGCGCCACAGCGCGCGA 3480
Db      3481 GAGCAGACACCAAGACCTGCTGACCGCGGCTCTTACGTCACAGGAGGAGGCGCGC 3540
Qy      3481 GAGCAGACACCAAGACCTGCTGACCGCGGCTCTTACGTCACAGGAGGAGGCGCGC 3540
Db      3541 CACACCGAGGCGCGACCGCTGGAGTCTGAGGCGCTGAGAGTGTGTCGCGCGCGC 3600
Qy      3541 CACACCGAGGCGCGACCGCTGGAGTCTGAGGCGCTGAGAGTGTGTCGCGCGCGC 3600
Db      3601 CATGTCGCGTGAAGGCTGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Qy      3601 CATGTCGCGTGAAGGCTGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Db      3661 GAGTGTCCAGCAACCTGCGCTTCACTTCCCAAGGCTGCGCTCGCTCCACCCCA 3720
Qy      3661 GAGTGTCCAGCAACCTGCGCTTCACTTCCCAAGGCTGCGCTCGCTCCACCCCA 3720
Db      3721 GGGCCAGCTTTTCTGACACGAGAGCCGCGCTTCACTTCCCAAGGCTGCGCTCGCTCCACCCCA 3780
Qy      3721 GGGCCAGCTTTTCTGACACGAGAGCCGCGCTTCACTTCCCAAGGCTGCGCTCGCTCCACCCCA 3780
Db      3781 CGAGATTCCGCAATGTTTCAACCTTCCGCTTCTTTCCTTCCACCCCAAGGCTGCGCT 3840
Qy      3781 CGAGATTCCGCAATGTTTCAACCTTCCGCTTCTTTCCTTCCACCCCAAGGCTGCGCT 3840
Db      3841 AGGTGAGAACCCCTGAGAGGAGCCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3900
Qy      3841 AGGTGAGAACCCCTGAGAGGAGCCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3900
Db      3901 CCCTGTACACAGGCGAGAGCCCTGACCTGAGTGGGGTCCCTGTGGGTCAAAATGGGG 3960
Qy      3901 CCCTGTACACAGGCGAGAGCCCTGACCTGAGTGGGGTCCCTGTGGGTCAAAATGGGG 3960
Db      3961 GAGGTGCTGTGGAGTAAATATGAAATATGAGTTTTCAGTTTGAAGAAAAA 4015
Qy      3961 GAGGTGCTGTGGAGTAAATATGAAATATGAGTTTTCAGTTTGAAGAAAAA 4015

```

RESULT 3

US-08-854-050-224

Sequence 224, Application US/08854050

Patent No. 6261836

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin

APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6261836el Telomerase

```

NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product="hTERT"
OTHER INFORMATION: /note="human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
OTHER INFORMATION:
US-08-854-050-224

```

Query Match 100.0%; Score 4015; DB 3; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 GAGGCGTGCCTCTGCTGCGCAGTGGAGAGCCCTGAGCCCGCGGAGATGCC 60
Db      1 GAGGCGTGCCTCTGCTGCGCAGTGGAGAGCCCTGAGCCCGCGGAGATGCC 60
Qy      61 GGGGCTCCCGCGCGGAGAGCCCTGAGCCCTGAGCCCGCGGAGATGCC 120
Db      61 GGGGCTCCCGCGCGGAGAGCCCTGAGCCCTGAGCCCGCGGAGATGCC 120
Qy      121 GCGGCTGCGCAGTTCGTCGCGCGCTGAGGAGCCCAAGGCTGAGGCTGAGGCTGAGGCT 180
Db      121 GCGGCTGCGCAGTTCGTCGCGCGCTGAGGAGCCCAAGGCTGAGGCTGAGGCTGAGGCT 180
Qy      181 GAGCCGCGGCGCTTCCGCGCGCTGAGGAGCCCAAGTGCCTGAGTGCCTGAGGAGCGC 240

```

Dp	181	GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAAGTGCCTGGTGTGCGTGGCCCTTGGAGCG	240
Qy	241	ACGGCCGCCCCCGCGCGCCCTCTCCGCGCAGGTGTCTGCTGAGAGAGCTGTAGC	300
Dp	241	ACGGCCGCCCCCGCGCGCCCTCTCCGCGCAGGTGTCTGCTGAGAGAGCTGTAGC	300
Qy	301	CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGAGAACCTGCTGGCTTTCCGCTTGGC	360
Dp	301	CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGAGAACCTGCTGGCTTTCCGCTTGGC	360
Qy	361	GCTGCTGAGCGGGGGCCGCGGGGGGGCCCCCGAGGGCTTCAACAACAGCGTGGCAGCTA	420
Dp	361	GCTGCTGAGCGGGGGCCGCGGGGGGGCCCCCGAGGGCTTCAACAACAGCGTGGCAGCTA	420
Qy	421	CTTGCCCAACACGATGACCGAACCTGCGGGAGCGGGGCGTGGGGCTGCTGGCG	480
Dp	421	CTTGCCCAACACGATGACCGAACCTGCGGGAGCGGGGCGTGGGGCTGCTGGCG	480
Qy	481	CCGCGTGGGGCAACGACGTGTGCTTCACTGTGCTGGCACGTGCGCGCTCTTTGTGTGGT	540
Dp	481	CCGCGTGGGGCAACGACGTGTGCTTCACTGTGCTGGCACGTGCGCGCTCTTTGTGTGGT	540
Qy	541	GGCTTCCACGTGCGCGCTACCGAGTGTGGGGGCGCGCGGTGACCAAGCTGGGCGGTGGCAC	600
Dp	541	GGCTTCCACGTGCGCGCTACCGAGTGTGGGGGCGCGCGGTGACCAAGCTGGGCGGTGGCAC	600
Qy	601	TCAAGCCCGGCGCCCGGCGACACGCTAATGAGAACCCCGAAGGCGTCTGGGATGCAACGGGC	660
Dp	601	TCAAGCCCGGCGCCCGGCGACACGCTAATGAGAACCCCGAAGGCGTCTGGGATGCAACGGGC	660
Qy	661	CTGGAACCATAGCCTCAGGGAGGGCGGGGGTCCCTTGCGCTGCGACGCCGGGGTGGAG	720
Dp	661	CTGGAACCATAGCCTCAGGGAGGGCGGGGGTCCCTTGCGCTGCGACGCCGGGGTGGAG	720
Qy	721	GAGGCGCGGGGGCAAGTGCACGCCCAAGCTCTGCGCTTGGCCCAAGAGCCCAAGCGTTGGCGC	780
Dp	721	GAGGCGCGGGGGCAAGTGCACGCCCAAGCTCTGCGCTTGGCCCAAGAGCCCAAGCGTTGGCGC	780
Qy	781	TGCCCCCTAGCGGAGCGGAGCGGCCGCTTGGGCAAGGATCTGTGGCCACCCGGGCAAGAC	840
Dp	781	TGCCCCCTAGCGGAGCGGAGCGGCCGCTTGGGCAAGGATCTGTGGCCACCCGGGCAAGAC	840
Qy	841	GCGTGGACCGAGTGAACGATGGTTTCTGTGTGTGTCACTTGCAGAACCCCGCGAAGAAC	900
Dp	841	GCGTGGACCGAGTGAACGATGGTTTCTGTGTGTGTCACTTGCAGAACCCCGCGAAGAAC	900
Qy	901	CACCTCTTTGAGGGGTGCGCTCTGTGGACCGCGCCACTTCCACCCATCCGTGGGCGCGCA	960
Dp	901	CACCTCTTTGAGGGGTGCGCTCTGTGGACCGCGCCACTTCCACCCATCCGTGGGCGCGCA	960
Qy	961	GACACACGCGGGGGCCCCCATCAACAATGCGGGGCAACAATGCCCTGGGACAATGCGCTTGGCC	1020
Dp	961	GACACACGCGGGGGCCCCCATCAACAATGCGGGGCAACAATGCCCTGGGACAATGCGCTTGGCC	1020
Qy	1021	CCCGGTGTAGCGCGAGACCAAGCACTTCTCTTACTCTCAGGCGACAGAGAGCACTGCG	1080
Dp	1021	CCCGGTGTAGCGCGAGACCAAGCACTTCTCTTACTCTCAGGCGACAGAGAGCACTGCG	1080
Qy	1081	GCCCTCTTTCCTACTCAGCTCTGTGAGGCGCAAGCTGTACTGCGCTCGAAGGCTGTGGA	1140
Dp	1081	GCCCTCTTTCCTACTCAGCTCTGTGAGGCGCAAGCTGTACTGCGCTCGAAGGCTGTGGA	1140
Qy	1141	GACCACTTTTCGGGTTCAAGGCGCTGAGTGCAGAGGACCTGCCGACAGTTGGCCCGGCT	1200
Dp	1141	GACCACTTTTCGGGTTCAAGGCGCTGAGTGCAGAGGACCTGCCGACAGTTGGCCCGGCT	1200
Qy	1201	GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTCTTCTGAGAGCTGTGGGAACAAGCGCA	1260
Dp	1201	GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTCTTCTGAGAGCTGTGGGAACAAGCGCA	1260
Qy	1261	GTCGCCCTTACGGGGTGTCTTCAAGACCACTGCCGCTGCGAGCTGCGGTCACCCCAGC	1320

[illegible]


```
Db 1681 CAAGTTCCTGACGCGCTGATGATGTGTATGTCGTGAGCTGCTCAGGCTTTCTTTA 1740
Qy 1741 TGTCAAGGAGACAGCTTTCAAAAGAACAGGCTTTTCTTCAACGGAAGTGTCTGAG 1800
Db 1741 TGTCAAGGAGACAGCTTTCAAAAGAACAGGCTTTTCTTCAACGGAAGTGTCTGAG 1800
Qy 1801 CAAGTTCAAAGCAATTGGAATCAGACAGCACTTGAAAGAGGTGACGTGCGGAGCTGTC 1860
Db 1801 CAAGTTCAAAGCAATTGGAATCAGACAGCACTTGAAAGAGGTGACGTGCGGAGCTGTC 1860
Qy 1861 GGAAGCAGAGTCAAGGACATCGGGAAGCCAGGCCCCCTGTTACGTCACAGACTCCG 1920
Db 1861 GGAAGCAGAGTCAAGGACATCGGGAAGCCAGGCCCCCTGTTACGTCACAGACTCCG 1920
Qy 1921 CTTCATCCCAAGGCTGACGGGCTGCGGCGATTTGTGAACATGGAACGTGCGGAGC 1980
Db 1921 CTTCATCCCAAGGCTGACGGGCTGCGGCGATTTGTGAACATGGAACGTGCGGAGC 1980
Qy 1981 CAGAACGTTCCGACAGAGAAAAGAGGCGCAGCGCTCTCACCTCGAGGGTGAAGGCACTGT 2040
Db 1981 CAGAACGTTCCGACAGAGAAAAGAGGCGCAGCGCTCTCACCTCGAGGGTGAAGGCACTGT 2040
Qy 2041 CAGGCTCTCAACATCAGAGGCGGCGCGCCCGGCTCTGAGGCGCTCTGCTGCGG 2100
Db 2041 CAGGCTCTCAACATCAGAGGCGGCGCGCCCGGCTCTGAGGCGCTCTGCTGCGG 2100
Qy 2101 CTTGAGCATATCCACAGGCGCTGCGCACCTTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 CTTGAGCATATCCACAGGCGCTGCGCACCTTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Qy 2161 GCGGCTCTGAGCTGTACTTTGTCAAGTGTGATGTGACGCGGCGCTGACGACATCCCCA 2220
Db 2161 GCGGCTCTGAGCTGTACTTTGTCAAGTGTGATGTGACGCGGCGCTGACGACATCCCCA 2220
Qy 2221 GGAAGGCTCAGGAGGTCAATCCGACAGCATCATCAACCCAGAACAGCATGCGTGC 2280
Db 2221 GGAAGGCTCAGGAGGTCAATCCGACAGCATCATCAACCCAGAACAGCATGCGTGC 2280
Qy 2281 TCGGATAGCGGTGATCCGACAGAGCCGCGCATGCGGACAGTCCGAGAGGCTTTCAAGGCCA 2340
Db 2281 TCGGATAGCGGTGATCCGACAGAGCCGCGCATGCGGACAGTCCGAGAGGCTTTCAAGGCCA 2340
Qy 2341 CGTCTCTACTTGAACAAGCTTCCAGCGCTGATGCGACAGTGTGCTGCTGCTGCTGCTG 2400
Db 2341 CGTCTCTACTTGAACAAGCTTCCAGCGCTGATGCGACAGTGTGCTGCTGCTGCTGCTG 2400
Qy 2401 GACCAAGCCGCTGAGGAGTCCGCTGATGAGCAGAGGCTCTCCCTGAAATGAGGCGAG 2460
Db 2401 GACCAAGCCGCTGAGGAGTCCGCTGATGAGCAGAGGCTCTCCCTGAAATGAGGCGAG 2460
Qy 2461 CAGTGGCTCTTTCAGCGTCTTCTTACGCTTCAATGTGCAACAGCCGCTGCGCATGAGGG 2520
Db 2461 CAGTGGCTCTTTCAGCGTCTTCTTACGCTTCAATGTGCAACAGCCGCTGCGCATGAGGG 2520
Qy 2521 CAAGTCTCTAGTCAAGTCCAGGGGATCCGCGAGGCTCATCTCTTCCAGCTGCTCTG 2580
Db 2521 CAAGTCTCTAGTCAAGTCCAGGGGATCCGCGAGGCTCATCTCTTCCAGCTGCTCTG 2580
Qy 2581 CAGCCTGTGCTACGCGACATGAGAAACAAGCTGTTGCGGAGATTCGCGGAGACGGGCT 2640
Db 2581 CAGCCTGTGCTACGCGACATGAGAAACAAGCTGTTGCGGAGATTCGCGGAGACGGGCT 2640
Qy 2641 GCTCTGCGCTTTGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAAAC 2700
Db 2641 GCTCTGCGCTTTGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAAAC 2700
Qy 2701 CTTCCTCAGGACCTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 2760
Db 2701 CTTCCTCAGGACCTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 2760
Qy 2761 GACAGTGTGAACTTCTCTGTAGAAACAGAGCCCTGAGTGTGCAAGCTTTTGTTCAGAT 2820
Db 2761 GACAGTGTGAACTTCTCTGTAGAAACAGAGCCCTGAGTGTGCAAGCTTTTGTTCAGAT 2820

Db 2761 GACAGTGTGAACTTCTCTGTAGAAACAGAGCCCTGAGTGTGCAAGCTTTTGTTCAGAT 2820
Qy 2821 GCGGCGCCACGCGCTATATCCCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 2821 GCGGCGCCACGCGCTATATCCCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Qy 2881 GCAGAGCGACTACTCCAGCTATGCGCGGACCTTCATCAGAGCAGTCTCACTTCAACCG 2940
Db 2881 GCAGAGCGACTACTCCAGCTATGCGCGGACCTTCATCAGAGCAGTCTCACTTCAACCG 2940
Qy 2941 CCGCTTCAAGGCTGAGGAGAACATGCTGTGCAAACTCTTTGCGGTCTTGGCTGAAGTG 3000
Db 2941 CCGCTTCAAGGCTGAGGAGAACATGCTGTGCAAACTCTTTGCGGTCTTGGCTGAAGTG 3000
Qy 3001 TCACAGCTGTTTCTGATTTGAGGTGAAACAGCTTCCAGAGGTGTGACCAACATCA 3060
Db 3001 TCACAGCTGTTTCTGATTTGAGGTGAAACAGCTTCCAGAGGTGTGACCAACATCA 3060
Qy 3061 CAAGATCTCTGCTGACAGCGCTACAGTGTGCTGACAGCTGCTGCTGCTGCTGCTGCTG 3120
Db 3061 CAAGATCTCTGCTGACAGCGCTACAGTGTGCTGACAGCTGCTGCTGCTGCTGCTGCTG 3120
Qy 3121 TCAGCAAGTTTGAAGAACCCCACTTTTCTGCGCGCTCATCTGACAGGCTCTCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCCACTTTTCTGCGCGCTCATCTGACAGGCTCTCT 3180
Qy 3181 CTGCTACTCATCTGTAAGAACCAAGAACGACAGAGATGTGCTGCGGAGCCAGAGGCGCG 3240
Db 3181 CTGCTACTCATCTGTAAGAACCAAGAACGACAGAGATGTGCTGCGGAGCCAGAGGCGCG 3240
Qy 3241 CCGGCTCTGCTGCTGCGAGGCGCTGACAGTGTGCTGCAACAGATTTCTGCTCAAGCT 3300
Db 3241 CCGGCTCTGCTGCTGCGAGGCGCTGACAGTGTGCTGCAACAGATTTCTGCTCAAGCT 3300
Qy 3301 GACTGACACCGGTGCTACCTAGTGCATCTCTGAGGTGCTGCTGAGACAGGCTGCTGCTG 3360
Db 3301 GACTGACACCGGTGCTACCTAGTGCATCTCTGAGGTGCTGCTGAGACAGGCTGCTGCTG 3360
Qy 3361 GCTGAGTCCGAAAGCTCCCGGAGACAGCGTGACTGCTGAGGCGCGACCAACCGGCG 3420
Db 3361 GCTGAGTCCGAAAGCTCCCGGAGACAGCGTGACTGCTGAGGCGCGACCAACCGGCG 3420
Qy 3421 ACTGCTCTGAGCTTCAAGAACATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3480
Db 3421 ACTGCTCTGAGCTTCAAGAACATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3480
Qy 3481 GAGGAGACACGAGAGCGCTGCTGACGCGGCTGCTGACGCTGCTGCTGCTGCTGCTGCTG 3540
Db 3481 GAGGAGACACGAGAGCGCTGCTGACGCGGCTGCTGACGCTGCTGCTGCTGCTGCTGCTG 3540
Qy 3541 CACACCCAGGCGCGACCGCTGAGGAGTGTGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTG 3600
Db 3541 CACACCCAGGCGCGACCGCTGAGGAGTGTGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTG 3600
Qy 3601 CATGTCCGCTGAAAGCTGAGTGTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Db 3601 CATGTCCGCTGAAAGCTGAGTGTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Qy 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3720
Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3720
Qy 3721 GGGCAGCTTCTTCTCACAGAGGCGCGCTTCCACTCCCAATAGAAATAGTCTATCC 3780
Db 3721 GGGCAGCTTCTTCTCACAGAGGCGCGCTTCCACTCCCAATAGAAATAGTCTATCC 3780
Qy 3781 CCAATTTGGCAATTTGTTCAACCCCTGCGCTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3840
Db 3781 CCAATTTGGCAATTTGTTCAACCCCTGCGCTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3840
Qy 3841 AGGTGGAAGCCCTGAGAGGAGCCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3900
Db 3841 AGGTGGAAGCCCTGAGAGGAGCCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3900
```


Db 1621 GAGCCAGGGGTTGGCTGTGTCGGGCGGAGACCCGTCTGCTGAGAGATCTTGGC 1680
Qy 1681 CAAATTCTGCACTGGCTGATGAGTGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
Db 1681 CAAATTCTGCACTGGCTGATGAGTGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
Qy 1741 TGTCAAGGAGACAGCTTTCAAAAAGAACAGGCTCTTTTCTACCGAGAGTGTGAG 1800
Db 1741 TGTCAAGGAGACAGCTTTCAAAAAGAACAGGCTCTTTTCTACCGAGAGTGTGAG 1800
Qy 1801 CAAATTGCAAAAGATTGGAATTCAGACAGCACTTGAAAGAGGTGACGTGCGGAGCTGTC 1860
Db 1801 CAAATTGCAAAAGATTGGAATTCAGACAGCACTTGAAAGAGGTGACGTGCGGAGCTGTC 1860
Qy 1861 GGAAGCAGAGGTGAGGAGATGAGGAGGCGAGGCGGCTGTGACCTGTGACGCTCCG 1920
Db 1861 GGAAGCAGAGGTGAGGAGATGAGGAGGCGAGGCGGCTGTGACCTGTGACGCTCCG 1920
Qy 1921 CTTCATCTCCCAAGCTTGAAGGCTGCGGCGGATTTGTGAACATGAGACTACGTGAGAGC 1980
Db 1921 CTTCATCTCCCAAGCTTGAAGGCTGCGGCGGATTTGTGAACATGAGACTACGTGAGAGC 1980
Qy 1981 CAGAACGTTCCGAGAGAAAAGAGGCGGAGCTGTCACTCGAGGAGTGAAGCACTGTT 2040
Db 1981 CAGAACGTTCCGAGAGAAAAGAGGCGGAGCTGTCACTCGAGGAGTGAAGCACTGTT 2040
Qy 2041 CAGCGTGTCAACTGAGGCGGCGGCGGCGGCGGCGGCTGTGAGGCGCTGTGAGTGG 2100
Db 2041 CAGCGTGTCAACTGAGGCGGCGGCGGCGGCGGCGGCGGCTGTGAGGCGCTGTGAGTGG 2100
Qy 2101 CTTGAGCAGATATCAAGAGGCTGTGAGCACTTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Db 2101 CTTGAGCAGATATCAAGAGGCTGTGAGCACTTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Qy 2161 GCGGCGTGAAGCTGTACTTTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220
Db 2161 GCGGCGTGAAGCTGTACTTTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220
Qy 2221 GGAAGGCTCAAGGAGGTCAATGCGCAGCACTCAATCAACCCAGAACAGTGTGCGTGC 2280
Db 2221 GGAAGGCTCAAGGAGGTCAATGCGCAGCACTCAATCAACCCAGAACAGTGTGCGTGC 2280
Qy 2281 TCGGTATGCGGTGTGTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
Db 2281 TCGGTATGCGGTGTGTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
Qy 2341 CGTCTCACTTGAAGCACTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2400
Db 2341 CGTCTCACTTGAAGCACTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2400
Qy 2401 GACCAAGCCGCTGAGGAGTGCCTGTCAATGAGAGAGTGTCTCTGATGAGGCGCAG 2460
Db 2401 GACCAAGCCGCTGAGGAGTGCCTGTCAATGAGAGAGTGTCTCTGATGAGGCGCAG 2460
Qy 2461 CAGTGGCTCTTGAAGTCTTCTCAAGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
Db 2461 CAGTGGCTCTTGAAGTCTTCTCAAGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
Qy 2521 CAAAGTCTTCAAGT 2580
Db 2521 CAAAGTCTTCAAGT 2580
Qy 2581 CAGGCTGTGCTAAGGAGCAATGAGAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Db 2581 CAGGCTGTGCTAAGGAGCAATGAGAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Qy 2641 GGTCTGT 2700
Db 2641 GGTCTGT 2700
Qy 2701 CTTTCTCAAGAACCTTGT 2760
Db 2701 CTTTCTCAAGAACCTTGT 2760

Qy 2761 GACAGTGTGAATCTTCCCTGTGAAGAACAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGT 2820
Db 2761 GACAGTGTGAATCTTCCCTGTGAAGAACAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGT 2820
Qy 2821 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2880
Db 2821 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2880
Qy 2881 GCAAGCGACTATCTCAAGT 2940
Db 2881 GCAAGCGACTATCTCAAGT 2940
Qy 2941 CCGCTTCAAGGCTGT 3000
Db 2941 CCGCTTCAAGGCTGT 3000
Qy 3001 TCAAGCCTGTTTCTGATTTGTCAAGTGAACAGCTTCAAGGCTGTGTGTGTGTGTGTGT 3060
Db 3001 TCAAGCCTGTTTCTGATTTGTCAAGTGAACAGCTTCAAGGCTGTGTGTGTGTGTGTGT 3060
Qy 3061 CAAAGTCTTGT 3120
Db 3061 CAAAGTCTTGT 3120
Qy 3121 TCAGCAAGTTGTGAAGAACCCCAATTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3180
Db 3121 TCAGCAAGTTGTGAAGAACCCCAATTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3180
Qy 3181 CTGTACTTCAATCTTGAAGAACCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
Db 3181 CTGTACTTCAATCTTGAAGAACCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
Qy 3241 CCGGCGT 3300
Db 3241 CCGGCGT 3300
Qy 3301 GACTGCAACCGT 3360
Db 3301 GACTGCAACCGT 3360
Qy 3361 GCTGAGTGTGAAGTCTTCCGAGGAGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3420
Db 3361 GCTGAGTGTGAAGTCTTCCGAGGAGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3420
Qy 3421 ACTGCGCTCAAGCTTCAAGAACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3480
Db 3421 ACTGCGCTCAAGCTTCAAGAACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3480
Qy 3481 GAGCAGACACAGCAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3540
Db 3481 GAGCAGACACAGCAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3540
Qy 3541 CACACCCAGGCGCGGAGCTGT 3600
Db 3541 CACACCCAGGCGCGGAGCTGT 3600
Qy 3601 CATGTCCGCGTGAAGGCTGT 3660
Db 3601 CATGTCCGCGTGAAGGCTGT 3660
Qy 3661 GAGTGTCAAGCAGCAGT 3720
Db 3661 GAGTGTCAAGCAGCAGT 3720
Qy 3721 GGGCAGGCTTTTCTCAACAGGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3780
Db 3721 GGGCAGGCTTTTCTCAACAGGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3780
Qy 3781 CCAAGTGTGCAATTTTCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3840
Db 3781 CCAAGTGTGCAATTTTCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3840

QY 3841 AGGTGAGAGACCTGAGAGACCTGAGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
DB 3841 AGGTGAGAGACCTGAGAGACCTGAGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3901 CCCTGTACACAGGCGGAGACCTGTGACCTGATGGGGGTCCCTGTGGTCAATTTGGGG 3960
DB 3901 CCCTGTACACAGGCGGAGACCTGTGACCTGATGGGGGTCCCTGTGGTCAATTTGGGG 3960
QY 3961 GAGGTGCTGTGGAGAAATACTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4015
DB 3961 GAGGTGCTGTGGAGAAATACTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4015

RESULT 6
US-09-128-354-1

/ Sequence 1, Application US/09128354
/ Patent No. 6337200
/ GENERAL INFORMATION:
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Geron Corporation
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
/ FILE REFERENCE: 015389-00310US
/ CURRENT APPLICATION NUMBER: US/09/128,354
/ CURRENT FILING DATE: 1998-08-03
/ EARLIER APPLICATION NUMBER: US 08/851,843
/ EARLIER FILING DATE: 1997-05-06
/ EARLIER APPLICATION NUMBER: US 08/854,050
/ EARLIER FILING DATE: 1997-05-09
/ EARLIER APPLICATION NUMBER: US 08/911,312
/ EARLIER FILING DATE: 1997-08-14
/ EARLIER APPLICATION NUMBER: US 08/912,951
/ EARLIER FILING DATE: 1997-08-14
/ EARLIER APPLICATION NUMBER: US 08/915,503
/ EARLIER FILING DATE: 1997-08-14
/ EARLIER APPLICATION NUMBER: WO PCT/US97/17618
/ EARLIER FILING DATE: 1997-10-01
/ EARLIER APPLICATION NUMBER: WO PCT/US97/17885
/ EARLIER FILING DATE: 1997-10-01
/ EARLIER APPLICATION NUMBER: US 08/974,549
/ EARLIER FILING DATE: 1997-11-19
/ EARLIER APPLICATION NUMBER: US 08/974,584
/ EARLIER FILING DATE: 1997-11-19
/ EARLIER APPLICATION NUMBER: US 09/052,864
/ EARLIER FILING DATE: 1998-03-31
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 4015
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (56)..
/ OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-128-354-1

Query Match 100.0%; Score 4015; DB 3; Length 4015;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGCTGCTGCTCTGCTGCACTGGGAAGCCCTGGCCGACCCCGCCGATGCG 60
DB 1 GGAGGCTGCTGCTCTGCTGCACTGGGAAGCCCTGGCCGACCCCGCCGATGCG 60
QY 61 GGGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGTGCGAGCACTACCGAGGTGT 120
DB 61 GGGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGTGCGAGCACTACCGAGGTGT 120
QY 121 GCGCGTGGCACTTGTGTGCGGCGCTGGGGCCCGAGGGTGTGAGAGCGCG 180
DB 121 GCGCGTGGCACTTGTGTGCGGCGCTGGGGCCCGAGGGTGTGAGAGCGCG 180
QY 181 GGACCCGCGGCTTTCCGCGCGCTGTGGCCAGTGCCTGTGTGTGCTGCGGACGC 240

DB 181 GGACCCGCGGCTTTCCGCGCGCTGTGGCCAGTGCCTGTGTGTGCTGCGGACGC 240
QY 241 AGGCG 300
DB 241 AGGCG 300
QY 301 CGGAGTGTGAGAGAGCTGTGAGAGCGGCGCGAGAGAGAGTGTGCTGTGCTGCG 360
DB 301 CGGAGTGTGAGAGAGCTGTGAGAGCGGCGCGAGAGAGAGTGTGCTGTGCTGCG 360
QY 361 GCTGTGAGCGGAGCT 420
DB 361 GCTGTGAGCGGAGCT 420
QY 421 CCTGCGCAACAGTGTGAGAGCGAGAGCTGCGGGGAGCGGGGGTGTGGGGTCTGTGG 480
DB 421 CCTGCGCAACAGTGTGAGAGCGAGAGCTGCGGGGAGCGGGGGTGTGGGGTCTGTGG 480
QY 481 CCGCGTGGCGAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 540
DB 481 CCGCGTGGCGAGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 540
QY 541 GCGTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCTGTACAGCTGCGGCTGCGAC 600
DB 541 GCGTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCTGTACAGCTGCGGCTGCGAC 600
QY 601 TGAAGCG 660
DB 601 TGAAGCG 660
QY 661 CTGGAACCATAGCTGAGGAGAGCGGAGTCCCTGTGGGCTGTGCGAGCGCGGAGTGCAG 720
DB 661 CTGGAACCATAGCTGAGGAGAGCGGAGTCCCTGTGGGCTGTGCGAGCGCGGAGTGCAG 720
QY 721 GAGGCGCGGCGCGAGTGCAGCGAGTGTGCGGCTGTGCGAGAGAGCGCGGCTGTGCG 780
DB 721 GAGGCGCGGCGCGAGTGCAGCGAGTGTGCGGCTGTGCGAGAGAGCGCGGCTGTGCG 780
QY 781 TGCCTGTGAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB 781 TGCCTGTGAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 841 GCGTGGACCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GCGTGGACCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 CACTCTTTTGAAGGCTGCTCTGTGCAAGCGCGCACTTCCACCAATCCGTGGGCGCGCA 960
DB 901 CACTCTTTTGAAGGCTGCTCTGTGCAAGCGCGCACTTCCACCAATCCGTGGGCGCGCA 960
QY 961 GCACCAAGCGGCG 1020
DB 961 GCACCAAGCGGCG 1020
QY 1021 CCGGAGTACGCGGAGCAACGACTTCTACTCTTACTCTTACTCTTACTCTTACTCTT 1080
DB 1021 CCGGAGTACGCGGAGCAACGACTTCTACTCTTACTCTTACTCTTACTCTTACTCTT 1080
QY 1081 GCGCTCTCTTCTACTCTTACTCTTCTGAGGCGCGAGCTGTGCGGCTGTGGA 1140
DB 1081 GCGCTCTCTTCTACTCTTACTCTTCTGAGGCGCGAGCTGTGCGGCTGTGGA 1140
QY 1141 GACCATCTTTTGTGGTTCAGGCGCGCTGTGAGTGTGCGAGAGTCTCCCGAGTGTGCG 1200
DB 1141 GACCATCTTTTGTGGTTCAGGCGCGCTGTGAGTGTGCGAGAGTCTCCCGAGTGTGCG 1200
QY 1201 GCGGAGGCTGTGAGCAATGCGGCGCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
DB 1201 GCGGAGGCTGTGAGCAATGCGGCGCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
QY 1261 GTGCGCTTACGAGGAGTGTGCTTCAAGAGCACTGCGCGCTGTGAGTGTGAGTGTGAGT 1320

Db 1261 GTGCCCTACGAGGAGTCTCTCAAGACGACTGCCGCTGAGCTGGATCAACCCAGC 1320
QY 1321 AGCCGATGCTGATGCTCCGAGGAGAGCCCAAGGCTCTGTGCGGCCCCCGAGAGAGGA 1380
Db 1321 AGCCGATGCTGATGCTCCGAGGAGAGCCCAAGGCTCTGTGCGGCCCCCGAGAGAGGA 1380
QY 1381 CACAGACCCCGGCTGCTGTGAGCTGCTCCGACAGACAGAGCCCTGAGAGGTA 1440
Db 1381 CACAGACCCCGGCTGCTGTGAGCTGCTCCGACAGACAGAGCCCTGAGAGGTA 1440
QY 1441 CGGTTTGTGCGGAGCTGCTGCGGCGGCTGTGTGCTCCAGGCTCTGAGGCA 1500
Db 1441 CGGTTTGTGCGGAGCTGCTGCGGCGGCTGTGTGCTCCAGGCTCTGAGGCA 1500
QY 1501 CAAGGAGCGCGCTTCTCAGAGAACACCAAGAGTTATCTCCCTGGGAGAGATGCA 1560
Db 1501 CAAGGAGCGCGCTTCTCAGAGAACACCAAGAGTTATCTCCCTGGGAGAGATGCA 1560
QY 1561 GCTCTGCTGCAAGAGCTGACGTGAAGATGAGCGTGGGACTGCGTTGCTGCGCAG 1620
Db 1561 GCTCTGCTGCAAGAGCTGACGTGAAGATGAGCGTGGGACTGCGTTGCTGCGCAG 1620
QY 1621 GAGCCGAGGAGTTGCTGTGTTCCGCGCCGAGAGACCTGCTGTGAGAGATCTGCGC 1680
Db 1621 GAGCCGAGGAGTTGCTGTGTTCCGCGCCGAGAGACCTGCTGTGAGAGATCTGCGC 1680
QY 1681 CAAGTTCTGCACTGAGCTGATGATGTGATGCTGCTGAGCTGCTGAGCTCTTCTTTA 1740
Db 1681 CAAGTTCTGCACTGAGCTGATGATGTGATGCTGCTGAGCTGCTGAGCTCTTCTTTA 1740
QY 1741 TGTTCAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGTCTGAG 1800
Db 1741 TGTTCAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGTCTGAG 1800
QY 1801 CAAGTTGCAAGAGATGAGATGAGACGACCTTGAAGAGGATGACCTGAGGAGCTGTTC 1860
Db 1801 CAAGTTGCAAGAGATGAGATGAGACGACCTTGAAGAGGATGACCTGAGGAGCTGTTC 1860
QY 1861 GGAAGCAGAGATGAGGAGCATCGGAGACGAGCCGCTCTGACGTCAGATCTCG 1920
Db 1861 GGAAGCAGAGATGAGGAGCATCGGAGACGAGCCGCTCTGACGTCAGATCTCG 1920
QY 1921 CTTTCACTCCCAAGCTGACGAGGCTGTGCGGCTGATTTGAACTGACTGATGCTGGAGC 1980
Db 1921 CTTTCACTCCCAAGCTGACGAGGCTGTGCGGCTGATTTGAACTGACTGATGCTGGAGC 1980
QY 1981 CAGAGCTTCCGAGAGAAAGAGGCGGAGCGCTCACTCGAGGCTGAAGCACTGTT 2040
Db 1981 CAGAGCTTCCGAGAGAAAGAGGCGGAGCGCTCACTCGAGGCTGAAGCACTGTT 2040
QY 2041 CAGCGTGTCAATCACTGAGCGGCGGCGGCGGCTCTGAGGCGCTCTGTGTGAG 2100
Db 2041 CAGCGTGTCAATCACTGAGCGGCGGCGGCGGCTCTGAGGCGCTCTGTGTGAG 2100
QY 2101 CCGGAGCATATCAAGAGGCGCTGAGCACTTCTGTGCTGCGTGTGCGGCGGAGAGCC 2160
Db 2101 CCGGAGCATATCAAGAGGCGCTGAGCACTTCTGTGCTGCGTGTGCGGCGGAGAGCC 2160
QY 2161 GCGCGCTGAGCTGTACTTGTCAAGGTGATGAGCGGCGGCTGAGCACTTCTGAGAGCC 2220
Db 2161 GCGCGCTGAGCTGTACTTGTCAAGGTGATGAGCGGCGGCTGAGCACTTCTGAGAGCC 2220
QY 2221 GGAAGAGCTCAAGAGGATGATGCGCAGCATCATCAAAACCCAGAACACGTAATCTGCG 2280
Db 2221 GGAAGAGCTCAAGAGGATGATGCGCAGCATCATCAAAACCCAGAACACGTAATCTGCG 2280
QY 2281 TCGGATGCGGATGATGAGAGGCGGCGGCGGCGGCTGAGGCGGCTTGAAGAGCA 2340
Db 2281 TCGGATGCGGATGATGAGAGGCGGCGGCGGCGGCTGAGGCGGCTTGAAGAGCA 2340
QY 2341 CGTCTTACCTTGAAGACCTCAAGCGCTGATGAGCAGTTGCTGCTGAGCACTGAGAG 2400
Db 2341 CGTCTTACCTTGAAGACCTCAAGCGCTGATGAGCAGTTGCTGCTGAGCACTGAGAG 2400

QY 2401 GACACGCGCTGAGGAGATCCGCTGCTCATGACAGACACTCTCTCTGAATGAGCGAG 2460
Db 2401 GACACGCGCTGAGGAGATCCGCTGCTCATGACAGACACTCTCTCTGAATGAGCGAG 2460
QY 2461 CAGTGCCTCTTGAAGATCTTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2520
Db 2461 CAGTGCCTCTTGAAGATCTTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2520
QY 2521 CAAGTCTACGTCAGATGCGAGAGATCCGAGGAGCTCATCTCTCCAGCTGCTG 2580
Db 2521 CAAGTCTACGTCAGATGCGAGAGATCCGAGGAGCTCATCTCTCCAGCTGCTG 2580
QY 2581 CAGCCTGCTACGCGAGATGAGAGAACAGAGCTGTTTGGGAGATTTGGGAGAGAGGCT 2640
Db 2581 CAGCCTGCTACGCGAGATGAGAGAACAGAGCTGTTTGGGAGATTTGGGAGAGAGGCT 2640
QY 2641 GCTCTGCTGATGATGATTTCTGTTGATGATGATGATGATGATGATGATGATGATG 2700
Db 2641 GCTCTGCTGATGATGATTTCTGTTGATGATGATGATGATGATGATGATGATGATG 2700
QY 2701 CTTTCTCAGAGACCTGCTGAGAGTGTCTGAGATGATGATGATGATGATGATGATG 2760
Db 2701 CTTTCTCAGAGACCTGCTGAGAGTGTCTGAGATGATGATGATGATGATGATGATG 2760
QY 2761 GACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
Db 2761 GACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
QY 2821 GCGGCGCAGCGCTATTCCTGCTGAGGCTGCTGCTGATGATGATGATGATGATGATG 2880
Db 2821 GCGGCGCAGCGCTATTCCTGCTGAGGCTGCTGCTGATGATGATGATGATGATGATG 2880
QY 2881 GAGAGCGATCTCTCAGCTATGCTGAGCTGCTGATGATGATGATGATGATGATGATG 2940
Db 2881 GAGAGCGATCTCTCAGCTATGCTGAGCTGCTGATGATGATGATGATGATGATGATG 2940
QY 2941 CCGCTTCAAGGCTGAGAGAACAGAGCTGAGAACTCTTTGGGAGCTTGGCGCTGAGAG 3000
Db 2941 CCGCTTCAAGGCTGAGAGAACAGAGCTGAGAACTCTTTGGGAGCTTGGCGCTGAGAG 3000
QY 3001 TCACAGCTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
Db 3001 TCACAGCTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
QY 3061 CAAGATCTCTGCTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 3120
Db 3061 CAAGATCTCTGCTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 3120
QY 3121 TCAGAGATGATGAGAGACCCACATTTTCTGCGCTGATCTCTGAGAGAGGCTGCT 3180
Db 3121 TCAGAGATGATGAGAGACCCACATTTTCTGCGCTGATCTCTGAGAGAGGCTGCT 3180
QY 3181 CTGCTACTCTCTCTGAGAGACCCACATTTTCTGCGCTGATCTCTGAGAGAGGCTGCT 3240
Db 3181 CTGCTACTCTCTCTGAGAGACCCACATTTTCTGCGCTGATCTCTGAGAGAGGCTGCT 3240
QY 3241 CCGGCTTCTGCTCTGAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3300
Db 3241 CCGGCTTCTGCTCTGAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3300
QY 3301 GACTGACACGCTGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3360
Db 3301 GACTGACACGCTGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3360
QY 3361 GCTGAGTGGAGATCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Db 3361 GCTGAGTGGAGATCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
QY 3421 ACTGCGCTCAGACTTCAAGACATCTGAGATGATGATGATGATGATGATGATGATGATG 3480
Db 3421 ACTGCGCTCAGACTTCAAGACATCTGAGATGATGATGATGATGATGATGATGATGATG 3480

Oy	3481	GAGCAGACACAGACGCCCTCACAAGCGGGCTACGTC	CCACAGGAGGAGGGGCGGCC	3540
Db	3481	GAGCAGACACAGCAGCCCTCTCACGCGGGCTCTCA	CTCCACAGGAGGAGGGCGGCC	3540
Oy	3541	CACACCCAGGCGCCGACCGCTGGAGGCTCTGAGG	AGCTGAGGCTTGAGCGAGGCTG	3600
Db	3541	CACACCCAGGCGCCGACCGCTGGAGGCTCTGAGG	AGCTGAGGCTTGAGCGAGGCTG	3600
Oy	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGACTGAGG	CGTTCAGGAGGAGTGTCCAGCCAAAGGCT	3660
Db	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGACTGAGG	CGTTCAGGAGGAGTGTCCAGCCAAAGGCT	3660
Oy	3661	GAGTGTCCAGACACCTGCGCTTCACTTCCCA	CAGGCTGGGCGCTCGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGACACCTGCGCTTCACTTCCCA	CAGGCTGGGCGCTCGCTCCACCCCA	3720
Oy	3721	GGGCGCAGTTTTCCTCACAGAGCGGCGTTCC	ATCCCAATAGGAATATGTCATCC	3780
Db	3721	GGGCGCAGTTTTCCTCACAGAGCGGCGTTCC	ATCCCAATAGGAATATGTCATCC	3780
Oy	3781	CCAGATTGCGCATTTGTTACCCCTGCGCTGCG	CCCTTTCGCTTCCACCCCCACATCC	3840
Db	3781	CCAGATTGCGCATTTGTTACCCCTGCGCTGCG	CCCTTTCGCTTCCACCCCCACATCC	3840
Oy	3841	AGGTGAGACCTTGAGAGGACCTTGAGGCTCT	GGGAAATTTGAGTAGTACCCAAAGTGTG	3900
Db	3841	AGGTGAGACCTTGAGAGGACCTTGAGGCTCT	GGGAAATTTGAGTAGTACCCAAAGTGTG	3900
Oy	3901	CCCTGTACACAGGCGAGGACCTTGCACTGGAT	GGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
Db	3901	CCCTGTACACAGGCGAGGACCTTGCACTGGAT	GGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
Oy	3961	GAGGTGCTGTGGGAGTAATAATCTGAATATAG	TAATTTTACGTTTGAATAAAAAA	4015
Db	3961	GAGGTGCTGTGGGAGTAATAATCTGAATATAG	TAATTTTACGTTTGAATAAAAAA	4015

RESULT 7
US-09-675-321-1
: Sequence 1, Application US/09675321

```

: Patent No.6440735
: GENERAL INFORMATION:
:
: APPLICANT: Gaeta, Federico C.A.
:
: APPLICANT: Garon Corporation
:
: TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
:
: TITLE OF INVENTION: Response to a Telomerase Antigen
:
: FILE REFERENCE: 015389-003500PC
:
: CURRENT APPLICATION NUMBER: US/09/675,321
:
: CURRENT FILING DATE: 2000-09-28
:
: PRIOR APPLICATION NUMBER: US 60/112,006
:
: PRIOR FILING DATE: 1998-03-31
:
: PRIOR APPLICATION NUMBER: WO PCT/US99/06898
:
: PRIOR FILING DATE: 1999-03-30
:
: NUMBER OF SEQ ID NOS: 2
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 1
:
: LENGTH: 4015
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (56)..(3454)
:
: OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
:
: US-09-675-321-1

```

Query Match	100.0%;	Score 4015;	DB 4;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4015; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

QY	61	GGGGCTCCCCGCGCGGAGGCGGAGCGCTCCCTGTCGTGGGAGGCACTACCGGAGGTC	120
Db	61	GGGGCTCCCCGCTCCGCGCGGAGCGGCGCTCCCTGTCGTGGAGCCACTACCGGAGGTC	120
QY	121	GCCGCTGGCCACGTTCTGTGCGGCGCTGTGGGCGCCAGAGGCTGGCGGTCGTAGCGCG	180
Db	121	GCCGCTGGCCACGTTCTGTGTGGGCGGCGCTGTGGGCGCCAGAGGCTGGCGGTCGTAGCGG	180
QY	181	GGAACCCGCGGCTTTCCGCGCGCTGTGGCCCAATGCTGTGGTCCTGCTGGAGCGC	240
Db	181	GGAACCCGCGGCTTTCCGCGCGCTGTGGCCCAATGCTGTGGTCCTGCTGGAGCGC	240
QY	241	ACGGCGCGCCCCCGCGCGCGCTCTTCCGCGAGGTCCTCGGCTGAAAGAGCTGTGGC	300
Db	241	ACGGCGCGCCCCCGCGCGCGCTCTTCCGCGAGGTCCTCGGCTGAAAGAGCTGTGGC	300
QY	301	CCGAGTGTGAGAGGCTGTGCGAGCGCGGCGCAAGAACGTCGTGACCTTCCGCTTCG	360
Db	301	CCGAGTGTGAGAGGCTGTGCGAGCGCGGCGCAAGAACCTGCTGGCTTCGCGCTTCG	360
QY	361	GCTGTGAGCGGGGCGCGCGGGGCGCGCGCGCGCGCTTCAACAACGCTGTGCGACCTA	420
Db	361	GCTGTGAGCGGGGCGCGCGGGGCGCGCGCGCGCGCTTCAACAACGCTGTGCGACCTA	420
QY	421	CCTGCCCCAACACGCTGACCGACATGTCGCGGGGAGCGGGCGTGGGGCGTCGTGCG	480
Db	421	CCTGCCCCAACACGCTGACCGACATGTCGCGGGGAGCGGGCGTGGGGCGTCGTGCG	480
QY	481	CCGCGTGGGCGAGACGCTGTGTTCACTCTGAGACGCTGCGCGCTCTTGTGTGTCGT	540
Db	481	CCGCGTGGGCGAGACGCTGTGTTCACTGCTGTGACGCTGCGCGCTCTTGTGTGTCGT	540
QY	541	GCGTCCACGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACAGCTCGGCGCTGCCAC	600
Db	541	GCGTCCACGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACAGCTCGGCGCTGCCAC	600
QY	601	TCAGGCG	660
Db	601	TCAGGCG	660
QY	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCTCGGAGCTGCGACGCGCGGTCGAG	720
Db	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCTCGGAGCTGCGACGCGCGGTCGAG	720
QY	721	GAGGCGCGGGGCGAGTGCACGCGAGCTGTCGTTGCCAAGAGGCCAGGCGTGGCGC	780
Db	721	GAGGCGCGGGGCGAGTGCACGCGAGCTGTCGTTGCCAAGAGGCCAGGCGTGGCGC	780
QY	781	TGCGCTTAGCGCGGAGCGGAGCGCGCTTGGGCGAGGTCCTGGGCGCACCGGCGAGAC	840
Db	781	TGCGCTTAGCGCGGAGCGGAGCGCGCTTGGGCGAGGTCCTGGGCGCACCGGCGAGAC	840
QY	841	GCGTGAACCGAGTACCGTGGTTTCTGTGTGTGTACCTGCGACGCGCGGAAAGAGC	900
Db	841	GCGTGAACCGAGTACCGTGGTTTCTGTGTGTGTACCTGCGACGCGCGGAAAGAGC	900
QY	901	CACCTCTTTGAGGGTGGCTCTCTGGGCACGCGACCTCCACCCATTCGTGGGCGCGCA	960
Db	901	CACCTCTTTGAGGGTGGCTCTCTGGGCACGCGACCTCCACCCATTCGTGGGCGCGCA	960
QY	961	GCACCAAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGTCC	1020
Db	961	GCACCAAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGTCC	1020
QY	1021	CCCGGTGAGCGCGGAGCAAGCACTTCTTACCTCTCAAGGCGCAAGAGGAGCGTCG	1080
Db	1021	CCCGGTGAGCGCGGAGCAAGCACTTCTTACCTCTCAAGGCGCAAGAGGAGCGTCG	1080
QY	1081	GCGCTCTTCTTACCTGAGCTCTGAGGCGCAGGCTGTGCGCTCGGAGGCTGTGGA	1140
Db	1081	GCGCTCTTCTTACCTGAGCTCTGAGGCGCAGGCTGTGCGCTCGGAGGCTGTGGA	1140
QY	1141	GACCATCTTCTGGGTTCCAGGCGCGCGGAGCTCCCGCAGGTTTCCCGCT	1200

Db 1081 GCCCTCCTTCACTCAGCTCTCTGAGGCCAGCCTCACTGCGCTCGAGAGCTCTGTGGA 1140

1141 GACCATCTTTCTGGGTTCCAGGCGCTGATGCGAGGACTCCCGCAGGTTGCCCCCT 1200
QY 1201 GCCCAGCGCTACGCGAAATGCGGCCCTGTTTCTGAGACTGCTTGGGAAACAACGGCA 1260
Db 1201 GCCCAGCGCTACTGGGAAATGCGGCCCTGTTTCTGAGACTGCTTGGGAAACAACGGCA 1260
QY 1261 GTGCCCCCTACGCGGAGTGTCTCTCAAGACGACTGCCCTGAGCTGCGGTCAACCCAGC 1320
Db 1261 GTGCCCCCTACGCGGAGTGTCTCTCAAGACGACTGCCCTGAGCTGCGGTCAACCCAGC 1320
QY 1321 AGCCGCTGTCTGTGCCCCGCGGAGAAAGCCCAAGGCTCTGTGCGGCCCCCAGAGAGAGA 1380
Db 1321 AGCCGCTGTCTGTGCCCCGCGGAGAAAGCCCAAGGCTCTGTGCGGCCCCCAGAGAGAGA 1380
QY 1381 CACAGACCCCGCTGAGCTGTGAGCTGTCCGCGACAGACAGAGAGCCCTGGAGAGGTGA 1440
Db 1381 CACAGACCCCGCTGAGCTGTGAGCTGTCCGCGACAGACAGAGAGCCCTGGAGAGGTGA 1440
QY 1441 CGGCTTGTGTCGCGGCGCTGCTGCGCGCGGCTGTGCCCCCAGGCTCTGCGGCTCAAGCA 1500
Db 1441 CGGCTTGTGTCGCGGCGCTGCTGCGCGCGGCTGTGCCCCCAGGCTCTGCGGCTCAAGCA 1500
QY 1501 CAACGAAACGCGCTTCTCTCAGGAAACACAGAAAGTTCTCTCCCTGGGAGCATGCAA 1560
Db 1501 CAACGAAACGCGCTTCTCTCAGGAAACACAGAAAGTTCTCTCCCTGGGAGCATGCAA 1560
QY 1561 GCTCTGCTGACAGAGCTGACGTGAAAGATGAGCTGCGGAGCTGCGGCTTGGCGGCA 1620
Db 1561 GCTCTGCTGACAGAGCTGACGTGAAAGATGAGCTGCGGAGCTGCGGCTTGGCGGCA 1620
QY 1621 GAGCCCAAGGGGTTGCTGTGTTCCGCGCGAGACACCGTCTGCGTGAAGATCTTGGC 1680
Db 1621 GAGCCCAAGGGGTTGCTGTGTTCCGCGCGAGACACCGTCTGCGTGAAGATCTTGGC 1680
QY 1681 CAAGTTCCTGCACTGCGCTGAATGAGTGTGATCGTCTGAGCTGCTCAAGTCTTTCTTAA 1740
Db 1681 CAAGTTCCTGCACTGCGCTGAATGAGTGTGATCGTCTGAGCTGCTCAAGTCTTTCTTAA 1740
QY 1741 TGTCAAGGAGACCACTTTCAAAAAGAACAGGCTCTTTTCTAACGGAAGATGTCTGAG 1800
Db 1741 TGTCAAGGAGACCACTTTCAAAAAGAACAGGCTCTTTTCTAACGGAAGATGTCTGAG 1800
QY 1801 CAAGTTCGAAGATTTGGAATCAGACGCACTTGAAGAGGTCAGCTGCGGAGCTGTC 1860
Db 1801 CAAGTTCGAAGATTTGGAATCAGACGCACTTGAAGAGGTCAGCTGCGGAGCTGTC 1860
QY 1861 GGAAGCAGAGGTGAGGACAGATGCGGAGCGAGCCCGCTGCTGAAGTCTCCAGACTCCG 1920
Db 1861 GGAAGCAGAGGTGAGGACAGATGCGGAGCGAGCCCGCTGCTGAAGTCTCCAGACTCCG 1920
QY 1921 CTTTCATCCCAAGCTGACGCGGCTGCGGCGATTTGAACATGATGATTAAGTCTGGAAC 1980
Db 1921 CTTTCATCCCAAGCTGACGCGGCTGCGGCGATTTGAACATGATGATTAAGTCTGGAAC 1980
QY 1981 CAGAAGCTTCCGAGAAAGAGAGGCGCAGGCTCTCACTCTGAGGCTGAAGCACTGTT 2040
Db 1981 CAGAAGCTTCCGAGAAAGAGAGGCGCAGGCTCTCACTCTGAGGCTGAAGCACTGTT 2040
QY 2041 CAGCGTGTCAACTACGAGCGGCGGCGGCGCCCGCTGCGGCGCTCTGTGTGAGG 2100
Db 2041 CAGCGTGTCAACTACGAGCGGCGGCGGCGCCCGCTGCGGCGCTCTGTGTGAGG 2100
QY 2101 CCTGAGCATATCACAAGGCGCTGCGGCACTTCTGCTGCTGCTGCTGCGGCGCAGAGCC 2160
Db 2101 CCTGAGCATATCACAAGGCGCTGCGGCACTTCTGCTGCTGCTGCTGCGGCGCAGAGCC 2160
QY 2161 GCGGCTGTGAGCTGTACTTTGTCAAGGTGATGAGCGGCGGTACGACCATCCCA 2220
Db 2161 GCGGCTGTGAGCTGTACTTTGTCAAGGTGATGAGCGGCGGTACGACCATCCCA 2220
QY 2221 GGAAGGCTCAGGAGGTGATGCGGCGCATCAAAACCCAGAACAGTACTGTGAGG 2280
Db 2221 GGAAGGCTCAGGAGGTGATGCGGCGCATCAAAACCCAGAACAGTACTGTGAGG 2280
2281 TCGGTAATGCGGTGCTCCAAAGAGCGGCCCATATGGGCACTGCCAGGCTTCAAGGCA 2340
Db 2281 TCGGTAATGCGGTGCTCCAAAGAGCGGCCCATATGGGCACTGCCAGGCTTCAAGGCA 2340
QY 2341 CGTCTTACCTTGAACAGACTCCAGCCGATGCGACAGTGTGAGGCTCACTGAGAGA 2400
Db 2341 CGTCTTACCTTGAACAGACTCCAGCCGATGCGACAGTGTGAGGCTCACTGAGAGA 2400
QY 2401 GACAGCCCGCTGAGGAGATGCGGTGCTATGAGAGAGCTCTCTGTAATGAGCGCAG 2460
Db 2401 GACAGCCCGCTGAGGAGATGCGGTGCTATGAGAGAGCTCTCTGTAATGAGCGCAG 2460
QY 2461 CAGTGGCTCTTCAAGCTTCTCACTGATGAGGCAACAGCGCTGCGGATCAAGGGG 2520
Db 2461 CAGTGGCTCTTCAAGCTTCTCACTGATGAGGCAACAGCGCTGCGGATCAAGGGG 2520
QY 2521 CAAGTCTTACGTCAGATGCGAGGAGATCCCGAGGAGCTCTCTCCACGCTGCTG 2580
Db 2521 CAAGTCTTACGTCAGATGCGAGGAGATCCCGAGGAGCTCTCTCCACGCTGCTG 2580
QY 2581 CAGCTGTGCTACGCGGACATGAGAACAGCTGTTGCGGAGATTGCGCGGAGCGGCT 2640
Db 2581 CAGCTGTGCTACGCGGACATGAGAACAGCTGTTGCGGAGATTGCGCGGAGCGGCT 2640
QY 2641 GCTCCGAGGTTGAGATGATTTCTGTGTGTGACACTCACTCAACCCAGCGGAAAC 2700
Db 2641 GCTCCGAGGTTGAGATGATTTCTGTGTGTGACACTCACTCAACCCAGCGGAAAC 2700
QY 2701 CTTCTCAGAGCCCTGATCCGAGGTGCTCTGAGTATGAGCTGCTGAGAACTTGGGAA 2760
Db 2701 CTTCTCAGAGCCCTGATCCGAGGTGCTCTGAGTATGAGCTGCTGAGAACTTGGGAA 2760
QY 2761 GACAGTGTGAACTTCCCTGTGAGAAAGAGAGCCCTGCGGTGACAGCTTTTGTCAAT 2820
Db 2761 GACAGTGTGAACTTCCCTGTGAGAAAGAGAGCCCTGCGGTGACAGCTTTTGTCAAT 2820
QY 2821 GCGGCGCCACAGGCTATTCCCGTGTGCGGCGCTGCTGCGGATCACCGGAGGAT 2880
Db 2821 GCGGCGCCACAGGCTATTCCCGTGTGCGGCGCTGCTGCGGATCACCGGAGGAT 2880
QY 2881 GCAGAGCGACTACTACAGCTATGCCCCGAGCTCTCATCAGAGCACTCTACCTTCAACG 2940
Db 2881 GCAGAGCGACTACTACAGCTATGCCCCGAGCTCTCATCAGAGCACTCTACCTTCAACG 2940
QY 2941 CCGCTTCAAGGCTGGAGAGAACTGCGCAACTCTTTGGGCTCTTGGCGTGAAGTG 3000
Db 2941 CCGCTTCAAGGCTGGAGAGAACTGCGCAACTCTTTGGGCTCTTGGCGTGAAGTG 3000
QY 3001 TCACAGCTGTTTCTGAAATTTGCAAGGCTCCAGAGCGGCTGACCAACATCTA 3060
Db 3001 TCACAGCTGTTTCTGAAATTTGCAAGGCTCCAGAGCGGCTGACCAACATCTA 3060
QY 3061 CAAGATCTCTGCTGAGAGGCTGACAGGCTTCAAGCATGTGCTGAGCTCCCATTTCA 3120
Db 3061 CAAGATCTCTGCTGAGAGGCTGACAGGCTTCAAGCATGTGCTGAGCTCCCATTTCA 3120
QY 3121 TCAGAAATTTGGAAGAACCCCACTTTTCTGTGCGGTCTATCTTGAACAGGCTCTCC 3180
Db 3121 TCAGAAATTTGGAAGAACCCCACTTTTCTGTGCGGTCTATCTTGAACAGGCTCTCC 3180
QY 3181 CTGCTACTCTCACTCAAGAGCAAGAAAGCAGAGGATGCTGCGGAGGCGAGGCGCGC 3240
Db 3181 CTGCTACTCTCACTCAAGAGCAAGAAAGCAGAGGATGCTGCGGAGGCGAGGCGCGC 3240
QY 3241 CCGGCTCTGCGCTTCCAGGCGGTGCACTGAGTGTGCGCAACAGACTCTGCTCAAGCT 3300
Db 3241 CCGGCTCTGCGCTTCCAGGCGGTGCACTGAGTGTGCGCAACAGACTCTGCTCAAGCT 3300
QY 3301 GACTTGAGAACGCTGTCACTACGTCGCACTCTGAGGAGCTTCAAGAGAGCGCAGAGCA 3360
Db 3301 GACTTGAGAACGCTGTCACTACGTCGCACTCTGAGGAGCTTCAAGAGAGCGCAGAGCA 3360

```
QY 3361 GCTGAGTGGAAAGCTCCGGGGAGAGAGCTGACTGCTGCTGGAGGCGGAGCAACCGGAC 3420
DB 3361 GCTGAGTGGAAAGCTCCGGGGAGAGAGCTGACTGCTGCTGGAGGCGGAGCAACCGGAC 3420
QY 3421 ACTGCGCTCAGACTTCAAGACCATCTCTGACTGATGAGCCACCGCCCAAGCCAGCGCA 3480
DB 3421 ACTGCGCTCAGACTTCAAGACCATCTCTGACTGATGAGCCACCGCCCAAGCCAGCGCA 3480
QY 3481 GAGCAGACACCAAGAGCCCTGTCTACGCGCGGCTTACGCTCCAGGAGGAGGAGGCGGCGC 3540
DB 3481 GAGCAGACACCAAGAGCCCTGTCTACGCGCGGCTTACGCTCCAGGAGGAGGAGGCGGCGC 3540
QY 3541 CACACCCAGGCGCGGAGCTGAGGAGTGAAGGCTGAGTGTGCTTTGGCGGAGGCGCTG 3600
DB 3541 CACACCCAGGCGCGGAGCTGAGGAGTGAAGGCTGAGTGTGCTTTGGCGGAGGCGCTG 3600
QY 3601 CATGTCGGCTGAAAGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGCGCT 3660
DB 3601 CATGTCGGCTGAAAGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGCGCT 3660
QY 3661 GAGTGTCCAGACACCTGCGCTCTTCACTTCCCAAGGCTGCGCTGCGCTCCACCCCA 3720
DB 3661 GAGTGTCCAGACACCTGCGCTCTTCACTTCCCAAGGCTGCGCTGCGCTCCACCCCA 3720
QY 3721 GGGCGAGCTTTCTCCACAGGAGCGCGCTTCCACTCCCAATAGGAAATGTCATCC 3780
DB 3721 GGGCGAGCTTTCTCCACAGGAGCGCGCTTCCACTCCCAATAGGAAATGTCATCC 3780
QY 3781 CCAGATTGCGCATTTGTTACCCCTGCGCTGCTTCTTGGCTTCAACCCCAACATCC 3840
DB 3781 CCAGATTGCGCATTTGTTACCCCTGCGCTGCTTCTTGGCTTCAACCCCAACATCC 3840
QY 3841 AGGTGAGACCTCTGAGAGACCTGCGAGCTCTGCGAAATTTGAGTGAACCAAGGTGTG 3900
DB 3841 AGGTGAGACCTCTGAGAGACCTGCGAGCTCTGCGAAATTTGAGTGAACCAAGGTGTG 3900
QY 3901 CCGGTGACACAGGCGGAGGAGCCCTGCACTGGAATGGGGGCTTGGGGGCAAAATGGGGG 3960
DB 3901 CCGGTGACACAGGCGGAGGAGCCCTGCACTGGAATGGGGGCTTGGGGGCAAAATGGGGG 3960
QY 3961 GAGGTGCTGTGGAGTAAATATCTGAAATATGAGTTTTTTCAGTTTTTGAAGAAAAA 4015
DB 3961 GAGGTGCTGTGGAGTAAATATCTGAAATATGAGTTTTTTCAGTTTTTGAAGAAAAA 4015
```

RESULT 8
US-09-052-919-1
Sequence 1, Application US/09052919
Patent No. 644650

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hartley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
NUMBER OF SEQUENCES: 72
TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```
QY 1 GAGGCGTGGCTGCTGCTGCGACGTTGGGAAGCCCTGCGCGCCAGCCCGCGATGCC 60
DB 1 GAGGCGTGGCTGCTGCTGCGACGTTGGGAAGCCCTGCGCGCCAGCCCGCGATGCC 60
QY 61 GCGGCTCTCCGCTGCGCGAGCGCTGCGCTCCCTGCTGCGAGCCACTACCGGAGGTCT 120
DB 61 GCGGCTCTCCGCTGCGCGAGCGCTGCGCTCCCTGCTGCGAGCCACTACCGGAGGTCT 120

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product="human telomerase reverse
US-09-052-919-1
Query Match 100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Indels 0; Gaps 0;
```

QY 121 GCCGCTGAGCAGGTTGTCGCGGCTTGAGGAGCCGACGAGGCTGAGGCTGAGGAGCGCG 180
DB 121 GCCGCTGAGCAGGTTGTCGCGGCTTGAGGAGCCGACGAGGCTGAGGAGCGCG 180
QY 181 GGAACCCGAGGCTTTCCGCGCTGAGTGGCCAGTGGCTGAGTGGCTGAGTGGCTGAGTGG 240
DB 181 GGAACCCGAGGCTTTCCGCGCTGAGTGGCCAGTGGCTGAGTGGCTGAGTGGCTGAGTGG 240
QY 241 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 CCGAGTGTCTGACAGAGGCTGTGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 CCGAGTGTCTGACAGAGGCTGTGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 GGTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 361 GGTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 421 CCTGCGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 CCTGCGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 CCGCGTGGGAGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGT 540
DB 481 CCGCGTGGGAGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGGCTGT 540
QY 541 GGTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 GGTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 TCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 TCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 CTGGAACCAATAGCTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 CTGGAACCAATAGCTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 GAG 780
DB 721 GAG 780
QY 781 TGCCCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 TGCCCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 GCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
DB 841 GCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 901 CACCTCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 CACCTCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB 961 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 CCGGAGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 CCGGAGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 GCGCTCTTCTCTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 GCGCTCTTCTCTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
DB 1141 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1201 GCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260

DB 1201 GCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1261 GTGCCCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
DB 1261 GTGCCCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
QY 1321 AGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
DB 1321 AGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
QY 1381 CACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
DB 1381 CACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
QY 1441 CCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
DB 1441 CCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
QY 1501 CAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
DB 1501 CAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
QY 1561 GCTCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
DB 1561 GCTCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
QY 1621 GAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
DB 1621 GAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
QY 1681 CAAGTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
DB 1681 CAAGTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
QY 1741 TGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
DB 1741 TGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
QY 1801 CAAGTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
DB 1801 CAAGTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
QY 1861 GGAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
DB 1861 GGAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
QY 1921 CTTATCTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
DB 1921 CTTATCTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1981 CAGAAGGAG 2040
DB 1981 CAGAAGGAG 2040
QY 2041 CAGGAG 2100
DB 2041 CAGGAG 2100
QY 2101 CTTGAGAG 2160
DB 2101 CTTGAGAG 2160
QY 2161 GCGCCTGAG 2220
DB 2161 GCGCCTGAG 2220
QY 2221 GGAAGGAG 2280
DB 2221 GGAAGGAG 2280
QY 2281 TCGGTATGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTrrT"
OTHER INFORMATION: /note= "human telomerase reverse
transcriptase (hTrrT) catalytic protein
OTHER INFORMATION: component"
US-08-912-951-1

Query Match 100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGCTCTCTCTGCGACGCGGGAAGCCCTGCGCCCGCCGACCCCGCCGATGCC 60
DB 1 GCAGCGCTGCTCTCTCTCTGCGACGCGGGAAGCCCTGCGCCCGCCGACCCCGCCGATGCC 60
QY 61 GCGCGCTCCCGCTGCGACGCGGCGCTGCGCTCCCTGCTGCGCAGCACTACCGGAGGTGCT 120
DB 61 GCGCGCTCCCGCTGCGACGCGGCGCTGCGCTCCCTGCTGCGCAGCACTACCGGAGGTGCT 120
QY 121 GCGCGCTGCGACGCTGCGGCGGCTGCGGCGCCCGAGGCTGCGGCTGCTGCAAGCGCG 180
DB 121 GCGCGCTGCGACGCTGCGGCGGCTGCGGCGCCCGAGGCTGCGGCTGCTGCAAGCGCG 180
QY 181 GGAACCGCGCGCTTTCGCGCGCTGCTGCGCCAGTGTCTGTGTGTGCTGCTGCGGAGCGC 240
DB 181 GGAACCGCGCGCTTTCGCGCGCTGCTGCGCCAGTGTCTGTGTGTGCTGCTGCGGAGCGC 240
QY 241 ACGGCGCGCCCGCGCGCCCTCTCTTCCGCAAGTGTCTGCTGCAAGAGACTGCTGAGC 300
DB 241 ACGGCGCGCCCGCGCGCCCTCTCTTCCGCAAGTGTCTGCTGCAAGAGACTGCTGAGC 300
QY 301 CGGAGTGTGCGAGAGCTGTGCGAGCGCGCGGAAAGAGTGTGCTGCTGCTGCTGCTGCTG 360
DB 301 CGGAGTGTGCGAGAGCTGTGCGAGCGCGCGGAAAGAGTGTGCTGCTGCTGCTGCTGCTG 360
QY 361 GCTGTGCGAGCGGCGCGCGCGCGCGCGCGCGCGAGGCTTCAACCAAGAGTGTGCGAGCTA 420
DB 361 GCTGTGCGAGCGGCGCGCGCGCGCGCGCGCGCGAGGCTTCAACCAAGAGTGTGCGAGCTA 420

DB 361 GCTGTGCGAGCGGCGCGCGCGCGCGCGCGCGCGAGGCTTCAACCAAGAGTGTGCGAGCTA 420
QY 421 CTTGCCAACCAGGTGACCGACGCTGCGGAGAGCGGAGCGTGTGCGCTGCTGCG 480
DB 421 CTTGCCAACCAGGTGACCGACGCTGCGGAGAGCGGAGCGTGTGCGCTGCTGCG 480
QY 481 CCGCGTGGGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 CCGCGTGGGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 GGTCTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 GGTCTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 TGAAGCG 660
DB 601 TGAAGCG 660
QY 661 CTGGAACATAGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCGCGCGCGCGCGCGCGCG 720
DB 661 CTGGAACATAGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCGCGCGCGCGCGCGCG 720
QY 721 GAGCGCGCGGCGCGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCGCGCGCGCGCGCG 780
DB 721 GAGCGCGCGGCGCGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCGCGCGCGCGCGCG 780
QY 781 TGCCTCTGAGCGGAGCGGAGCGCGGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCGCG 840
DB 781 TGCCTCTGAGCGGAGCGGAGCGCGGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCGCG 840
QY 841 GCGTGAACAGAGTGTGCGGAGAGCGCGGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCG 900
DB 841 GCGTGAACAGAGTGTGCGGAGAGCGCGGAGTGTGCGGAGAGCGCGGAGTCCCTGCGGCG 900
QY 901 CACTCTTTTGAAGGCTGCGCTCTGCGACGCGCGCACTTCCACCGATCGTGTGCGCGCA 960
DB 901 CACTCTTTTGAAGGCTGCGCTCTGCGACGCGCGCACTTCCACCGATCGTGTGCGCGCA 960
QY 961 GAGCAGCGGCG 1020
DB 961 GAGCAGCGGCG 1020
QY 1021 CCGGCTGTACGCGCGAGACCAAGCACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 CCGGCTGTACGCGCGAGACCAAGCACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 GCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1081 GCGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 GACCATCTTTTCTGAGGTTCTGAGGCTGCTGAGTGTGCGGAGTGTGCGGAGTGTGCG 1200
DB 1141 GACCATCTTTTCTGAGGTTCTGAGGCTGCTGAGTGTGCGGAGTGTGCGGAGTGTGCG 1200
QY 1201 GCGCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 GCGCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 GTGCGCGCTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 GTGCGCGCTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 AGCGGCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1321 AGCGGCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 CACAGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 CACAGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 CGGCTTGTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 CGGCTTGTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

1501 CAACGAAAGCGCGTTCTCTGAGGAACACAAAGATTATCTCCCTGGGGAGATGCGAA 1560
1501 CAACGAAAGCGCGTTCTCTGAGGAACACAAAGATTATCTCCCTGGGGAGATGCGAA 1560
1561 GCTCTCGCTGAGAGACTGACGTGGAAGATGAGCCGTGCGGAGACTGCGCTTGGCTGCGAG 1620
1561 GCTCTCGCTGAGAGACTGACGTGGAAGATGAGCCGTGCGGAGACTGCGCTTGGCTGCGAG 1620
1621 GAGCCCAAGGGTTGGCTGTGTTCCGCGCAGAGCAACCGTCTGCGTGAAGATCTCTGCG 1680
1621 GAGCCCAAGGGTTGGCTGTGTTCCGCGCAGAGCAACCGTCTGCGTGAAGATCTCTGCG 1680
1681 CAAGTTCCTGCACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1681 CAAGTTCCTGCACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1741 TGTCAAGAGACCACTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGCTTGAG 1800
1741 TGTCAAGAGACCACTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGCTTGAG 1800
1801 CAAGTTCGAAGATTGGAATCAGACGCACTTGAAGAGGTTGACCTGCGGAGCTGTC 1860
1801 CAAGTTCGAAGATTGGAATCAGACGCACTTGAAGAGGTTGACCTGCGGAGCTGTC 1860
1861 GGAAGCAGAGGTGAGGACGATCGGGAAGCAGAGCCCGCGCTGACGCTGAGACTGCG 1920
1861 GGAAGCAGAGGTGAGGACGATCGGGAAGCAGAGCCCGCGCTGACGCTGAGACTGCG 1920
1921 CTTCATCCCCAAGCTGAGCGGGCTGCGCGATTTGAAACATGACTGATGATGATGATGATGAT 1980
1921 CTTCATCCCCAAGCTGAGCGGGCTGCGCGATTTGAAACATGACTGATGATGATGATGATGAT 1980
1981 CAGAAGCTTCCGAGAGAAAGAGGCGCAGAGCTCTACCTCGAGGTTGAGGCACTGTT 2040
1981 CAGAAGCTTCCGAGAGAAAGAGGCGCAGAGCTCTACCTCGAGGTTGAGGCACTGTT 2040
2041 CAGCGGTCTCACTAGAGCGGGCGGGGCGCGCGCTCTGAGGAGCTGATGATGATGATGATGAT 2100
2041 CAGCGGTCTCACTAGAGCGGGCGGGGCGCGCGCTCTGAGGAGCTGATGATGATGATGATGAT 2100
2101 CCTGAGCATATCCACAGGGCCCTGCGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
2101 CCTGAGCATATCCACAGGGCCCTGCGGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
2161 GCGCGCTGAGCTGTACTTTGTCAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2161 GCGCGCTGAGCTGTACTTTGTCAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2221 GGAAGGCTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2221 GGAAGGCTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2281 TCGGTATGCGGTGATCAGAAAGGCGCGCATGAGGCACTGCGCAAGGCTTCAAGAGCA 2340
2281 TCGGTATGCGGTGATCAGAAAGGCGCGCATGAGGCACTGCGCAAGGCTTCAAGAGCA 2340
2341 TGGGTATGCGGTGATCAGAAAGGCGCGCATGAGGCACTGCGCAAGGCTTCAAGAGCA 2400
2341 TGGGTATGCGGTGATCAGAAAGGCGCGCATGAGGCACTGCGCAAGGCTTCAAGAGCA 2400
2401 GAGCAGCGCGCTGAGGAGATGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
2401 GAGCAGCGCGCTGAGGAGATGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
2461 GAGTGGCTCTTTCAGAGCTTCTCTACGCTTCAATGATGATGATGATGATGATGATGATGATGAT 2520
2461 GAGTGGCTCTTTCAGAGCTTCTCTACGCTTCAATGATGATGATGATGATGATGATGATGATGAT 2520
2521 CAAGTCTTACGCTCAGTGGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG 2580
2521 CAAGTCTTACGCTCAGTGGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG 2580

2581 CAGCTGTGCTACGCGGACATGAGAAACAGCTGTTTGGGGGATTTCCGCGGAGCGGCT 2640
2581 CAGCTGTGCTACGCGGACATGAGAAACAGCTGTTTGGGGGATTTCCGCGGAGCGGCT 2640
2641 GCTCTCGCTTGTGATGATTTCTTGTGTGACACTCACTTCAACCCAGCGGAAAC 2700
2641 GCTCTCGCTTGTGATGATTTCTTGTGTGATGATTTCTTGTGTGATGATTTCTTGTGTGATGAT 2700
2701 CTTCCTCAGAGACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
2701 CTTCCTCAGAGACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
2761 GACAGTGTGAACTTCCCTGTGAAAGACAGAGCCCTGAGTGCACGCTTTTGTGAT 2820
2761 GACAGTGTGAACTTCCCTGTGAAAGACAGAGCCCTGAGTGCACGCTTTTGTGAT 2820
2821 GCGCGCCCAAGGCTTATCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
2821 GCGCGCCCAAGGCTTATCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
2881 GGAAGCAGACTACTCAGCTATGCGCGGACCTTCATCAGAGCAGCTTCAACCG 2940
2881 GGAAGCAGACTACTCAGCTATGCGCGGACCTTCATCAGAGCAGCTTCAACCG 2940
2941 CGGCTTCAAGGCTGAGAGAAATGCGTGCAGAACTTTTGGGGTCTTGGCTGAAGT 3000
2941 CGGCTTCAAGGCTGAGAGAAATGCGTGCAGAACTTTTGGGGTCTTGGCTGAAGT 3000
3001 TCACAGCTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
3001 TCACAGCTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
3061 CAGAATCTCTGCTGAGAGGCTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCA 3120
3061 CAGAATCTCTGCTGAGAGGCTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCA 3120
3121 TCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACAGCGGCTCCCT 3180
3121 TCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACAGCGGCTCCCT 3180
3181 CTGCTATCTCATCTGAAAGCCAAAGACGAGGATGTCGCTGAGGAGCCAGGCGCGC 3240
3181 CTGCTATCTCATCTGAAAGCCAAAGACGAGGATGTCGCTGAGGAGCCAGGCGCGC 3240
3241 CGGCTCTGCTGCTGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3300
3241 CGGCTCTGCTGCTGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3300
3241 CGGCTCTGCTGCTGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3300
3241 CGGCTCTGCTGCTGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3300
3301 GACTGAGCAGCGGTGACCTAGTGCACCTCCGAGGCTGACTCAGGACAGCCAGAGCA 3360
3301 GACTGAGCAGCGGTGACCTAGTGCACCTCCGAGGCTGACTCAGGACAGCCAGAGCA 3360
3361 GCTGAGTGGAAAGCTCCCGGAGACGACGCTGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3420
3361 GCTGAGTGGAAAGCTCCCGGAGACGACGCTGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3420
3421 ACTGAGCTCAGAGCTTCAAGACCATCTGAGTGAATGAGGCAACCGGCCAAGAGGCGCA 3480
3421 ACTGAGCTCAGAGCTTCAAGACCATCTGAGTGAATGAGGCAACCGGCCAAGAGGCGCA 3480
3481 GAGCAGACAGCAGAGCCCTGCAAGCGCGGCTTCAAGTCCAGAGGAGAGAGGAGGAGGAGGAGG 3540
3481 GAGCAGACAGCAGAGCCCTGCAAGCGCGGCTTCAAGTCCAGAGGAGAGAGGAGGAGGAGGAGG 3540
3541 CACACCCAGGCGCGCAGCTGAGAGTGAAGGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3600
3541 CACACCCAGGCGCGCAGCTGAGAGTGAAGGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3600
3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
3661 GAGTGTCCAGCAACCTGCGCTTCTTCACTTCCCAAGGCTGAGGCTGAGGCTTCCACCCCA 3720
3661 GAGTGTCCAGCAACCTGCGCTTCTTCACTTCCCAAGGCTGAGGCTGAGGCTTCCACCCCA 3720

Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGGCTGGCTCCACCCCA 3720
QY 3721 GGGGCGAGTTTCTTCCACAGAGACCCGGCTTCCACTCCCAATAGAAATGTCATCC 3780
Db 3721 GGGGCGAGTTTCTTCCACAGAGACCCGGCTTCCACTCCCAATAGAAATGTCATCC 3780
QY 3781 CCAGATTGCGCATGTTTCAACCCCTGGCCCTTCCCTTCCCTTCCACCCCAATCC 3840
Db 3781 CCAGATTGCGCATGTTTCAACCCCTGGCCCTTCCCTTCCCTTCCACCCCAATCC 3840
QY 3841 AGGTGGAGACCTTGAAGAGACCTTGGAGCTTGGAAATTTGAGTGAACCAAGGTGTG 3900
Db 3841 AGGTGGAGACCTTGAAGAGACCTTGGAGCTTGGAAATTTGAGTGAACCAAGGTGTG 3900
QY 3901 CCCTGTACACAGGAGGACCTTCCCTGATGGAGGCTCCCTGGAGTCAAAATTTGGGGG 3960
Db 3901 CCCTGTACACAGGAGGACCTTCCCTGATGGAGGCTCCCTGGAGTCAAAATTTGGGGG 3960
QY 3961 GAGGTGCTGTGGAGTAAATATCTGAATATATGATTTTCAATTTGAAAAAAA 4015
Db 3961 GAGGTGCTGTGGAGTAAATATCTGAATATATGATTTTCAATTTGAAAAAAA 4015

RESULT 10
US-09-733-294A-3
Sequence 3, Application US/09733294A
Patent No. 6492171
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: William Gaarde
APPLICANT: Susan M. Freiler
APPLICANT: Edward V. Wanciewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0527
CURRENT APPLICATION NUMBER: US/09/733,294A
CURRENT FILING DATE: 2000-12-07
PRIORITY FILING DATE: 09/572,423
PRIORITY FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 3
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)...(3454)
US-09-733-294A-3

Query Match 100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGCGTCTGCTGCGCACTGGAGAGCTTGGCCCGGACCAACCCCGCATGCG 60
Db 1 GCAGCGCTGCGTCTGCTGCGCACTGGAGAGCTTGGCCCGGACCAACCCCGCATGCG 60
QY 61 GCGCGCTCCCGCTGCGAGCCGTGGCTCTCTGTCGCGACGCTACCGCGAGGTGCT 120
Db 61 GCGCGCTCCCGCTGCGAGCCGTGGCTCTCTGTCGCGACGCTACCGCGAGGTGCT 120
QY 121 GCGCGTGGCCAGTGTGCGGCGCTGGGGGCGCGGCTGGCGGCTGGTGAAGCGCG 180
Db 121 GCGCGTGGCCAGTGTGCGGCGCTGGGGGCGCGGCTGGCGGCTGGTGAAGCGCG 180
QY 181 GGAACCGCGGCGCTTTCGCGCGCTGGTGGCCAGTGGCTGTGTGCTGGAGCGC 240
Db 181 GGAACCGCGGCGCTTTCGCGCGCTGGTGGCCAGTGGCTGTGTGCTGGAGCGC 240
QY 241 AGCGCGCGCGCGCGCGCGCGCTTTCGCGCGAGTGTCTTGTGCTGAAGAGCTGGTGC 300
Db 241 AGCGCGCGCGCGCGCGCGCGCTTTCGCGCGAGTGTCTTGTGCTGAAGAGCTGGTGC 300

QY 301 CCGAGTGTGCAAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCTTGGCTTGGC 360
Db 301 CCGAGTGTGCAAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCTTGGCTTGGC 360
QY 361 GCTGTGAGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 361 GCTGTGAGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 CTTGCCCAACAGGTGACCGGACCTGCGGGGAGCGGGCGTGGGGCTGTGCTGCG 480
Db 421 CTTGCCCAACAGGTGACCGGACCTGCGGGGAGCGGGCGTGGGGCTGTGCTGCG 480
QY 481 CCGCGTGGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 CCGCGTGGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GGTCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTAACAGCTGCGGCTGCAC 600
Db 541 GGTCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTAACAGCTGCGGCTGCAC 600
QY 601 TCAGGCG 660
Db 601 TCAGGCG 660
QY 661 CTGGAACCATTAAGGTGAGGGAGCGCGGGTCCCTGCGCTGCGAGCCCGGCTGCGAG 720
Db 661 CTGGAACCATTAAGGTGAGGGAGCGCGGGTCCCTGCGCTGCGAGCCCGGCTGCGAG 720
QY 721 GAGGCGCGGGGAGTGTGCGAGCGCGAAATGTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 GAGGCGCGGGGAGTGTGCGAGCGCGAAATGTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TGCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 781 TGCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 841 GCGTGGACCGAGTGAACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 841 GCGTGGACCGAGTGAACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 CACTCTTTTGAAGGATGTGCTGTGCGACGCGGCACTCCCACTCATCGTGGCGCGCA 960
Db 901 CACTCTTTTGAAGGATGTGCTGTGCGACGCGGCACTCCCACTCATCGTGGCGCGCA 960
QY 961 GCACCAAGCGGCG 1020
Db 961 GCACCAAGCGGCG 1020
QY 1021 CCGGCTGTACGCGGAGACCAACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
Db 1021 CCGGCTGTACGCGGAGACCAACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
QY 1081 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
Db 1081 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
QY 1141 GACCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
Db 1141 GACCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 1201 GCGCCAGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
Db 1201 GCGCCAGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
QY 1261 GTGCCCTTACAGGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
Db 1261 GTGCCCTTACAGGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
QY 1321 AGCGGT 1380
Db 1321 AGCGGT 1380
QY 1381 CACAGACCCCGGTGCTGT 1440

Dp	1381	CACAGACCCCGTGGCTGGTGGAGCTGCTCCGCAAGACAGACGCCCTTGGAGAGTGTAA	1440
Qy	1441	CGGCTTCGTGGGGGCTGGCTGGGCGCGGCTGGTGCCGCCAGGCGCTTGGGGGCTCCAGGCA	1500
Dp	1441	CGGCTTCGTGGGGGCTGGCTGGGCGCGGCTGGTGCCGCCAGGCGCTTGGGGGCTCCAGGCA	1500
Qy	1501	CAACGAAACGCCGCTTCTCCAGAGAACACCAAGAAAGTTCACTCTCTGGGAGAGATGCCAA	1560
Dp	1501	CAACGAAACGCCGCTTCTCCAGAGAACACCAAGAAAGTTCACTCTCTGGGAGAGATGCCAA	1560
Qy	1561	GCTCTCCCTGAGAGAGCTGAAGTGAGAGATGAGCGGGAGATGGCGTTGGCTGGCGAG	1620
Dp	1561	GCTCTCCCTGAGAGAGCTGAAGTGAGAGATGAGCGGGAGATGGCGTTGGCTGGCGAG	1620
Qy	1621	GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGCAAGACACCGCTCTGCGTAGAGAGATCCCTGAC	1680
Dp	1621	GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGCAAGACACCGCTCTGCGTAGAGAGATCCCTGAC	1680
Qy	1681	CAAGTTCCTGCACTGGCTGAATGAGTGTATCGTCTGAGCTGCTCAGGCTCTTTCTTTTAA	1740
Dp	1681	CAAGTTCCTGCACTGGCTGAATGAGTGTATCGTCTGAGCTGCTCAGGCTCTTTCTTTTAA	1740
Qy	1741	TGTCACGAGAACCAAGCTTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGTGTCTGGAG	1800
Dp	1741	TGTCACGAGAACCAAGCTTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGTGTCTGGAG	1800
Qy	1801	CAAGTTCCAAAGCAATTTGGAATACAGACAGCACTTGAAGAGGATGACACTCGGAGAGCTGTC	1860
Dp	1801	CAAGTTCCAAAGCAATTTGGAATACAGACAGCACTTGAAGAGGATGACACTCGGAGAGCTGTC	1860
Qy	1861	GGAAGCAGAGGTCAGGAGCATGGGAGAGCCAGGCGCCCTTGCTGACGTCACAGACTCCG	1920
Dp	1861	GGAAGCAGAGGTCAGGAGCATGGGAGAGCCAGGCGCCCTTGCTGACGTCACAGACTCCG	1920
Qy	1921	CTTATATCCCAAGCCTGACGGGCTGGGCTGGGATTTGGAAATAGATCTACTGTGGAGAC	1980
Dp	1921	CTTATATCCCAAGCCTGACGGGCTGGGCTGGGATTTGGAAATAGATCTACTGTGGAGAC	1980
Qy	1981	CAGAACGTTCCGACAGAAAGAGAGGCGGAGCGCTCTCACTCGAGGGTGAAGGCACTGTT	2040
Dp	1981	CAGAACGTTCCGACAGAAAGAGAGGCGGAGCGCTCTCACTCGAGGGTGAAGGCACTGTT	2040
Qy	2041	CAGCGTCTCACTACAGAGCGGGCGCGGCGCCCGGCTCTGAGGCGCTCTGTGTGGAG	2100
Dp	2041	CAGCGTCTCACTACAGAGCGGGCGCGGCGCCCGGCTCTGAGGCGCTCTGTGTGGAG	2100
Qy	2101	CTTGGAGATATCCAGAGGCGCTGGCGCACCTTCTGTGTGTGGGCGGCCAGAGACCC	2160
Dp	2101	CTTGGAGATATCCAGAGGCGCTGGCGCACCTTCTGTGTGTGGGCGGCCAGAGACCC	2160
Qy	2161	GCGGCTGAGCTGATCACTTTGTCAAGGTGATGTGAAGGGCGGTTAGACACCATCCGCCCA	2220
Dp	2161	GCGGCTGAGCTGATCACTTTGTCAAGGTGATGTGAAGGGCGGTTAGACACCATCCGCCCA	2220
Qy	2221	GGAAGGCTCAAGAGGATCAATGCGCAGCATCAATCAAAACCCAGAAACAGTACTGCGTGG	2280
Dp	2221	GGAAGGCTCAAGAGGATCAATGCGCAGCATCAATCAAAACCCAGAAACAGTACTGCGTGG	2280
Qy	2281	TGCGTATGCGGTGTCCAGAAAGGCGCGCCATGGGCGAGTCCGCAAGGCTTTCAAGAGCA	2340
Dp	2281	TGCGTATGCGGTGTCCAGAAAGGCGCGCCATGGGCGAGTCCGCAAGGCTTTCAAGAGCA	2340
Qy	2341	CGTCTCAACCTTGAACAGACCTTCAGCGGTACATGCGCAAGTTGTGGGTCTCACTGGAGGA	2400
Dp	2341	CGTCTCAACCTTGAACAGACCTTCAGCGGTACATGCGCAAGTTGTGGGTCTCACTGGAGGA	2400
Qy	2401	GACCAAGCCGCTGAGGAGATGCGGTCTCATGAGCAGAGAGCTCTCTCTGAATAGAGCCAG	2460
Dp	2401	GACCAAGCCGCTGAGGAGATGCGGTCTCATGAGCAGAGAGCTCTCTCTGAATAGAGCCAG	2460
Qy	2461	CAGTGGCTCTTGAAGCTTCTCTAAGCTTATGTGCAACACAGCGCGTGGCATCAAGGGG	2520

QY	3601	CATGTCGGAGCTGAAGAGCTGAGTGTCCGGCTAGAGCTGAGGAGAGTGTCAAGCAAGGGCT	3666
Db	3601	CATGTCGGAGCTGAAGAGCTGAGTGTCCGGCTAGAGCTGAGGAGAGTGTCAAGCAAGGGCT	3666
QY	3661	GAGTGTCCAGCAACACTGCGGTCTTCACTTCCCAAGAGTGGACCTGAGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGCAACACTGCGGTCTTCACTTCCCAAGAGTGGACCTGAGCTCCACCCCA	3720
QY	3721	GGGCGAGCTTTTCTCTACCAAGAGCCGGGCTTCCACTCCGCCACATAGGAATATGTCATCC	3780
Db	3721	GGGCGAGCTTTTCTCTACCAAGAGCCGGGCTTCCACTCCGCCACATAGGAATATGTCATCC	3780
QY	3781	CCAGATTGCGCAATTGTTACCCCTGCGCCTGCGCCCTTTCGCTTCCACCCCAACATCC	3840
Db	3781	CCAGATTGCGCAATTGTTACCCCTGCGCCTGCGCCCTTTCGCTTCCACCCCAACATCC	3840
QY	3841	AGGTGAGAACCTGTGAGAAGAACCTGTGAGAGCTCTGGAAATTGGAGTAGTACCAAAAGGTGTG	3900
Db	3841	AGGTGAGAACCTGTGAGAAGAACCTGTGAGAGCTCTGGAAATTGGAGTAGTACCAAAAGGTGTG	3900
QY	3901	CCCTGTACACAGGCGAGGACCTGTGACCTTGATGGGGGTCCCTGTGGTCAAAATTGGGGG	3960
Db	3901	CCCTGTACACAGGCGAGGACCTGTGACCTTGATGGGGGTCCCTGTGGTCAAAATTGGGGG	3960
QY	3961	GAGGTGCTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTCAAAATTTGAAAAA	4015
Db	3961	GAGGTGCTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTCAAAATTTGAAAAA	4015

RESULT 11
 US-09-402-161B-1
 ; Sequence 1, Application US/09402161B
 ; Patent No. 6610839
 GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,161B
 FILING DATE: 29-Sep-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997

```

1      APPLICATION NUMBER: US 08/912,951
2      FILING DATE: 14-AUG-1997
3      APPLICATION NUMBER: US 08/915,503
4      FILING DATE: 14-AUG-1997
5      APPLICATION NUMBER: WO PCT/US97/17885
6      FILING DATE: 01-OCT-1997
7      ATTORNEY/AGENT INFORMATION:
8          NAME: Ausehuus, Scott L.
9          REGISTRATION NUMBER: 42,271
10         REFERENCE/DOCKET NUMBER: 015389-002620US
11         TELECOMMUNICATION INFORMATION:
12             TELEPHONE: (415) 576-0200
13             TELEFAX: (415) 576-0300
14         INFORMATION FOR SEQ ID NO: 1:
15             SEQUENCE CHARACTERISTICS:
16                 LENGTH: 4015 base pairs
17                 TYPE: nucleic acid
18                 STRANDEDNESS: single
19                 TOPOLOGY: linear
20             MOLECULE TYPE: cDNA
21             FEATURE:
22                 NAME/KEY: CDS
23                 LOCATION: 56...3454
24                 OTHER INFORMATION: /product="hTRT"
25                 /note="human telomerase reverse
26                 transcriptase (hTRT) catalytic protein
27                 component"
28         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
29         US-09-402-181B-1

```

Query Match	100.0%;	Score 4015;	DB 4;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4015;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GCAGCCGCTGCGTCTTGTCTGCGCAGCTGTGGAGAGCCCTTGCCGCCGCCACCCCGCGATGCC	60	
Db	1	GCAGCGCTGTGCTCTTGTCTGCGCAGTGTGGAGAGCCCTTGCCGCCGCCACCCCGCGATGCC	60	
QY	61	GCGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTCTGCTGCGCAGCCACTTACCGCGAGTGTCT	120	
Db	61	GCGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTCTGCTGCGCAGCCACTTACCGCGAGTGTCT	120	
QY	121	GCGCGTGGCCACGTTGCTGTGGGGCGCCCTTGGGGGCCCCAGAGGCTGGGGGCTGTGTGACGCGG	180	
Db	121	GCGCGTGGCCACGTTGCTGTGGGGCGCCCTTGGGGGCCCCAGAGGCTGGGGGCTGTGTGACGCGG	180	
QY	181	GAGACCCGCGCGCTTTCGCGCGCTGTGTGTGCGCAGATGCTGTGTGTGCGTGGCCCTTGAGCGC	240	
Db	181	GAGACCCGCGCGCTTTCGCGCGCTGTGTGTGCGCAGATGCTGTGTGTGCGTGGCCCTTGAGCGC	240	
QY	241	ACGGCGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGGTGTCTGTGCTTGAAGAGCTGTGTGGC	300	
Db	241	ACGGCGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGGTGTCTGTGCTTGAAGAGCTGTGTGGC	300	
QY	301	CCGAGTGTCTCAGAGGCTGTGTGCGAGCGCGCGCGCAGAGAACTGTGTGCGCTTTCGCGCTTCGC	360	
Db	301	CCGAGTGTCTCAGAGGCTGTGTGCGAGCGCGCGCGCAGAGAACTGTGTGCGCTTTCGCGCTTCGC	360	
QY	361	GCTGCTGAGAGGGGGCCCGCGGGGGCCCCCGCAGAGCCTTACACACAGCGTGGCGCAGCTA	420	
Db	361	GCTGCTGAGAGGGGGCCCGCGGGGGCCCCCGCAGAGCCTTACACACAGCGTGGCGCAGCTA	420	
QY	421	CTTGCACCAACGCGTGAACCGACGCACTTGCGGGGAGCGGGGCGCTGTGGGAGCTGTGCTTGC	480	
Db	421	CTTGCACCAACGCGTGAACCGACGCACTTGCGGGGAGCGGGGCGCTGTGGGAGCTGTGCTTGC	480	
QY	481	CCGCGTGGGCGAGACGCTGTGCTTCACTCTGTGTGACGCTGCGCGCTCTTTGTGTGTGT	540	
Db	481	CCGCGTGGGCGAGACGCTGTGCTTCACTCTGTGTGACGCTGCGCGCTCTTTGTGTGTGT	540	
QY	541	GCGCTCCACGCTGTGCGCTTACAGGTGTGTGGGGCGCGCTGTACCACTTGTGGCGCTGTGCAC	600	
Db	541	GCGCTCCACGCTGTGCGCTTACAGGTGTGTGGGGCGCGCTGTGTACCACTTGTGGCGCTGTGCAC	600	

OY	601	CAAGGCCCCGGCCCCCGCCACACGCTAGTGAACCCCGAAGGGGCTCTGGGAAATCGGAACGGGC	660
Db	601	TCAGGCCCCGGCCCCCGCCACACGCTAGTGAACCCCGAAGGGGCTCTGGGAAATCGGAACGGGC	660
OY	661	CTGGAACCATATAGCGTCAGAGAGAGCCGGGGGTCCCCCTGGGAGCTGGCAGCCCGGGATGGCAG	720
Db	661	CTGGAACCATATAGCGTCAGAGAGAGCCGGGGGTCCCCCTGGGAGCTGGCAGCCCGGGATGGCAG	720
OY	721	GAGGCGCGGGGGCAGTGCGCAAGCTTGCCGTTGCTCCAAAGAGCCCAAGGCGTGGCGC	780
Db	721	GAGGCGCGGGGGCAGTGCGCAAGCTTGCCGTTGCTCCAAAGAGCCCAAGGCGTGGCGC	780
OY	781	TGCCCCTAGGCCCCGAGGGGAGCGCCCGTTGGGAGAGGGGCTGGGGCCACCCGGGCAAGGAC	840
Db	781	TGCCCCTAGGCCCCGAGGGGAGCGCCCGTTGGGAGAGGGGCTGGGGCCACCCGGGCAAGGAC	840
OY	841	GCGTGGACCGAGTGAACGCTGGTCTCTGTGTGATGTCACCTGCGAGACCCCGCGGAAGAGC	900
Db	841	GCGTGGACCGAGTGAACGCTGGTCTCTGTGTGATGTCACCTGCGAGACCCCGCGGAAGAGC	900
OY	901	CACCTCTTTTGGAGGGTGGGCTCTCTGGGACCGCGCACTCCCAACCCATCCGTGGGCGGCCA	960
Db	901	CACCTCTTTTGGAGGGTGGGCTCTCTGGGACCGCGCACTCCCAACCCATCCGTGGGCGGCCA	960
OY	961	GCACCAGCCGGGCCCCCCCATCCACATCCGCGGCAACAAGTCCCTTGGGACAAGCCTTGTGC	1020
Db	961	GCACCAGCCGGGCCCCCCCATCCACATCCGCGGCAACAAGTCCCTTGGGACAAGCCTTGTGC	1020
OY	1021	CCCGGTGTACGCGCGAGACCAAGACATTCCTCTACTCTCTCAGGCGACANAGAGACTGGC	1080
Db	1021	CCCGGTGTACGCGCGAGACCAAGACATTCCTCTACTCTCTCAGGCGACANAGAGACTGGC	1080
OY	1081	GCCCTCCTTCTACTCAGCTCTCTGAGGCGCAGCCCTGAATGGGCGCTGGGAGAGCTGGTGA	1140
Db	1081	GCCCTCCTTCTACTCAGCTCTCTGAGGCGCAGCCCTGAATGGGCGCTGGGAGAGCTGGTGA	1140
OY	1141	GACCAATCTTTCTGGGTTCCAGGCCCCCTGAGTGCAGGAGACTCCCGCAGGTTGCCCGGCT	1200
Db	1141	GACCAATCTTTCTGGGTTCCAGGCCCCCTGAGTGCAGGAGACTCCCGCAGGTTGCCCGGCT	1200
OY	1201	GCCCCAGGGCTACTGGGAAATGCGGCGCCCTGTTCTGAGAGCTGCTTGGGAAACAGCGCA	1260
Db	1201	GCCCCAGGGCTACTGGGAAATGCGGCGCCCTGTTCTGAGAGCTGCTTGGGAAACAGCGCA	1260
OY	1261	GTCGCCCTACGGGGGTCTCTCAAGAGCCAGTCCGCTGGAGCTGGGCTCACCCAGC	1320
Db	1261	GTCGCCCTACGGGGGTCTCTCTAAGAGCCAGTCCCGCTGGAGCTGGGCTCACCCAGC	1320
OY	1321	AGCGGCTCTGTGTGCTCCGGAGAGAGCCCCCAGGCTCTGTGCGCGCCCCGAGGAGAGGA	1380
Db	1321	AGCGGCTCTGTGTGCTCCGGAGAGAGCCCCCAGGCTCTGTGCGCGCCCCGAGGAGAGGA	1380
OY	1381	CACAGAGCCCGCTGCGCTGAGAGCTCTCCGACGACAGAGAGCCCTGGGAGAGTGA	1440
Db	1381	CACAGAGCCCGCTGCGCTGAGAGCTCTCCGACGACAGAGAGCCCTGGGAGAGTGA	1440
OY	1441	GCGCTTCTGTGCGGCTGCTGCGCGGCTGATGCCCCCAGAGCCTCTGGGCTCCAGGCA	1500
Db	1441	GCGCTTCTGTGCGGCTGCTGCGCGGCTGATGCCCCCAGAGCCTCTGGGCTCCAGGCA	1500
OY	1501	CAGAGAAAGCGCGCTTCTCAGAGAAACCAAGAAATTCCTCCCTGGGAAAGATGCCAA	1560
Db	1501	CAGAGAAAGCGCGCTTCTCAGAGAAACCAAGAAATTCCTCCCTGGGAAAGATGCCAA	1560
OY	1561	GCTCTCGCTGAGAGCTGAGCTGGAGATGAGCTGGGAGACTGCTTGGCTGGCAG	1620
Db	1561	GCTCTCGCTGAGAGCTGAGCTGGAGATGAGCTGGGAGACTGCTTGGCTGGCAG	1620
OY	1621	GAGCCCAAGGGTGGCTGTGTTCCGGCGCAGAGACCTGTGCTGGTGAAGATCTGGC	1680
Db	1621	GAGCCCAAGGGTGGCTGTGTTCCGGCGCAGAGACCTGTGCTGGTGAAGATCTGGC	1680

[illegible]

Db 2761 GACAGTGGTGAACCTTCCCTGTAGAAGAGGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT 2820
Qy 2821 GCCGGCCCAACGGGCTATTTCCCTGTGGTGGGCTGTGTGTGATATCCCGAACCTTGAAGGT 2880
Db 2821 GCCGGCCCAACGGGCTATTTCCCTGTGGTGGGCTGTGTGTGATATCCCGAACCTTGAAGGT 2880
Qy 2881 GCAGAGCACTACTCCAGCTATGCCCCGACCTTCATGAGAGCAGTCTCACTTCAACCG 2940
Db 2881 GCAGAGCACTACTCCAGCTATGCCCCGACCTTCATGAGAGCAGTCTCACTTCAACCG 2940
Qy 2941 CGGCTTCAAGGCTGGAGAGAAATATGCGTCCGAACTTTTGGGGTCTTGGCGGTGAAGT 3000
Db 2941 CGGCTTCAAGGCTGGAGAGAAATATGCGTCCGAACTTTTGGGGTCTTGGCGGTGAAGT 3000
Qy 3001 TCACAGGCTGTTTGTGATTTGGAGGTGAACAGCTTCACAGCGTGGACCAACATCTA 3060
Db 3001 TCACAGGCTGTTTGTGATTTGGAGGTGAACAGCTTCACAGCGTGGACCAACATCTA 3060
Qy 3061 CAAGATCCTCTGCTGAGAGGCGTACAGATTTCAGCATATGTGTGAGCTCCCATTTCA 3120
Db 3061 CAAGATCCTCTGCTGAGAGGCGTACAGATTTCAGCATATGTGTGAGCTCCCATTTCA 3120
Qy 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTGTGACAGGCTTCCCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTGTGACAGGCTTCCCT 3180
Qy 3181 CTGCTACTCCATCCTTGAAGCAAGAGGAGTGTGCTGGGGGCGCAAGGCGCGCGC 3240
Db 3181 CTGCTACTCCATCCTTGAAGCAAGAGGAGTGTGCTGGGGGCGCAAGGCGCGCGC 3240
Qy 3241 CGGCGCTCTGCTGCGAGGCGCGTGAAGTGTGCTGTCACCAAGCATTTCTGCTCAAGCT 3300
Db 3241 CGGCGCTCTGCTGCGAGGCGCGTGAAGTGTGCTGTCACCAAGCATTTCTGCTCAAGCT 3300
Qy 3301 GACTCGACACCGTGTCACTTACGTCACCTTCTGGGGTCACTAGAGCAACCCAGCGCA 3360
Db 3301 GACTCGACACCGTGTCACTTACGTCACCTTCTGGGGTCACTAGAGCAACCCAGCGCA 3360
Qy 3361 GCTGAGTGGAGAGTCCCGGGGAGCAGCGTGAAGTCCCTGAGGCGCAGCAACCGCG 3420
Db 3361 GCTGAGTGGAGAGTCCCGGGGAGCAGCGTGAAGTCCCTGAGGCGCAGCAACCGCG 3420
Qy 3421 ACTGCGCTGAGCTTCAAGACATCTGTGATGAGCCACCGCGCAACGAGGCGCA 3480
Db 3421 ACTGCGCTGAGCTTCAAGACATCTGTGATGAGCCACCGCGCAACGAGGCGCA 3480
Qy 3481 GAGCAGACACGAGAGCCCTGTACAGCGCGGCTCTACTGCCAGGAGGAGGAGGCGGC 3540
Db 3481 GAGCAGACACGAGAGCCCTGTGTACAGCGCGGCTCTACTGCCAGGAGGAGGAGGCGGC 3540
Qy 3541 CACACCCAGGCGCGCACCGCTGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCTG 3600
Db 3541 CACACCCAGGCGCGCACCGCTGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCTG 3600
Qy 3601 CATGTCGGGTGAAGGTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGCT 3660
Db 3601 CATGTCGGGTGAAGGTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGCT 3660
Qy 3661 GAGTGTCAAGACACCTGCTTCACTTCCCAAGAGGTGGGCTCCAGCCCA 3720
Db 3661 GAGTGTCAAGACACCTGCTTCACTTCCCAAGAGGTGGGCTCCAGCCCA 3720
Qy 3721 GGGCCAGCTTTTCTGACAGAGGCGGCTTCACTTCCCAAGATGATGATC 3780
Db 3721 GGGCCAGCTTTTCTGACAGAGGCGGCTTCACTTCCCAAGATGATGATC 3780
Qy 3781 CCAGATTGCGCATATTTCAACCTTCCGCTTCTTGGCTTCAACCCCAATC 3840
Db 3781 CCAGATTGCGCATATTTCAACCTTCCGCTTCTTGGCTTCAACCCCAATC 3840
Qy 3841 AGGTGAGACCTTGAAGAGACCTGGAGCTCTGGGAATTTGAGTGAACAAAGGTG 3900
Db 3841 AGGTGAGACCTTGAAGAGACCTGGAGCTCTGGGAATTTGAGTGAACAAAGGTG 3900

Db 3841 AGGTGAGACCTTGAAGAGACCTTGGAGCTCTGGGAATTTGAGTGAACAAAGGTG 3900
Qy 3901 CCTGTACACAGGCGAGAACCTTGCACCTGATGAGGGGTCCCTGTGGATCAAAATGGGG 3960
Db 3901 CCTGTACACAGGCGAGAACCTTGCACCTGATGAGGGGTCCCTGTGGATCAAAATGGGG 3960
Qy 3961 GAGGTGCTGGGAGTAAATCTGAATATATGAGTTTCACTTTGAAAAAA 4015
Db 3961 GAGGTGCTGGGAGTAAATCTGAATATATGAGTTTCACTTTGAAAAAA 4015

RESULT 12
US-09-721-456-1
Sequence 1, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721.456
FILING DATE: 22-NOV-6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974.549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724.643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844.419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846.017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851.843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854.050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911.312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912.951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915.503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

QY	1021	CCCCGTGACGCCAGACCAAGACCTTCCTCTACCTCCACAGCGACAAGAGACAGCTGCG	1080
Db	1021	CCCGGTGACGCCAGACCAAGACCTTCTCTACCTCCACAGCGACAAGAGAGAGCTGCG	1080
QY	1081	GCCCTCTTCTCTACCTGACGCTCTTGAGGCCAGGCTGACTGCGGCTCGAGAGGCTGTGGA	1140
Db	1081	GCCCTCTTCTCTACTGACGCTCTTGAGGCCAGGCTGACTGCGGCTCGAGAGGCTGTGGA	1140
QY	1141	GACCACTTTTCTGGGTTTCCAGGCTTCGGAATGCGAGGACTCCCGCAGGTTGGCCCGCT	1200
Db	1141	GACCACTTTTCTGGGTTTCCAGGCTTCGGAATGCGAGGACTCCCGCAGGTTGGCCCGCT	1200
QY	1201	GCCCCAGCGCTACTGCGCAAAATGCGGCCCTGTATTTCTGAGCTGCTTGAGGAAACAAGCGCA	1260
Db	1201	GCCCCAGCGTACTGCGCAAAATGCGGCCCTGTATTTCTGAGAGCTGTGAGAAACAAGCGCA	1260
QY	1261	GTGCCCTCTACGGGGGTGCTCTCCAGACCACTGCGCCGTGAGCTGGTCACCCCAGC	1320
Db	1261	GTGCCCTCTACGGGGGTGCTCTCCAGACCACTGCGCCGTGAGCTGGTCACCCCAGC	1320
QY	1321	AGCCGATCTGTGCGCCGGGAGAAAGCCCAGGGGCTGTGGCGGCCCCCGAGAGAGAGGA	1380
Db	1321	AGCCGATCTGTGCGCCGGGAGAAAGCCCAGGGGCTGTGGCGGCCCCCGAGAGAGAGGA	1380
QY	1381	CACAGACCCCGCTGCGCTGTGACCTGCTCCGACAGACAGCAAGCCCTTGAGAGTGA	1440
Db	1381	CACAGACCCCGCTGCGCTGTGACCTGCTCCGACAGACAGCAAGCCCTTGAGAGTGA	1440
QY	1441	CGGCTCTGTGGGGGCTGCGCCGCTGCGCTGCTGCTGCGCCACAGGCTCTGAGGCTCCAGCA	1500
Db	1441	CGGCTCTGTGGGGGCTGCGCCGCTGCGCTGCTGCTGCGCCACAGGCTCTGAGGCTCCAGCA	1500
QY	1501	CAAGCAACGCGCTTCTCCTCAGAGAACCAACAAAGATTCACTCCCTGGGGAAGATGCGAA	1560
Db	1501	CAAGCAACGCGCTTCTCCTCAGAGAACCAACAAAGATTCACTCCCTGGGGAAGATGCGAA	1560
QY	1561	GCTCTCTGCTGAGAGAGCTGACGTGGAATGAGCGTGTGCGGACTGCGCTTGGCTGCGAG	1620
Db	1561	GCTCTCTGCTGAGAGAGCTGACGTGGAATGAGCGTGTGCGGACTGCGCTTGGCTGCGAG	1620
QY	1621	GAGCCACAGGGGTTGGCTGTGTCGGCGCGACAGACACCGTCTGGGTGAGAGATCTGCGC	1680
Db	1621	GAGCCACAGGGGTTGGCTGTGTCGGCGCGACAGACACCGTCTGGGTGAGAGATCTGCGC	1680
QY	1681	CAAGTTCTCTGCACTGCGCTGATGAGTGTGTAAGTGTGCAAGTCTCAAGTCTTCTTTTA	1740
Db	1681	CAAGTTCTCTGCACTGCGCTGATGAGTGTGTAAGTGTGCAAGTCTCTTCTTTTA	1740
QY	1741	TGTCACCGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACACGGAAGTGTCTGAG	1800
Db	1741	TGTCACCGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACACGGAAGTGTCTGAG	1800
QY	1801	CAAGTTGCAAGACTTGGAAATCAGACAGCACTTGAAGAGGGTGTGAGCTGCGGAGCTGTC	1860
Db	1801	CAAGTTGCAAGACTTGGAAATCAGACAGCACTTGAAGAGGGTGTGAGCTGCGGAGCTGTC	1860
QY	1861	GGAAGCAGAGGTCACGGACGACTGTGGAAAGCCAGGCCCGCTCTGCTGACGTCTCAACTCCG	1920
Db	1861	GGAAGCAGAGGTCACGGACGACTGTGGAAAGCCAGGCCCGCTCTGCTGACGTCTCAACTCCG	1920
QY	1921	CTTCAATCCCAAGGCTGACGGGCTGTGCGGCGAATGTGAACATGGAATCAATGCTGTGGAGC	1980
Db	1921	CTTCAATCCCAAGGCTGACGGGCTGTGCGGCGAATGTGAACATGGAATCAATGCTGTGGAGC	1980
QY	1981	CAGAACGTTCCGCAAGAAAGAGGGCCGAGCGTCTCACTTGAAGGTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTCCGCAAGAAAGAGAGGGCCGAGCGTCTCACTTGAAGGTGAAGGCACTGTT	2040
QY	2041	CAGCGTGTCTCAACTACAGCGGGGCGCGCGCTCCCTGGGGGCTCTGTGCTGGG	2100
Db	2041	CAGCGTGTCTCAACTACAGCGGGGCGCGCGCTCCCTGGGGGCTCTGTGCTGGG	2100
QY	2101	CTTGAGCAATATCCAGAGGCGCTGCGCACCTTGTGTGCTGTGTGCGGCGCCAGAGCC	2160

Db	2101	CCGGAAGATATCCACAGGACCTTGCGCACTTCGTGCTGCGTGGGCGCCAGAACCC	2160
OY	2161	GCGGCTGAGCTGTACTTTGTCAAGGTGATGACGGGCGCGTACGACACCATCCCCA	2220
Db	2161	GCGGCTGAGCTGTACTTTGTCAAGGTGATGACGGGCGCGTACGACACCATCCCCA	2220
OY	2221	GGACAGGCTCACGGAGGTATGCGCCAGCATCATMAACCCAGAACACGTATCGCTGG	2280
Db	2221	GGACAGGCTCACGGAGGTATGCGCCAGCATCATMAACCCAGAACACGTATCGCTGG	2280
OY	2281	TGGTATGCGCTGATCCAGAAAGGCGCCATGAGGACGTCCGCAAGGCTTCAAGAGCA	2340
Db	2281	TGGTATGCGCTGATCCAGAAAGGCGCCATGAGGACGTCCGCAAGGCTTCAAGAGCA	2340
OY	2341	CGTCTCTACCTTGAACACCTCCAGCCGTACATGACACAGTTGTTGCTTACCTGACGA	2400
Db	2341	CGTCTCTACCTTGAACACCTCCAGCCGTACATGACACAGTTGTTGCTTACCTGACGA	2400
OY	2401	GACGAGCCGCTGAGGGAATGCGGTGTATCGAGACGACCTCCCTGTAATGAGGCAAG	2460
Db	2401	GACGAGCCGCTGAGGGAATGCGGTGTATCGAGACGACCTCCCTGTAATGAGGCAAG	2460
OY	2461	CAGTGGCCTCTTGAAGCTTCTCAAGCTTCAATGTCACACAGCCGTCGACATGAGGG	2520
Db	2461	CAGTGGCCTCTTGAAGCTTCTCAAGCTTCAATGTCACACAGCCGTCGACATGAGGG	2520
OY	2521	CAGTCTCTACGTTCCAGTGCAGAGTCCCGCAGGGCTCATCTCTTCCACGTGCTCTG	2580
Db	2521	CAGTCTCTACGTTCCAGTGCAGAGTCCCGCAGGGCTCATCTCTTCCACGTGCTCTG	2580
OY	2581	CAGCCTGTGCTACGCGGACATGAGAACAGAGCTGTTTGCGGGATTCGCGCGGAGCT	2640
Db	2581	CAGCCTGTGCTACGCGGACATGAGAACAGAGCTGTTTGCGGGATTCGCGCGGAGCT	2640
OY	2641	GCTCTCTGCGTGTGTGATGATTTCTTGTGTGACACTCACCTCACCCAGCGGAAAC	2700
Db	2641	GCTCTCTGCGTGTGTGATGATTTCTTGTGTGACACTCACCTCACCCAGCGGAAAC	2700
OY	2701	CTTCTCTCAGAACCTTGATCCAGAGTGTCCCTAGATATGCTGCTGAGTGAACCTTGCGAA	2760
Db	2701	CTTCTCTCAGAACCTTGATCCAGAGTGTCCCTAGATATGCTGCTGAGTGAACCTTGCGAA	2760
OY	2761	GACAGTGTGAACCTTCCCTGTGAAACGAGGCCCTTGAGTGCACGCGTTTGTTCAGAT	2820
Db	2761	GACAGTGTGAACCTTCCCTGTGAAACGAGGCCCTTGAGTGCACGCGTTTGTTCAGAT	2820
OY	2821	GCGGCGCCACGCGCTAATCCCTGATGCGGCGCTGCTGCTGATACCCGGAACCTTGAGGT	2880
Db	2821	GCGGCGCCACGCGCTAATCCCTGATGCGGCGCTGCTGCTGATACCCGGAACCTTGAGGT	2880
OY	2881	GCGAGCGCATACTCCAGCTATCCCGGACCTCATCAGAGCCAGTCTCACCTTCAACCG	2940
Db	2881	GCGAGCGCATACTCCAGCTATCCCGGACCTCATCAGAGCCAGTCTCACCTTCAACCG	2940
OY	2941	CGGCTTCAAGGTTGGGAGGAATGCGGTGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGTTGGGAGGAATGCGGTGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG	3000
OY	3001	TCAAGCCTGTTTCTGGAATTTGCAAGTGAACAGCTCCGAGCGGTGTGACCAACATCTTA	3060
Db	3001	TCAAGCCTGTTTCTGGAATTTGCAAGTGAACAGCTCCGAGCGGTGTGACCAACATCTTA	3060
OY	3061	CAGATCTCTCTGTGTCAGGCGTACAGGTTTCAAGCATGTGTGTGTCAGCTCCCATTTCA	3120
Db	3061	CAGATCTCTCTGTGTCAGGCGTACAGGTTTCAAGCATGTGTGTGTCAGCTCCCATTTCA	3120
OY	3121	TCAGAAATTTGGAAGAACCCCAATTTTCTGTGCGGTCACTCTGACACGCGCTCCCT	3180
Db	3121	TCAGAAATTTGGAAGAACCCCAATTTTCTGTGCGGTCACTCTGACACGCGCTCCCT	3180
OY	3181	CTGCTACTCAATCTTGAAGCCAAACGACAGGATGTGTGCTGGGGGCCAAGGCGCCGCG	3240

Db	3181	TTGCTACTCCATCCTGTAAGCAGAAAGACGAGGATGCTGGGGGCGAAAGGCGCGC	3240
Qy	3241	CGGCGCTTCTGCGCTTCCGAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTTCTGTCTCAAGCT	3300
Db	3241	CGGCGCTTCTGCGCTTCCGAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTTCTGTCTCAAGCT	3300
Qy	3301	GACTCGACACCGGTGCACCTTACGTGSCACTCTGTGGGGTCACTCAGAGCAGGCGCCAGAGCGCA	3360
Db	3301	GACTCGACACCGGTGCACCTTACGTGSCACTCTGTGGGGTCACTCAGAGCAGGCGCCAGAGCGCA	3360
Qy	3361	GCTGAGTCGGAAGCTCCCGGGGAGCGAGCTGACTGCTCTGTGAGGCGCGCAAGCCAACTCCGGC	3420
Db	3361	GCTGAGTCGGAAGCTCCCGGGGAGCGAGCTGACTGCTCTGTGAGGCGCGCAAGCCAACTCCGGC	3420
Qy	3421	ACTGCGCTTCAGACTTTCAGAACCAATCCCTGGAATGATATGCGCACACCGCGCCCAAGCCAGGCGCA	3480
Db	3421	ACTGCGCTTCAGACTTTCAGAACCAATCCCTGGAATGATATGCGCACACCGCGCCCAAGCCAGGCGCA	3480
Qy	3481	GAGCAGACACCGAGAGCCCTGTGCACGCGCGGCTTACGTCCCAAGAGAGGAGGGCGGCGC	3540
Db	3481	GAGCAGACACCGAGAGCCCTGTGCACGCGCGGCTTACGTCCCAAGAGAGGAGGGCGGCGC	3540
Qy	3541	CACACCCAGGCGCGSCACCGCTGGGAGTGTGAGGCGCTTGAAGTGTGTTGGCGAGGCGCTG	3600
Db	3541	CACACCCAGGCGCGSCACCGCTGGGAGTGTGAGGCGCTTGAAGTGTGTTGGCGAGGCGCTG	3600
Qy	3601	CATGTCCGCGCTGGAAGGCTGAGTGTTCGCGCTAGGCGCTGAGGGAATGTTCACGCCAAGGGCT	3660
Db	3601	CATGTCCGCGCTGGAAGGCTGAGTGTTCGCGCTAGGCGCTGAGGGAATGTTCACGCCAAGGGCT	3660
Qy	3661	GAGTGTCCAGACACCTGCGCTTTCATTCTCCCAAGGCTGGGCGCTCGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGACACCTGCGCTTTCATTCTCCCAAGGCTGGGCGCTCGCTCCACCCCA	3720
Qy	3721	GGGCGAGCTTTCCTCACACAGAGCGCGGCTTTCATTCTCCCAATAGGAATAGTCCATCC	3780
Db	3721	GGGCGAGCTTTCCTCACACAGAGCGCGGCTTTCATTCTCCCAATAGGAATAGTCCATCC	3780
Qy	3781	CCAATTTGCCATTGTTCACCCCTTCGCGCTCCCTCTTTCGCTTCCACCCCCACCATTC	3840
Db	3781	CCAATTTGCCATTGTTCACCCCTTCGCGCTCCCTCTTTCGCTTCCACCCCCACCATTC	3840
Qy	3841	AGGTGAGAGACCTTAGAAGAGACCTCGGAGGCTTCTGGGAATTTGGAGTGAACCAAGGTGTG	3900
Db	3841	AGGTGAGAGACCTTAGAAGAGACCTCGGAGGCTTCTGGGAATTTGGAGTGAACCAAGGTGTG	3900
Qy	3901	CCCTGTACACAGGCGAGGACCTTCGACTCTGAGTGGGGTCCCTGTGGTCAAAATTGGGGG	3960
Db	3901	CCCTGTACACAGGCGAGGACCTTCGACTCTGAGTGGGGTCCCTGTGGTCAAAATTGGGGG	3960
Qy	3961	GAGGTGCTGTGGAGTAAATATACGAATATATGATTTTTCAGTTTGAATAAAAAA	4015
Db	3961	GAGGTGCTGTGGAGTAAATATACGAATATATGATTTTTCAGTTTGAATAAAAAA	4015

RESULT 15
 US-08-974-549A-343
 : Sequence 343, Application US/08974549A
 : Patent No. 6166178
 : GENERAL INFORMATION:
 : APPLICANT: Cech, Thomas R.
 : APPLICANT: Lingner, Joachim
 : APPLICANT: Nakamura, Toru
 : APPLICANT: Chapman, Karen B.
 : APPLICANT: Morin, Gregg B.
 : APPLICANT: Harley, Calvin B.
 : APPLICANT: Andrews, William H.
 : TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 : NUMBER OF SEQUENCES: 727
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, Eighth Floor
 : CITY: San Francisco

```

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTERT CDNA"

```

[illegible]

QY 121 GCCGCTGAGCACTTTCGTCGAGCGCTGAGGAGCCCAAGGAGCTGAGGAGTGAAGCGCGG 180
Db 121 GCCGCTGAGCACTTTCGTCGAGCGCTGAGGAGCCCAAGGAGCTGAGGAGTGAAGCGCGG 180
QY 181 GAGACCGGAGCTTTCGTCGAGCGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 240
Db 181 GAGACCGGAGCTTTCGTCGAGCGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 240
QY 241 AGCGGAGCG 300
Db 241 AGCGGAGCG 300
QY 301 CCGAGTCTGAGAGAGCTGTCAGAGCGAGCGAGCGAGAGAGTGTGAGCTTTCGAGCTTTCGAG 360
Db 301 CCGAGTCTGAGAGAGCTGTCAGAGCGAGCGAGCGAGAGAGTGTGAGCTTTCGAGCTTTCGAG 360
QY 361 GCTGCTGAGAGAGAGCG 420
Db 361 GCTGCTGAGAGAGAGCG 420
QY 421 CCGTCCCAACAGAGTGAACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 480
Db 421 CCGTCCCAACAGAGTGAACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 480
QY 481 CCGGCTGAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 540
Db 481 CCGGCTGAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 540
QY 541 GCGTCCCAACAGAGTGAACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 600
Db 541 GCGTCCCAACAGAGTGAACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 600
QY 601 TCAAGCCCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 660
Db 601 TCAAGCCCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 660
QY 661 CTGAGAACATAGAGCTGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 720
Db 661 CTGAGAACATAGAGCTGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 720
QY 721 GAGGCGCGGAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 780
Db 721 GAGGCGCGGAGAGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 780
QY 781 TGCCTCCGAGAGCGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 840
Db 781 TGCCTCCGAGAGCGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 840
QY 841 GCGTGAACAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAG 900
Db 841 GCGTGAACAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAG 900
QY 901 CACCTCTTTCGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 960
Db 901 CACCTCTTTCGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 960
QY 961 GAGACAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 1020
Db 961 GAGACAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 1020
QY 1021 CCGGCTGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAG 1080
Db 1021 CCGGCTGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAG 1080
QY 1081 GCGCTCTTTCGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 1140
Db 1081 GCGCTCTTTCGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 1140
QY 1141 GAGCATCTTTCGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 1200
Db 1141 GAGCATCTTTCGAGAGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAGCG 1200

QY 1201 GCCCAGCGCTACTGGCAAAATGGGCGCCCTGTTTCTGAGAGCTCTTGGGAAACCAAGCGCA 1260
Db 1201 GCCCAGCGCTACTGGCAAAATGGGCGCCCTGTTTCTGAGAGCTCTTGGGAAACCAAGCGCA 1260
QY 1261 GTGCCCCCTTACGAGAGTCTCTTCAAGACGACCTGCGCGAGAGCTGAGAGTCAAGCGAG 1320
Db 1261 GTGCCCCCTTACGAGAGTCTCTTCAAGACGACCTGCGCGAGAGCTGAGAGTCAAGCGAG 1320
QY 1321 AGCGGCTGCTGTTGCGCGGAGAGAGCGCGAGAGCTTGTGAGCGAGCGCGCGAGAGAGAG 1380
Db 1321 AGCGGCTGCTGTTGCGCGGAGAGAGCGCGAGAGCTTGTGAGCGAGCGCGCGAGAGAGAG 1380
QY 1381 CACAGACCCCGGCTGAGTGAAGTGTCTCCGCGACAGACAGAGCGCGCGAGAGAGTGA 1440
Db 1381 CACAGACCCCGGCTGAGTGAAGTGTCTCCGCGACAGACAGAGCGCGCGAGAGAGTGA 1440
QY 1441 CCGCTTTCGTCGAGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1500
Db 1441 CCGCTTTCGTCGAGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1500
QY 1501 CAAAGAACCGCGCTTCTTCAAGAACCAAGAAATTCATCTCTGAGAGACATGCGCA 1560
Db 1501 CAAAGAACCGCGCTTCTTCAAGAACCAAGAAATTCATCTCTGAGAGACATGCGCA 1560
QY 1561 GCTCTGCTGACAGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
Db 1561 GCTCTGCTGACAGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
QY 1621 GAGCCAGAGAGGTTGAGTGTGTTCCGAGCGCAGAGACCGCTGAGTGAAGAGATCTGAGC 1680
Db 1621 GAGCCAGAGAGGTTGAGTGTGTTCCGAGCGCAGAGACCGCTGAGTGAAGAGATCTGAGC 1680
QY 1681 CAAAGTTCGTCGACGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1740
Db 1681 CAAAGTTCGTCGACGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1740
QY 1741 TGTCAAGAGACCAAGTTCAAAGAACAGAGCTCTTTCCTTCAAGAGAGAGTGTGAGAG 1800
Db 1741 TGTCAAGAGACCAAGTTCAAAGAACAGAGCTCTTTCCTTCAAGAGAGAGTGTGAGAG 1800
QY 1801 CAAAGTTCGTCGACGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
Db 1801 CAAAGTTCGTCGACGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860
QY 1861 GGAAGAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAG 1920
Db 1861 GGAAGAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAG 1920
QY 1921 CTTCAATCCCAAGAGCTGAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAG 1980
Db 1921 CTTCAATCCCAAGAGCTGAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAGAGAGTCAAG 1980
QY 1981 CAGAACGTTTCGAG 2040
Db 1981 CAGAACGTTTCGAG 2040
QY 2041 CAGAGTCTCAACTCAAG 2100
Db 2041 CAGAGTCTCAACTCAAG 2100
QY 2101 CCGTGAAGATATCAAG 2160
Db 2101 CCGTGAAGATATCAAG 2160
QY 2161 GCGGCTGAGAGTGTCTTTCGAG 2220
Db 2161 GCGGCTGAGAGTGTCTTTCGAG 2220
QY 2221 GGAAG 2280
Db 2221 GGAAG 2280
QY 2281 TCGATATCCGTTGTCAG 2340

```

Db 2281 TCGGATGCGGTCGACGAAAGCGCGCCATG3GCACTCCGCAAGCCCTTCAAGAGCA 2340
QY 2341 CGTCTCTACCTGACAGACCTCAGCCGCAATGACAGAGTTCGAGGCTCAGCTGAGGA 2400
Db 2341 GGTCTCTACCTGACAGACCTCAGCCGCAATGACAGAGTTCGAGGCTCAGCTGAGGA 2400
QY 2401 GACAGCCCGCTGAGGAGATGCGCTGCTCATGACAGAGCTCCTCCATGATAGAGCCAG 2460
Db 2401 GACAGCCCGCTGAGGAGATGCGCTGCTCATGACAGAGCTCCTCCATGATAGAGCCAG 2460
QY 2461 CAGTGGCTCTTTCAGAGCTTCTCTACGCTTCAATGTCACACAGCCGTCGATCAAGG 2520
Db 2461 CAGTGGCTCTTTCAGAGCTTCTCTACGCTTCAATGTCACACAGCCGTCGATCAAGG 2520
QY 2521 CAGTGGCTCTTTCAGAGCTTCTCTACGCTTCAATGTCACACAGCCGTCGATCAAGG 2580
Db 2521 CAGTGGCTCTTTCAGAGCTTCTCTACGCTTCAATGTCACACAGCCGTCGATCAAGG 2580
QY 2581 CAGCTCTGACGAGGAGCATGAGAAACAAGCTGTTTGGGGATTCGAGGAGCGGCT 2640
Db 2581 CAGCTCTGACGAGGAGCATGAGAAACAAGCTGTTTGGGGATTCGAGGAGCGGCT 2640
QY 2641 GCTCTGCGTTCGAGGAGCATGAGAAACAAGCTGTTTGGGGATTCGAGGAGCGGCT 2700
Db 2641 GCTCTGCGTTCGAGGAGCATGAGAAACAAGCTGTTTGGGGATTCGAGGAGCGGCT 2700
QY 2701 CTTCTCTCAGAGACCTGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2760
Db 2701 CTTCTCTCAGAGACCTGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2760
QY 2761 GACAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2820
Db 2761 GACAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2820
QY 2821 GCGGCGGCGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2880
Db 2821 GCGGCGGCGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2880
QY 2881 GAGAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2940
Db 2881 GAGAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 2940
QY 2941 GCGGCTTCAAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3000
Db 2941 GCGGCTTCAAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3000
QY 3001 TCACAGGCTGTTTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3060
Db 3001 TCACAGGCTGTTTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3060
QY 3061 CAAGATCTCTCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3120
Db 3061 CAAGATCTCTCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3120
QY 3121 TCAGGAGGTTTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3180
Db 3121 TCAGGAGGTTTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3180
QY 3181 CTGCTACTCTCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3240
Db 3181 CTGCTACTCTCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3240
QY 3241 CGGCGCTCTCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3300
Db 3241 CGGCGCTCTCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3300
QY 3301 GACTGAGACCGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3360
Db 3301 GACTGAGACCGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3360
QY 3361 GCTGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3420

```

```

Db 3361 GCTGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3420
QY 3421 ACTGCGCTCAGACTTCAAGAACCATCTGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3480
Db 3421 ACTGCGCTCAGACTTCAAGAACCATCTGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3480
QY 3481 GAGCAGACACGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3540
Db 3481 GAGCAGACACGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3540
QY 3541 CACACCCAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3600
Db 3541 CACACCCAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3600
QY 3601 CAGTCCGCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3660
Db 3601 CAGTCCGCTGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3660
QY 3661 GAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3720
Db 3661 GAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3720
QY 3721 GGGCAGGCTTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3780
Db 3721 GGGCAGGCTTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3780
QY 3781 CAGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3840
Db 3781 CAGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3840
QY 3841 AGTGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3900
Db 3841 AGTGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3900
QY 3901 CCTGTACACAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3960
Db 3901 CCTGTACACAGGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 3960
QY 3961 GAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 4015
Db 3961 GAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAGTTCGAGGAG 4015

```

Search completed: October 30, 2004, 03:18:16
 Job time : 321 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 09:37:02 ; Search time 209 Seconds
(without alignments)
3849.823 Million cell updates/sec

Title: US-10-044-692-2

Perfect score: 5961
Sequence: 1 MPRAFCRAVSLRSHYRE.....TALEMANPALPSDEKTLID 1132

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 10.0, Fgapext 0.5
Delop 6.0, Delext 7.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US10044692/runat.28102004.103655.1383/app.query.fasta.1.1287
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10044692 @cgn2_1.1.89 @runat.28102004.103655.1383 -NCPUS=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5961	100.0	3396	3	US-08-974-549A-638 Sequence 638, App
2	5961	100.0	3396	3	US-08-974-549A-639 Sequence 639, App
3	5961	100.0	3396	3	US-08-974-549A-640 Sequence 640, App
4	5961	100.0	3396	3	US-08-974-549A-641 Sequence 641, App
5	5961	100.0	3396	3	US-08-974-549A-642 Sequence 642, App
6	5961	100.0	3396	4	US-09-721-456-638 Sequence 638, App
7	5961	100.0	3396	4	US-09-721-456-639 Sequence 639, App
8	5961	100.0	3396	4	US-09-721-456-640 Sequence 640, App
9	5961	100.0	3396	4	US-09-721-456-641 Sequence 641, App
10	5961	100.0	3396	4	US-09-721-456-642 Sequence 642, App
11	5961	100.0	3451	3	US-08-974-549A-721 Sequence 721, App
12	5961	100.0	3451	4	US-09-721-456-721 Sequence 721, App

13	5961	100.0	4015	3	US-08-851-843A-224 Sequence 224, App
14	5961	100.0	4015	3	US-08-974-549A-1 Sequence 1, Appl
15	5961	100.0	4015	3	US-08-854-050-224 Sequence 224, App
16	5961	100.0	4015	3	US-09-430-323-224 Sequence 224, App
17	5961	100.0	4015	3	US-09-572-423B-3 Sequence 3, Appl
18	5961	100.0	4015	3	US-09-128-354-1 Sequence 1, Appl
19	5961	100.0	4015	4	US-09-675-321-1 Sequence 1, Appl
20	5961	100.0	4015	4	US-09-052-919-1 Sequence 1, Appl
21	5961	100.0	4015	4	US-08-912-951-1 Sequence 1, Appl
22	5961	100.0	4015	4	US-09-733-294A-3 Sequence 3, Appl
23	5961	100.0	4015	4	US-09-402-181B-1 Sequence 1, Appl
24	5961	100.0	4015	4	US-09-721-456-1 Sequence 1, Appl
25	5961	100.0	4015	4	US-09-953-052-1 Sequence 1, Appl
26	5961	100.0	4015	4	US-09-465-491-1 Sequence 1, Appl
27	5961	100.0	4037	3	US-08-974-549A-343 Sequence 343, App
28	5962	99.8	4037	4	US-09-402-181B-343 Sequence 343, App
29	5962	99.8	4037	4	US-09-721-456-343 Sequence 343, App
30	5593.5	93.8	3855	3	US-08-974-549A-4 Sequence 4, Appl
31	5593.5	93.8	3855	4	US-08-912-951-4 Sequence 4, Appl
32	5593.5	93.8	3855	4	US-08-402-181B-4 Sequence 4, Appl
33	5593.5	93.8	3855	4	US-09-402-181B-4 Sequence 4, Appl
34	5579	93.6	4029	3	US-08-851-843A-173 Sequence 173, App
35	5579	93.6	4029	3	US-08-974-549A-292 Sequence 292, App
36	5579	93.6	4029	3	US-08-854-050-173 Sequence 173, App
37	5579	93.6	4029	3	US-09-430-323-173 Sequence 173, App
38	5579	93.6	4029	4	US-09-402-181B-292 Sequence 292, App
39	5579	93.6	4029	4	US-09-721-456-292 Sequence 292, App
40	3505	58.8	3496	4	US-09-042-460-1 Sequence 1, Appl
41	3134	52.6	1866	4	US-09-582-924B-11 Sequence 11, Appl
42	2789	46.8	51552	4	US-09-733-294A-30 Sequence 30, Appl
43	2782	46.7	4200	4	US-08-912-951-6 Sequence 6, Appl
44	2782	46.7	4321	4	US-09-402-181B-6 Sequence 6, Appl
45	2782	46.7	4335	3	US-08-974-549A-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-974-549A-638
Sequence 638, Application US/08/974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lindner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974.549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015889-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 638:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396 /note= "hTERT-encoding sequence employing
OTHER INFORMATION: alternative codon distributions for
OTHER INFORMATION: E. coli (all genes)"
US-08-974-549A-638
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-044-692-2 (1-1132) x US-08-974-549A-638 (1-3396)
QY 1 MeProrAAlaArproArGysaArgAlaValArSerLeuLeuArGSerHisTyrArgGlu 20
Db 1 ATGCCCGCGCGCGCGCTGCGCGAGCTGTCGCGAGCCATTATTCGCGAA 60
QY 21 ValLeuProLeuAlaThrPheValArGArgLeuGlyProGlnGlyTrrPArgLeuValGln 40
Db 61 GTGCTCCGCTGGCGACCTTTGTGCGCGCTGCGCGCGCGAGGCTGGCGCTGGTGCGAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysValProTrr 60
Db 121 CGCGGCGATCCGCGCGGCTTCCGCGCTGCTGCGAGAGTCCCTGGTGCTGCGCGTGG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysValLeuArgGlu 80
Db 181 GATGCGCGCGCGCGCGCGCGCGAGCTTTCGCGAGGTGAGCTGCTGAAAGAACTG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaValAsnValLeuAlaPheGly 100

241 GTGGCGCGCTGCTGCGAGCGCTGCGAAGCGCGCGAAGAAAGTGTGCGCTTGGC 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
Db 301 TTTGGCGCTGCTGAGTGGCGCGCGCGCGCGCGCGCGGAAAGCTTTACCAACGAGCTGGC 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValatrrGlyLeuLeu 140
Db 361 AGCTATCTGCGAACAACGTGACCAATGCGCTGCGCGAGCGCGCGCGGAGCTGCTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 421 CTGCGCGCGCGCGAGATGATGTGCTGGATCTGCTGCGCGCTGCGCGCTGTTGG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuValAla 180
Db 481 CTGGTGGCGCGCGAGCTGCGCTATCAGGTGCGCGCGCGCGCTGTATCAGCTGGCGCG 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 541 GCGACCCAGCGCGCGCGCGCGCGCATGCGAGCGCGCGCGCGCGCTGGGGCTGGCGA 600
QY 201 ArgAlaTrrPAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 601 CGCGCTGGAAACATATAGCTGCGCGAAGCGCGCTGCGCTGGCGCTGCGCGCGCGG 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProAlaProArgArg 240
Db 661 GCGCGCGCGCGCGCGCGCGCGAGCGCGAGCGCGAGCTGCGCTGCGAAGCGCGCGCG 720
QY 241 GlyAlaAlaProGlyProGlyLuarGThrProValGlyGlnGlySerTrrAlaHisProGly 260
Db 721 GCGCGCGCGCGCGAAGCGGAACGCAACCGCGCTGGCGCGAGGCGAGCTGGCGCATCGG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
Db 781 CCGACCGCGCGCGCGAGCATGCGCGCTTTGCGTGTCAGCCCGCGCGCGCGCGA 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 841 GAAGCGAAGCGCTGGAAGCGCGCTGAGCGCGCGCGCGCATATGCGAGCTGGAGC 900
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrrPAsnThrPro 320
Db 901 CGCGAGCATCATGCGCGCGCGCGCGCGAGCACACCGCGCGCGCGCGCGGATACCCG 960
QY 321 CysProProValTrrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
Db 961 TCGCGCGCGGTATGCGGAAACCAAACTTTCTGTATAGCAGCGCGCATTAAGAACAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuAlaArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1021 CTGCGCGCGAGCTTCTGCTGAGCAGCTGCGCGCGAGCTACCGCGCGCGCGCTG 1080
QY 361 ValGluThrIlePheLeuGlySerArgProTrrPMeProGlyThrProArgArgLeuPro 380
Db 1081 GTGGAAACATTTTCTGAGGACCGCGCGCGCTGATGCGGAGACCCCGCGCGCTGCG 1140
QY 381 ArgLeuProGlnArgTrrGlnMetArgProLeuPheLeuGlnLeuGlnLysHis 400
Db 1141 CGCTGCGCGACGCTATGCGAGATGCGCGCTGTTCTGGAACCTGCTGGGCAACCAT 1200
QY 401 AlaGlnCysProTrrGlyValLeuLeuLysThrHisCysProLeuAlaArgAlaValThr 420
Db 1201 GCGCAGTGGCGGTATGCGTGTGCGAAGAACCATATGCGCGCTGCGCGCGGAGACC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGln 440
Db 1261 CGCGCGCGCGCGGTGCGCGCGCGCGGAAACCGCGAGGAGAGCTGGCGCGCGCGAAGA 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrrGln 460

Db 1321 GAAGATACCGATCCGCGCGCTGGTGCAGTCTGCCGACAAATAGACAGCCCTGGTCCAG 1380
 QY 461 VAIITRYGlyPheValArgAlaCySLeuAArgLeuValProProGlyLeuThrProGlySer 480
 Db 1381 GGTGTGGCTTTGTGCGCGCGCTGCCCGCCCGCTGGTGCAGCCCGCGCTGGTGGGACAC 1440
 QY 481 ARGHISaenGlyArgArgPheLeuArgAntThrLySLeuPhe11eSerLeuGlyLySHis 500
 Db 1441 CCGCATTAACGAAACCGCGCTTTCTGGCGCAACCAAAAATTTATTTAGCTGGGCAAAACAT 1500
 QY 501 AAlaLySLeuSerLeuGlnGlnLeuThrTrpLySMeSerValArgAspCyAla1TrpLeu 520
 Db 1501 GCGAAACCTGAGCTGCGAGAACCTGCACTCGAAATAGAGCGTGCAGATTGGCCGCTGGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCySValProAlaAlaGlnHisArgLeuArgGlnGln 540
 Db 1561 CCGCCACAGCCCGCGCGCTGGCTGGCGCGCGCGCAATCGCTGGCGCAAGAAAT 1620
 QY 541 LeuAlaLySLeuPheLeuH1eTrpLeuMetSerVal1TrpValValGlnLeuLeuArgSerPhe 560
 Db 1621 CTGGCGAAATTTCTGCATTGGCTGATGAGCGTGTATGTGTGTAAGTGTGCTGGCGAGCTTT 1680
 QY 561 PheTyTrVal1ThrGlnThrThrPheGlnLySAsnArgLeuPhePheTyTrArgLySVal 580
 Db 1681 TTTTATGTACCGAAACCACTTTTCAGAAAAACCGCTGTTTATGTGCAAAAAGCGTG 1740
 QY 581 TrpSerLySLeuGlnSer11eGly11eArgGlnHisLeuLySArgValGlnLeuArgGln 600
 Db 1741 TGGAGCAAACTGACAGCATTTGGCATTCGCGACCACTGAACCGCTGACGCTGGCGCA 1800
 QY 601 LeuSerGlyAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGACGGAAGCGGAATGCGCGCAAGCATTCGCGAAAGCGCGCGCGCTGCTGACAGCCCG 1860
 QY 621 LeuArgPhe11eProLySProAspGlyLeuArgPro11eValAsnMetAspTyTrVal 640
 Db 1861 CTGGCGTTTATTCGGAACCGGATGCGCTGGCGCGCATTTGTGAACATGATTAATGTGTG 1920
 QY 641 GlyAlaArgThrPheArgArgGlnLySArgAlaGlnArgLeuThrSerArgValLySAla 660
 Db 1921 GCGCGCGCGCACTTTGCGCGCGCAAAACCGCGGAACGCGCTGACCGCGCGGAAGCG 1980
 QY 661 LeuPheSerValLeuAsnTyTrGlnArgAlaArgArgProGlyLeuLeuGlnAlaSerVal 680
 Db 1981 CTGTTTAGCTGTGTAACCTAGAACCGCGCGCGCGCGCGCTGCTGGGCGCGAGCCGTG 2040
 QY 681 LeuGlyLeuAspAsp11eHisArgAla1ArgArgThrPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGGCGCTGGAATTTATTCATGCGCGCTGGCGCACTTTGTGCTGGCGCGCGCGCAG 2100
 QY 701 AspProProProGlyLeuTyTrPheValLySValAspValThrGlyAla1ArgPheThr11e 720
 Db 2101 GATCCCGCCCGCGAACCTGATTTTGTGAAGTGTGATGACCGCGCGCGATGATGATCAAT 2160
 QY 721 ProGlnAspArgLeuThrGlnVal11eAlaSer11e11eLySProGlnAsnThrTyTrCys 740
 Db 2161 CCGCAGAGATGCGCTGACCGAATGATTTGGAGCATTTAAACCGCAACCACTATTCG 2220
 QY 741 ValArgArgTyTrAlaValAlaGlnLySAlaAlaHisGlyHisValArgLySAlaPheLyS 760
 Db 2221 GTGGCGCGCTATGCGGTGTGAGAAAGCGCGCATGGCCATGTGCGCAAAAGCGTTTAA 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyTrMetArgGlnPheValAlaHisLeu 780
 Db 2281 AGCCATGTAGACACCTGACCGATCTGACCGCTATATGTGCCAGATTTTGGGGCGCATCTG 2340
 QY 781 GlnGlnThrSerProLeuArgAspAlaVal11eGlnGlnSerSerSerLeuAsnGln 800
 Db 2341 CAGGAACCAAGCCCGCTGCGCGCATGCGGTGTGATTTGAACAGACGACCACTGAACGA 2400
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgGlie 820
 Db 2401 GCGAGCAGCGCGCTGTTTGTATGTGTTTCTGCGCTTATGTGCAATGCGGTGGCGCAT 2460

QY 821 ArgGlyLySLeuTyTrValGlnCysGlnGly11eProGlnGlySer11eLeuSerThrLeu 840
 Db 2461 CCGCGCAAAAGCTATGTGTGACGTGCGAGGGCATTTCCGCAAGGAGAGATTTGAGCACCTCTG 2520
 QY 841 LeuCySLeuLeuCyTyTrGlyAspMetGlnAsnLySLeuPheAlaGly11eArgArgAsp 860
 Db 2521 CTGTGACGCTGTGTATGTGCGATATGGAACCAAACTGTTTGGCGGCAATTTGGCGCGCAT 2580
 QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 Db 2581 GCGCTGCTGCTGCGCTGTGTGATATTTCTGCTGTGAGACCCGCACTGACCCATGCG 2640
 QY 881 LySThrPheLeuArgThrLeuValArgGlyValProGlnTyTrGlyCySValValAsnLeu 900
 Db 2641 AAAACCTTTCTGCGCAACCTGTGTGCGCGCGCTGGCGGAATATGCTGCTGTGTAACCTG 2700
 QY 901 ArgLySThrValAsnPheProValGlnAspGlnAlaLeuGlyGly1TrpAlaPheVal 920
 Db 2701 CCGCAAAACCTGTGATCTTTCCGGTGGAAATGAAGCGCTGGCGGCAACCGCTTTGTG 2760
 QY 921 GlnMetProAlaHisGlyLeuPheProTrpCySgLyLeuLeuLeuAspThrArgThrLeu 940
 Db 2761 CAGATGCGGCGCGCATGGCGCTGTTCCGTGTGCGCGCTGCTGCTGATACCGGCACTCTG 2820
 QY 941 GlnValGlnSerAspTyTrSerSerTyTrAlaArgThrSer11eArgAlaSerLeuThrPhe 960
 Db 2821 GAAGTGCAGAGCATTTATAGCATAGCTATGCGCGCACACAGATTTCCGCGCAAGCTTCTT 2880
 QY 961 AsnArgGlyPheLySAlaGlyValArgAsnMetArgArgLySLeuPheGlyValLeuArgLeu 980
 Db 2881 AACCGCGGCTTTAAAGCGGGCGGCAACATGCGCCGCAAACTGTTTGGCGTGTGCGCGCTG 2940
 QY 981 LySHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCySThrAsn 1000
 Db 2941 AAATGCCATAGGCTGTTCTGTGATCTGACAGTGAAACAGCTGCACAGCCGTGTGCACAAAC 3000
 QY 1001 11eTyTrLyS11eLeuLeuLeuGlnAlaTyTrArgPheHisAlaCySValLeuGlnLeuPro 1020
 Db 3001 ATTTATTAATTTCTGCTGCTGAGGCGGTATTCCTTTTCATGCTGCTGCTGCAAGCTGCGG 3060
 QY 1021 PheHisGlnGlnVal1TrpLySAspProThrPhePheLeuArgVal11eSerAspThrAla 1040
 Db 3061 TTTTATGACAGAGGTGTGGAACCAACCACTTTTTCGCGGTATTTAGCATACCGCG 3120
 QY 1041 SerLeuCyTyTrSer11eLeuLySAlaLySAsnAlaGlyMetSerLeuGlyAlaLySgLy 1060
 Db 3121 AGCTGTGCTATAGCATTTCTGAACGAAACCGCGGCGATGAGCTGGGCGCGGAAGGC 3180
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValAlaGlnTrpLeuCySHisGlnAlaPheLeuLeu 1080
 Db 3181 GCGGCGGGCGCGCTGCGAGCAAGGGGTGAGTGTGTGTCATACAGCGCTTTCTGCTG 3240
 QY 1081 LySLeuThrArgHisArgValThrTyTrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3241 AAATGACCGCGCATTCGCTGATATGTGCGCGCTGCGGCAAGCGCTGGCAACCGGCGAG 3300
 QY 1101 ThrGlnLeuSerArgLySLeuProGly1TrpThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 Db 3301 ACCCAGCTGAGCGCGAAACCTGCGGGGCAACCACTGACCGCGCTGGAACGCGGCGAAC 3360
 QY 1121 ProAlaLeuProSerAspPheLySThr11eLeuAsp 1132
 Db 3361 CCGGCGCTGCGAGCATTTTAAACCACTTCTGAT 3396

RESULT 2

US-08-974-549A-639
 ; Sequence 639, Application US/08974549A

; Patent No. 616178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 639:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3396 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..3396
 OTHER INFORMATION: /note="hTERT-encoding sequence employing
 OTHER INFORMATION: alternative codon distributions for
 OTHER INFORMATION: enteric bacteria (high expressing
 OTHER INFORMATION: genes)"

US-08-974-549A-639
 Alignment Scores:
 Pred. No.: 0
 Score: 5961.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 3
 Gaps: 0
 US-10-044-692-2 (1-1132) x US-08-974-549A-639 (1-3396)
 QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgInu 20
 DB 1 ATGGCGCGTCTCCGGGTGGCGTCTGCTTCCCTGCTCCGTTCCACACCTGAA 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
 DB 61 GTTCTGCCGCTGCTACCTTCGTTGCTGCTGCGGTCGCGAGGGTGGCTGCTGAG 120
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 DB 121 CCGTGACCCGCGCTGCTTCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGlnLeu 80
 DB 181 GACGCTCGTCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 81 ValAlaArgValLeuGlnArgLeuGlyGlnArgGlyAlaValAsnValLeuAlaPheGly 100
 DB 241 GTTGCTCGTCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 101 PheAlaLeuLeuAspGlyValAlaArgGlyProProGlnAlaPheThrThrSerValArg 120
 DB 301 TTCGCTCTGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
 DB 361 TCCTACTGCGGACACCGCTTACCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 DB 421 CTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlyLeuGlyAla 180
 DB 481 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
 DB 541 GCTACCCAGCTCGTCCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 201 ArgAlaTyrPheHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB 601 CCGTCTGTAACCACTCCGTTGTAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB 661 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrPheHisProGly 260
 DB 721 GGTGCTGCTCCGGAACCGGAACGTAACCCGGTGGTCAAGGGTTCCTGGGCTCACCCGG 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 DB 781 CGTACCGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 DB 841 GAGGTACTCTCCCTGGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrPhePro 320

```
Db 901 CCGTCAGCACAGCTGGTCCGCGCTCCACCTCCGCGCTCCGCGGTCCGCGGACACCCCG 960
Qy 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyValAspLysGluGln 340
Db 961 TCCCGCCGCGGTTTACCGCTAAACCAACATCTCTCTACTCTCCGCGTACCAAGAACAG 1020
Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyValArgArgLeu 360
Db 1021 CTGGCGTCCGCTCTCTCTGCTGCTCTCTGCGGCTCCGCTGACCGGTGCTGCTGCTCG 1080
Qy 361 ValGluThrLlePheLeuGlySerArgProTyrPheProGlyLysProArgArgLeuPro 380
Db 1081 GTTGAACACATCTCTCTGGGTTCCCGCTCCGCGATCCCGGTACCCCGGCTGCTCCCG 1140
Qy 381 ArgLeuProGlnArgTyrLTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400
Db 1141 CGCTGCGCGAGCGTTACTGGCAGATGCGCTCCGCTGCTGGAACCTGGGGTAAACCAAC 1200
Qy 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db 1201 GCTCAGTGCCTGACCGGTGTTCTGCTGAACCACTGCGCGCTGCTGCTGCTGCTTACC 1260
Qy 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
Db 1261 CCGCGCTGCTGGTGTGGCGCTCGTGAACCAACGACGGGTTCGCTGCTGCTCGGAAAGAA 1320
Qy 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
Db 1321 GAAAGAACCGACCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
Db 1381 GTTTACGGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheLleSerLeuGlyLysHis 500
Db 1441 CCGTCACACGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Qy 501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTyrPhe 520
Db 1501 GCTAAACCTGCTGAGGAACTGACCTGAAATATCCGTTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlu 540
Db 1561 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Qy 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1621 CTGGCTAAATTCCTGCACTGGCTGATGCTCGTTTACGTTGAACTGCTGCTGCTCTTC 1680
Qy 561 PheTyrValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1681 TTCTACGTTACCGAAACCACTTCAGAAACCGGCTGTTCTTCTTACCGTAAATCCGTT 1740
Qy 581 TrpSerLysLeuGlnSerLleGlyLleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db 1741 TGGTCCAACTGACGATCCGATCCGCTGACCACTGAAACGTTTACAGCTGCGCTGAA 1800
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 CTGTCCGAAGCTGAAGTTCGTGACGACCGTGAAGCTGCTCCGCTGCTGCTGCTCCGT 1860
Qy 621 LeuArgPheLleProLysProAspGlyLeuArgProLleValAsnMetAspTyrValVal 640
Db 1861 CTGCGTTTATCCCGAAACCGACCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Qy 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1921 GGTGCTCGTACCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Qy 661 LeuPheSerValLeuLeuSerTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1981 CTGTTCTCCGTTCTGAACACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Qy 681 LeuGlyLeuAspAspAlaLleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGTCTGAGACATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Qy 701 AspProProProGluLeuTyrPheValLysValAspValThrGlyValAlaTyrAspThrLle 720
Db 2101 GACCCGCGCGCGAAGCTGACTTCCGTTAAAGTTGACGTTACCGGCTGCTTACGACACCATC 2160
Qy 721 ProGlnAspArgLeuThrGluValLleAsnSerLleLleLysProGlnAsnThrTyrCys 740
Db 2161 CCGCAGAACCGTTACCGAAAGTTATCGCTTCAATCATCAACCGGACGAAACCTACTGCTC 2220
Qy 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2221 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2281 TCCACGTTTCCACCTGACCGACCTGACCGCTGACCGCTGACCGCTGACCGCTGCTGCTG 2340
Qy 781 GlnGluThrSerProLeuArgAspAlaValValLleGlnGlnSerSerSerLeuLeuGln 800
Db 2341 CAGGAACCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLle 820
Db 2401 GCTTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyLleProGlnGlySerLleLeuSerThrLeu 840
Db 2461 CCGTGAATTCCTACGTTACGATCCAGGCTATCCGACGGGTTCATCTGTCACACCTG 2520
Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyLleArgArgAsp 860
Db 2521 CTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2641 AAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Qy 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2701 CGTAAACCGTGTAACTTCCCGGTGAAAGCAAGCTCTGGGTGCTACCCGCTTTCGTT 2760
Qy 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCGGCTCAGAGTGTGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2800
Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerLleArgAlaSerLeuThrPhe 960
Db 2821 GAAGTTCAGTCCGACTACTCTCTTACGCTGCTACTCATCGCTGCTTCCCTGACCTTC 2880
Qy 961 AsnArgGlyPheLysAlaGlyValArgAsnMetArgLysLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGTGTTCGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValLysThrAsn 1000
Db 2941 AATATCCACTCTCTCTCTGACCTGACGTTAACTCCCTGACACCGTTCGACCAAC 3000
Qy 1001 IleTyrLysLleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTACAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Qy 1021 PheHisGlnGlnValTTrpLysAsnProThrPheLeuArgValLleSerAspThrAla 1040
Db 3061 TTCCACACGACGTTTGGAACCAACCGACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
```



```
|||||
Db 481 TTGGTGTCTCATCTTGTGCTTATCAAGTTGTGGTCCACCATGTGTATCAATGGGTGCT 540
Qy 181 ALaThrGlnAlaArgProProProHiSaIaSerGlyProAlaArgArgLeuGlyCybeGlu 200
Db 541 GCTCTCAAGCTAAGCCACACCATCTTGTGTCCAGAAAGAAATGGGTGTGA 600
Qy 201 ArgAlaTTPaenHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 601 AGAGCTTGAATCATCTTGTGTAGAGAGCTGTGTCCAATGGGTTTGCACGCTCAAGT 660
Qy 221 ALaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProGlyArgProArgArg 240
Db 661 GCTAGAAAGAGGGGTGTGTCTCTCTAGATCTTTGGCATTTGCCAAAAAGACCAAGAGA 720
Qy 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
Db 721 GGTGTGTCTCCAGAACCAAGAAAGAACTCAGTTGGTCAAGGTTCTTGGGCTCATCCAGGT 780
Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
Db 781 AGAAGTAAAGGTCCATCTGATAGAGGTTTTGTGTGTTTCTCCAGCTAGACCACTGA 840
Qy 281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 841 GAAGTACTTCTTTGGAAGGTGCTTGTCTGTGTACTAGACATTCATCCATCTGTGGT 900
Qy 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro 320
Db 901 AGACAAACATCATGCGTGTCCACCATCTCTTAAACCAACCAAGACATGGGATCTCTCA 960
Qy 321 CysProProValTyrAlaGluThrIleHisIlePheLeuTyrSerSerGlyAspLeuGluGln 340
Db 961 TGTCCACCAAGTTATGCTGAACCTAAACATTTTGTATTTCTTGTGGATTAAGAACAA 1020
Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1021 TTGAGACATCTTTTGTGTCTTCTTGAAGACATCTTTGACCTGGGTCAAGAGATTG 1080
Qy 361 ValGluThrIlePheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
Db 1081 GTTGAACATATTTTGTGGTCTTGAACATGGAACGAGTACTCCAAAGATTTGCA 1140
Qy 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuGlyAsnHis 400
Db 1141 AGATTGCCCAAGAAATATTTGGCAATGAAGACATGTTTGGAAATGTGGGTAATCAT 1200
Qy 401 AlaGlnCysProTyrGlyValLeuLeuLeuYsThrHisCysProLeuArgAlaAlaValThr 420
Db 1201 GCTCAATGTCCATATAGTGTGTGTGTGAAGAACTCATTTGCCATTAGAGCTGTCTTACT 1260
Qy 421 ProAlaAlaGlyValCysAlaArgGluLeuYsProGlnGlySerValAlaAlaProGluGlu 440
Db 1261 CCAGCTGCTGGGTGTGTGTGCTAGAGAAAAACCAAGAGTTCTGTGTGCTCCAAAGAAA 1320
Qy 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
Db 1321 GAAGTACTGATCCAAAGAAATGGTTCATATTTGGAACCAACATTTCTTCCATGGCAA 1380
Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrProGlySer 480
Db 1381 GTTATGTGTTTGTGTAGAGCTTGTGTGAAGATGCTTCCACCAAGTTTGTGGGTTCT 1440
Qy 481 ArgHisaGlnGluArgArgPheLeuArgAsnThrIleYsPhePheIleSerLeuGlyIleYsHis 500
Db 1441 AGACATAATGAAGAAAGATTTTGTGAAGAAATATAAAAAATTAATTTCTTGGGTAAACAT 1500
Qy 501 AlaIleYsLeuSerLeuGlnGluLeuThrTTPYsMetSerValArgAspCysAlaThrLeu 520
Db 1501 GCTAAATTTGTTCTTCCAAAGAAATGACTTGAAAGATGCTGTATGAGATTGTGCTGGTTG 1560
Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGluIle 540
|||||

Db 1561 AGAAGATCTCCAGGTTGTGTGTGTCTCCAGCTGTAACATAGATTGAGAGAAATTT 1620
Qy 541 LeuAlaYsPheLeuHisTTPLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
Db 1621 TTGGCTAAATTTTGCATTTGGTTGATGTCTGTGTATGTGTGAATTTGTAATCTTTT 1680
Qy 561 PheTyrValThrGluThrThrPheGlnHisAsnArgLeuPhePheTyrArgYsSerVal 580
Db 1681 TTTTATGTACTGAACATCACTTTCAAAAAATAGATTGTTTTTTATAGAAAAATCTGTT 1740
Qy 581 TTPSerYsLeuGlnSerIleGlyIleArgGlnHisIleLeuYsAlaGlyGlnLeuArgGlu 600
Db 1741 TGTCTAAATTTGCATCTATTTGTATTTAGACAAATTTGAAAGAGTTCAATTAGAGAA 1800
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 TTGCTGAAGCTGAAGTTAGCAACATAGAGACCTAGACCAAGCTTTGTGTACTTCTAGA 1860
Qy 621 LeuArgPheIleProYsProAspGlyLeuArgProIleValaAsnMetAspTyrValVal 640
Db 1861 TTGAGATTTATTCAAAAACAGATGGTTTGAAGCAATTTGTAATATAGATTATGTTGTT 1920
Qy 641 GlyAlaArgThrPheArgArgGluLeuArgAlaGluArgLeuThrSerArgValYsAla 660
Db 1921 GGTCTAGAACTTTTGAAGAGAAAGAAAAAGCTGAAGATTTGACTTCTAGAGATTAAAGCT 1980
Qy 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1981 TTGTTTCTGTTTGAATATTAAGAAAGCTAGAAAGCCAGGTTTGTGGGTCTGTGTT 2040
Qy 681 LeuGlyLeuAspAspIleHisArgAlaTTPArgThrPheValLeuArgValArgAlaGln 700
Db 2041 TTGGGTTTGAATATTAATCAATAGAGCTTTGAGAACTTTTGTGTTGAAGTTAGAGCTAA 2100
Qy 701 AspProProProGluLeuTyrPheValIleYsAlaAspValThrGlyAlaTyrAspThrIle 720
Db 2101 GATCCACACACAGAAATGTATTTTGTAAAGTTATGTATCTGAGTCAATAGATCATATT 2160
Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleYsProGlnAsnThrTyrCys 740
Db 2161 CCACAGATTAATGACAGAAAGTTATGCTTCTATATTAATTAACCAACAAATACATTAATGT 2220
Qy 741 ValArgArgTyrAlaValAlaValGlnYsAlaHisIleGlyHisValArgYsAlaPheYs 760
Db 2221 GTTAGAAGATATGCTGTTGTTCAAAAGCTGCTCATGTGTATGAGAAAGCTTTTAA 2280
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
Db 2281 TCTCATGTTTCTACTTTGACATGATTGGCAACATATATGAGACAAATTTGTGCTCATTTGG 2340
Qy 781 GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu 800
Db 2341 CAAGAACTTCTCATTAAGAGATGCTGTGTATGAAACAATCTTCTTCTTGATGATA 2400
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2401 GCTTCTTGTGTTGTTGTAAGTTTATTTTGAATTTATATGTGTATCATAGCTGTATGAAAT 2460
Qy 821 ArgGlyYsSerTyrValGlnCysGlnGlyIleProGlnGlySerTTPLeuSerThrLeu 840
Db 2461 AGAGGTAAATCTTATGTTCAATGTCAAGGTATTCACAAAGGTTCTAATTTTGTCACTTTG 2520
Qy 841 LeuYsSerLeuCysTyrGlyAspMetGlnAsnYsLeuPheAlaGlyIleArgArgAsp 860
Db 2521 TTGTGTTCTTGTGTATGAGGATATGAGAAATAAATTTGTTGCTGTATTAAGAGAT 2580
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisIleLeuThrHisAla 880
Db 2581 GGTGTTGTTGTAAGATTTGTTGATGATTTTGTGTTGTTTGTCTCAATTTATACATACCT 2640
Qy 881 YsThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValaAsnLeu 900
Db 2641 AAACTTTTGTGAAGACTTGTGTATGAGGTGTCCAGAAATATGTGTGTGTATTAATTTG 2700
|||||
```

QY 901 ArgLysThrValIAsnProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
| | | | |
Db 2701 AGAAAAAGCTGTTGTTAATTTTCCAGTTGAAGATGAAGCTTTGGGTGGTACTCTTTGTT 2760
| | | | |
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
| | | | |
Db 2761 CAAATGCCAGCTCATGGTTGTTTCCATGGTGTGGTTGTTGTTGGATCTAGCACTTTG 2820
| | | | |
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
| | | | |
Db 2821 GAAGTTCATCTGATTAATTTCTTATAGCTAAGCTTCATTAGAGCTTCCTTTGACTTT 2880
| | | | |
QY 961 AsnArgGlyPheLeuAlaGlyArgAsnMetArgArgLeuPheGlyValLeuArgLeu 980
| | | | |
Db 2881 AATAGAGGTTTAAAGCTGGTGAAGATTAAGAGAGAAATTTTGGTGTGTTGAGATTG 2940
| | | | |
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
| | | | |
Db 2941 AATGTCATCTTTGTTGTTTGGATTGCAAGTTAATTTCTTCCAAAGCTGTTGTTACTAT 3000
| | | | |
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
| | | | |
Db 3001 AATTATTAATTTGTTGTTGCAAGCTTAATGATTTTCATGCTTGTGTTGCAATTGCCA 3060
| | | | |
QY 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
| | | | |
Db 3061 TTTTCATCAACAGGTTTGAAGAAATTCACACTTTTGGAGGTTAATTTTCATGACTGCT 3120
| | | | |
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGly 1060
| | | | |
Db 3121 TCTTTGTTGTTATTTATTTTGAAGCTAATAATGCTGGATGCTTTGGGTGCTAAAGGT 3180
| | | | |
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
| | | | |
Db 3181 GCTGCTGGTCCATTCATCACTGAACCTGTCATGTTGTCATCAAGCTTTTGTGTTG 3240
| | | | |
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
| | | | |
Db 3241 AATATGACAGACATAGAGTTCTTATGTTCCATGTTGGTCTTTGAGAACCTGCTCAA 3300
| | | | |
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
| | | | |
Db 3301 ACTCAATTCGTCTAGAAATTCGACAGTACTACTTTGACGCTTTGGAAGCTGCTCTAAT 3360
| | | | |
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
| | | | |
Db 3361 CCAGCTTGGCATTGATTTTAAACTAATTTTGAT 3396
| | | | |
RESULT 4
US-08-974-549A-641
Sequence 641. Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 641:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396 /note= "HRT-encoding sequence employing
OTHER INFORMATION: alternative codon distributions for
OTHER INFORMATION: yeast (high expressing genes)"
US-08-974-549A-641
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-044-692-2 (1-1132) x US-08-974-549A-641 (1-3396)
QY 1 MetProAlaIAsnProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 20
| | | | |
Db 1 ATGCCAAGAGCTCCAAAGATGTAAGCTGTTGATCTTTGATCTCACTAAGAGAA 60
| | | | |
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPArgLeuValGln 40
| | | | |

```

Db      61 GTTTGGCATTTGGTACTTTCGTTAGAGATTGGGCTCCAGAGTTGGAGATTGGTCA 120
Qy      41 ArgGlyAspProAlaIlePheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
Db      121 AGAGGTGACCCAGCTGCTTTCAGAGCTTGGTGCATAGTTGGTGTGTTGCTCATGG 180
Qy      61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
Db      181 GACGCTAGACCAACCAAGCTCTCCATCTTTCAGACAGATTCTTGTGTAAGAAATTG 240
Qy      81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaIleValAsnValLeuAlaPheGly 100
Db      241 GTTGTAGAGTTTTCAAAGATTGTGTGTAAGAGGCTAAGAACGTTTGGCTTCGGT 300
Qy      101 PheAlaLeuLeuAspGlyAlaArgGlyValProProGlnAlaPheThrSerValArg 120
Db      301 TTCGCTTGTGTGACGCGTCTAGAGGTGGTCCACCAAGAGCTTTCATCTTCTGTAGA 360
Qy      121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrpGlyLeuLeu 140
Db      361 TCTTACTTCCAAACACCTGTACTGACGCTTGAAGAGTTCTGGTCTTGGGGTTTGTG 420
Qy      141 LeuArgArgValGlyAspAspValLeuValIleLeuLeuAlaArgCysAlaLeuPheVal 160
Db      421 TTGAGAAAGAGTTGGTGAACAGCTTTTGGTCACTTGTGGTAGAATGTCTTGTGCTT 480
Qy      161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db      481 TTGGTGTCTCCATCTTGTGCTTACCAAGTTGTGTGCACATGTGACCAATTTGGTGTG 540
Qy      181 AlaThrGlnAlaArgProProProIleAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db      541 GCTACTCAAGCTAGACACCAACCAACGCTTCTGGTCCAGAAAGAAATTGGGTTGTGA 600
Qy      201 ArgAlaAlaTrpAsnIleSerValAlaArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
Db      601 AGAGCTTGGAAACCATCTGTAGAGAGCTGGGTGTTCCATTGGGTTTGCACGCTCCAGGT 660
Qy      221 AlaAlaArgArgArgGlyValSerAlaSerAlaSerArgLeuProLeuValArgProArgArg 240
Db      661 GCTAAGAAAGAGGTGTCTGTCTGTAGACTTGTGCTTGTGCTCCAAAGAGACCAAGAA 720
Qy      241 GlyAlaAlaProGlnProGlnArgThrProValGlnGlySerThrAlaIleProGly 260
Db      721 GGTGCTGCTCCAGAACCAAAAGAACTCCAGTTGGTCAAGGTTCTTGGGCTCAACCGGT 780
Qy      261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
Db      781 AGAAGCTAGAGGTCCATCTGACAGAGGTTCTGTGTTGTTCTCCAGCTAGACCAAGCTGA 840
Qy      281 GlnAlaAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgIleSerHisProSerValGly 300
Db      841 GAAGCTACTTCTTGTGAAAGGTCTTGTGTCTGTAGTCTAGACACTTCAACCATCTGTGTGT 900
Qy      301 ArgGlnIleHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
Db      901 AGACAAACACGAGCTGCTCCACATTTACTTCTAGACCAACCAAGACCAAGGAGACTCCA 960
Qy      321 CysProProValTyrAlaGlnThrIleHisPheLeuTyrSerSerGlyValAspGlyGln 340
Db      961 TGTCCACCAAGTTTAAAGCTAAAGCACTTCTGTACTTCTTGGTGAACAAGAACAA 1020
Qy      341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db      1021 TTGAGACCAATCTTCTTGTGTCTTCTTGTGAGCCATCTTGACTGGTCTGAAGATTG 1080
Qy      361 ValGlnThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
Db      1081 GTTGAACATATTTCTTGGGTTCTAGACATGAGATCCAGGTACTCCAAAGAAATTGGCA 1140
Qy      381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
|||
Db      1141 AGATTGCCAAGAAATCTGGCAAAATGAGACCATTTGTTCTTGGAAATTGTTGGTAAACAC 1200
Qy      401 AlaGlnCysProTyrGlyValLeuLeuIleYThrHisCysProLeuArgAlaAlaValThr 420
Db      1201 GCTCATGTCCATAGCGGTTTGTGTAAGACTCTGTCCATTTAGAGCTGCTGTACT 1260
Qy      421 ProAlaAlaGlyValCysAlaArgGlnIlePheProGlnGlySerValAlaAlaProGlnGln 440
Db      1261 CCAGCTGCTGGTGTGTGTGCTAGAGAAAGACCAAGGTTCTGTGCTGCTCCAGAGAA 1320
Qy      441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db      1321 GAAGACACTGAACCAAGAAAGATTGGTTCAAATTTGTGAACAACACTTCTTCCATGGCAA 1380
Qy      461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db      1381 GTTTACGGTTTGTGTAAGACTTGTGTGAAGATTGGTTCCACAGGTTTGTGGGTTCT 1440
Qy      481 ArgHisAsnGlnArgArgPheLeuArgAsnThrIleValSerLeuGlyIleHis 500
Db      1441 AGACAAACAAAGAAAGATTCTTGAGAAACCTAAGAAATTCTTCTTGGGTAAGCAC 1500
Qy      501 AlaIleLeuSerLeuGlnGlnLeuThrTrpIleValMetSerValArgAspCysAlaTrpLeu 520
Db      1501 GCTAAGTTGTCTTGTCCAAAGATTGACTTGAAAGATGCTGTGTAGAGACTGTGCTTGGTGT 1560
Qy      521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlyGlnIle 540
Db      1561 AGAAGATCTCCAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Qy      541 LeuAlaIlePheLeuHisTrpLeuMetSerValTyrValAlaGlnLeuLeuArgSerPhe 560
Db      1621 TTGGCTAAGTTCTTGCACGTTGATGTCTGTTACGTTGATTGTTGATTGTTGATGCTTTC 1680
Qy      561 PheTyrValThrGlnThrThrPheGlnIleValAsnArgLeuPhePheTyrArgIleSerVal 580
Db      1681 TTCTACGTTTACTGAACATCTTCCAAAGAAACATATTGTTCTTCTTCAAGAAAGCTGTT 1740
Qy      581 TrpSerIleValLeuGlnSerIleGlyIleArgGlnHisLeuValArgValGlnLeuArgGln 600
Db      1741 TGTCTAAGTTGCAATCTAATGTGTATGTAGACAACTTGAAAGAGTTCAATTGAGAGAA 1800
Qy      601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db      1801 TTGTCTGAAGCTGAAGTTAGACACACAGAGAAAGCTTACACGCTTGTGTGACTTCTAGA 1860
Qy      621 LeuArgPheIleProIleProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db      1861 TTGAGATTCAATCCAAAGCCAGACGTTTGAACCAATTGTTAACTAGACTAGCTGTGTT 1920
Qy      641 GlyAlaArgThrPheArgArgGlnIleValArgAlaGlnArgLeuThrSerArgValIleVal 660
Db      1921 GGTGTCTAAGACTTGAAGAGAAAGAGAGCTGAAGATGTACTTCTAGAGTTTAAAGCTT 1980
Qy      661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyValaSerVal 680
Db      1981 TTGTTCTCTGTTTAACTACGAAGAAGACTAGAAACACAGTTTGTGGGTCTCTGTGT 2040
Qy      681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
Db      2041 TTGGGTTTGAACGATTCACAGAGCTTGAAGAACTTTCGTTTGTGAGATTGAGACTCAA 2100
Qy      701 AspProProProGlnLeuTyrPheValIleValAspValThrGlyValaTyrAspThrIle 720
Db      2101 GACCCACCAACGAATTTGACTGTTAAGGTTGACGTTACGTTGCTTACGACACTAAT 2160
Qy      721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleIleValProGlnAsnThrTyrCys 740
Db      2161 CCACAGACAGATTGACTGAAGTTATGTCTTATATTAGGCCCAAAACACTTAACTGT 2220
Qy      741 ValArgArgTyrAlaValValGlnIleValAlaHisGlyHisValArgGlyAlaPheIleVal 760
Db      2221 GTTAGAAGATACGCTGTGTTCAAAGGCTGCTACGCTGTACGTTAGAAAGGCTTTCAG 2280
```

QY	761	SeRh1sValSerThrLeuThrProAspLeuGlnProCysThrArgGlnPheValAlaHisLeu	780
Db	2281	TCACACGTTCTCACTTGTGACTGACTTGCAACCAACATCAGACAAATTCGTGGCTCACTTG	2340
QY	781	GlnGlnThrSerProLeuArgAspAlaValValIleGlnGlnSerSerSerLeuAsnGln	800
Db	2341	CAAGAAACTTCCTCATTTGAGAGACGCGTGTATTGAAACAATCTTCTTTGAACGAA	2400
QY	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValAlaGlyIle	820
Db	2401	GCTTCCTTCGTGGTTGGTTCGACGTTTCTTGAGATTCATGTCACCAACGCGTGTAGAAAT	2460
QY	821	ArgGlyLysSerSerTyraValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
Db	2461	AGAGTAGAGTTCATCGTTCAATGTCAGAGATTCACAAAGGTTCTATTGTGTCACTTGG	2520
QY	841	LeuCysSerLeuCysTyrglyAspMetGlnAsnLysLeuPheAlaGlyIleAlaGlyAsp	860
Db	2521	TTGTGTTCTTGTGTTCACGGTGCATGAAACCAAGTGTGCGTGTATTAGAAAGAC	2580
QY	861	GlyLeuLeuLeuAlaGlyLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
Db	2581	GGTTTGTTGTAAGATTCGTTGACGACTCTCTGTGGTACTCCACACTTGACACGCT	2640
QY	881	LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrglyCysValValAsnLeu	900
Db	2641	AAGACTTCTTGAAACACTTGGTTAGAGGTGTCACAAATCGGTTGTGTGTTAACTGG	2700
QY	901	ArgIleThrValIvalAsnProValGlnAspGlnAlaLeuGlyValThrAlaPheVal	920
Db	2701	AGAAAGACTGTGTGTTAACTCTCCAGTTGAAACAGACTTTGGGTGGTACCTTCGTT	2760
QY	921	GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu	940
Db	2761	CAATGCCAGCTCACGGTTGTGCCAAGCGTGGTTGTTGTTGGACACTAGAACTTGG	2820
QY	941	GluValGlnSerAspTyrSerSerSerTyraAlaArgThrSerIleAlaGlnAlaSerLeuThrPhe	960
Db	2821	GAAGTTCATCTGACTACTCTCTCTTCAACCTTGAACCTCTATTAAAGCTCTTTGACCTTC	2880
QY	961	AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	980
Db	2881	AACAGAGGTTCCAGCGCTGTAAGAAACATGAGAAAGAAAGTTGTCGGGTTCAGATTGG	2940
QY	981	LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
Db	2941	AAGTGTCACTCTTGTGTCCTGGACCTTGCAAGTTAACTTTTGCAACCGTGTGTAACAAC	3000
QY	1001	IleTyrIleValIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
Db	3001	ATTTCAGAGATTTTGTGTTCAGACTTACAGATTCCACGCGTTGTGTTTCATTCGCA	3060
QY	1021	PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
Db	3061	TTCCACCAACAAGTTTGGAGAAACCCCACTTCTCTTGAAAGATTAATTCGACACAGCT	3120
QY	1041	SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlnAlaLysGly	1060
Db	3121	TCTTTGTGTACTCAATTTTGAAGGCTAAGAACGCTGTGATGTCTTTGGGTCTAAGGCT	3180
QY	1061	AlaAlaGlyProLeuProSerGlnAlaValGlnTyrLeuCysHisGlnAlaPheLeuLeu	1080
Db	3181	GCTGTGTGGCTCATTCGCATCGAACCTGTCAATGTTGTGTGCACCAAGCTTCTTGTGG	3240
QY	1081	LysLeuThrArgHisArgValThrTyraValProLeuLeuGlySerLeuArgThrAlaGln	1100
Db	3241	AAGTTGACTAGACACAGAGTTACTTAACGTTCCATGTGTGGGTTCTTTAGAACGCTCAA	3300
QY	1101	ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAlaAsn	1120
Db	3301	ACTCAATGTCTAGAAAGTTGCCAAGTACTCTTGAACCTGCTTTGGAAAGCTCTCTCAAC	3360

QY 621 LeuArgPheIleProIysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 DB 1861 TTGGCGTTCAATTCACAAACCAAGTGGTTGGCGCAATTTGTAACATGGAATTAAGTTGTT 1920
 QY 641 G1YAlaArgThrPheArgArgGluYsArgAlaGluArgLeuThrSerArgValIysAla 660
 DB 1921 GGGGCCCGTACCTTCGTCGTGAAAACCGGCCGAAGCTTTGACCTTCGTGTTAAAGCC 1980
 QY 661 LeuPheSerValLeuAsnTyrGluValAlaArgArgProGlyLeuLeuGluYalAsnVal 680
 DB 1981 TTGGTCTCTGTTTGAACCTACGAAACGTCGCCGTCGCAAGTTTGTGGGTGCTCTGTT 2040
 QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
 DB 2041 TTGGGTTGGATATATTCACCGCGCCGCGTACCTTCGTTTGGCTTGGTGGCCCA 2100
 QY 701 AspProProGluLeuTyrPheValIysValAspValThrGlyAlaTyrAspThrIle 720
 DB 2101 GATCCACCAACCAAAATTTGACTTCGTTAAAGTTGATGTTACCGGTGCTACATACCAATT 2160
 QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleIysProGlnAsnThrTyrCys 740
 DB 2161 CCAAGAGATCGTTGACCGAAGTATTGCTCTATTATTAACCAACAAACACTTACTGT 2220
 QY 741 ValArgArgTyrAlaValIleGlnYsAlaAlaHisGlyHisValArgIysAlaPheIys 760
 DB 2221 GTTCGTCGTTACCGCGTTGTTCAAAAAGCCGCCACGTCACGTTGTAAGCCTTCAAA 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
 DB 2281 TCTCAGCTTCTACCTTGACCGATTTGCAACCACTACCTGCTCAATTCGTTGCCCACTTG 2340
 QY 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerIleuAsnGlu 800
 DB 2341 CAAGAAACCTCTCCATTCGATGAGAGCCGTGTATTGAAACAATCTCTCTTTGAACGA 2400
 QY 801 AlAsnSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
 DB 2401 GCCTCTCTGCTGTTGTTGCGATGTTTCTTCGTTTCAATGATGTCACCAACGCGTTCGATT 2460
 QY 821 ArgGlyIysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleuSerThrIleu 840
 DB 2461 CGTGGTAAATCTTACGTTCAATGCAAGGTATTCACAAAGTCTTATTGTTGCTTACCTTG 2520
 QY 841 LeuCysSerIleuCysTyrGlyIysAspMetGluAsnIysLeuPheAlaGlyIleArgArgAsp 860
 DB 2521 TTGTGTTCTTGTGTTACGGGATGATGAAACAAATTTGTCGCCGATTTCTCGTGAT 2580
 QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 DB 2581 GGTTCGTTGTTGGCTTGGTTGATGATTTCTGTGTGTTACCCCACTTGACCCACGCGC 2640
 QY 881 LysThrPheLeuArgThrIleuValArgGlyValProGluTyrGlyCysValIleAsnLeu 900
 DB 2641 AAAACCTTCTTCGCTTACCTGTTGCGTGTTCACAAACACGTTGTTGTTAACTTG 2700
 QY 901 ArgGlyThrValIleAsnProValGluAspGluAlaLeuGlyGlyTrrAlaPheVal 920
 DB 2701 CGTAAACCGTTGTTAACTTCCCGCTGGAATGAAACCTTGGGTGTTACCGCTTCGTT 2760
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrIleu 940
 DB 2761 CAATGCGCAAGCCACGCGTTTGTCCCATGATGTTGTTGTTGATACCCGTAACCTTG 2820
 QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 DB 2821 GAAATTCATCTGATCTCTCTTACGCGCTTACCTCTATTCGTGCTCTTGAACCTTC 2880
 QY 961 AsnArgGlyPheIysAlaGlyArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu 980
 DB 2881 AACCGTGTTCACAAACCGCGTCTGTAACATGCTGTAAATTTGTTGCGGTTTTCGTTTG 2940
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

DB 2941 AAATGTCACTCTTGTCTTGATTTGCAAGTTAACTTTGCAACCGTTGTGTAACCAAC 3000
 QY 1001 IleTyrIysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGluLeuPro 1020
 DB 3001 ATTACAAAAATTTGTTGTGTAAGCCCTACCGCTTTCACGCGCTGTGTTGCAATTGCCA 3060
 QY 1021 PheHisGlnGlnValTrrIleAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 DB 3061 TTCCACCAACAAAGTTTGGAAAAACCAACCTTCTTCGCGTTATTTCGATACCGCC 3120
 QY 1041 SerIleuCysTyrSerIleLeuIysAlaIysAsnAlaGlyMetSerLeuGlyAlaYsGly 1060
 DB 3121 TCTTGTGTACTATTTTGGAAACCAAAAAACCGCGTATGTCCTTGGGTGCCAAAGT 3180
 QY 1061 AlaIaGlyProLeuProSerGluAlaValGlnTrrPheCysHisGlnAlaPheLeuLeu 1080
 DB 3181 GCCGCGGTCATTCACATGAAAGCCGTCATATGTTGTACCAAGCCTTCTTGTG 3240
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 DB 3241 AAATTGACCCGTCACCGTTTACCTACGTTCACTTGTGGTTCTTGGTACCGCCCA 3300
 QY 1101 ThrGlnLeuSerArgIysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 DB 3301 ACCCAATGTCTCGTAAATTCACAGTACCACTTGACCGCTTGAAAGCCGCCCAAC 3360
 QY 1121 ProAlaLeuProSerAspPheIysThrIleLeuAsp 1132
 DB 3361 CCAAGCCTTGCATCTGATTTCAAAACCAATTTGGAT 3396

RESULT 6

US-09-721-456-638
 Sequence 638, Application US/09721456
 Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Linsner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-Nov-6617110-2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 638:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396 /note="hTBT-encoding sequence employing
OTHER INFORMATION: alternative codon distributions for
E. coli (all genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 638:
US-09-721-456-638
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-044-692-2 (1-1132) x US-09-721-456-638 (1-3396)
QY 1 MetProAlaArgProAlaArgCysAlaValAlaArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATGCCGCGCGCGCGCGCGCTTGGCGCGCTGTCGCGCAGTGCCTGGATGCGCGGAA 60
QY 21 ValLeuProLeuAlaThrPheValAlaArgArgLeuGlyProGlnGlyTTrpArgLeuValGln 40
DB 61 GTGCTGCGCGCGCGCGCGCTTGTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGCGGCGCGCGCGCGCGCGCTTGGCGCGCTGTCGCGCAGTGCCTGGATGCGCGGAA 180
QY 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuValGln 80
DB 181 GATGCG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyValArgGlyAlaLeuValAlaPheGly 100
DB 241 GTGGCGCGCGCGCGCGCGCGCTGTCGCGCAGTGCCTGGATGCGCGGAA 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGGCG 360
QY 121 SerTyrLeuProAlaThrValAlaPheAlaLeuArgGlySerGlyAlaTrrpGlyLeu 140
DB 361 AGCTATCTCG 420
QY 141 LeuArgArgValGlyAspArgValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

DB 421 CTGCGCGCGCGCGCGCGCGATGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGGTGGCGCGCGCGCGCGCGTATCAGGATGTCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 181 AlaThrGlnAlaArgProProAlaAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCGACCG 600
QY 201 ArgAlaTrrpAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGCGCGTGAACCATAGCGTGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCG 720
QY 241 GlyAlaAlaProGlnProGlnAlaArgThrProValGlyGlnGlySerTrrpAlaHisProGly 260
DB 721 GCG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 CGCACCGCGCGCGCGCGCGATCGCGGCTTTCGCTGAGCGCGCGCGCGCGCGCGCGCGGAA 840
QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyTrrpArgHisSerHisProSerValGly 300
DB 841 GAAGGACCAAGCGCTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrrpAspThrPro 320
DB 901 CGCGACGATCATGCG 960
QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 961 TCGCGCGCGCGTATGCGCGGAAACCAACATTTTGTATAGACGCGCGCATGAAGAACAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuAlaArgProSerLeuThrGlyAlaArgGlyLeu 360
DB 1021 CTGCGCGCGCGCGCTTCTGCTGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
QY 361 ValGlnThrTrrpPheLeuGlySerArgProTrrpMetProGlyTrrpProArgArgLeuPro 380
DB 1081 GTGGAAACATTTTCTGGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 381 ArgLeuProGlnArgTyrTrrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1141 CGCGTGGCG 1200
QY 401 AlaGlnCysProTrrpGlyValLeuLeuLysThrHisCysProLeuAlaAlaValTrrp 420
DB 1201 GCGCGTGGCG 1260
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
DB 1261 CG 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrrpGln 460
DB 1321 GAAAGATCCGATCCG 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuAlaArgGlyLeuValProProGlyLeuTrrpGlySer 480
DB 1381 GTGTATGGCTTGTGCG 1440
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheHisSerLeuGlyLysHis 500
DB 1441 CGCGATTAAGAACCGCGCTTTCGCGCAACCAAAAATTTATTAAGCTGGCGCAACAT 1500
QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrrpLysMetSerValArgAspCysAlaTrrpLeu 520

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 639:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note="NTRT-encoding sequence employing
alternative codon distributions for
enteric bacteria (high expressing
genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 639:
US-09-721-456-639
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-044-692-2 (1-1132) x US-09-721-456-639 (1-3396)
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATGCGCGGCTCCGCGGTGCGGTGCTGCTCCCTGCTGCTCCACCTACCGGTAA 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40

DB 61 GTTCTGCGCGCTGCTACCTTCCTGCTGCTGCGGTCCGACGGTTCGGCTGCTGAC 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGTGGTGAACCGCGCTGCTTCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGlnLeu 80
DB 181 GACGCTCGTCCGCGCGCGCTGCTCCGCTTCCTCCGACGGTTTCTGCTGACAAAGACTG 240
QY 81 ValAlaArgValLeuGlnArgLeuGlyValArgGlyAlaValAsnValLeuAlaPheGly 100
DB 241 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 101 PheAlaLeuLeuAspGlyValAlaArgGlyGlyProProGlnValAlaPheThrSerValArg 120
DB 301 TTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
DB 361 TCTTACCTGCGGACACCGCTTACCGGCTGCGGTTCGGGTCTGCGGTCTGCTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 181 AlaThrGlnAlaArgProProProAlaAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCTACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGTCTGTTGAACACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProAlaArg 240
DB 661 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 721 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
DB 781 CGTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAAGTACCTCCCTGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
DB 901 CGTACACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 961 TGGCGCGCGTTCAGCTGAACCAAACTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgGlyLeu 360
DB 1021 CTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 361 ValGlnThrHisPheLeuGlySerArgProTyrPheProGlyTyrThrProArgArgLeuPro 380
DB 1081 GTTGAACACATCTCTGCGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1141 CGTCTGCGCAGCTTACTGCGAGATGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200

QY	401	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaValThr	420
Db	1201	GCTCACTGCCCTTACGGTCTTCTGCTGAAACCCTGCCGCTCGTCTGCTTACC	1260
QY	421	ProAlaAlaGlyValCysAlaArgLysProGlnGlySerValAlaAlaProGlnLys	440
Db	1261	CCGGCTGCTGGGTGTTTGCCCTGCTGTAACAAACCGACAGGGTTCGGTGTCCGGAGAA	1320
QY	441	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProGln	460
Db	1321	GAAAGACACCGACCCGGGCTGCTTGGTTCAAGCTGCTCGTCAACACTCTCCCGGTGGAG	1380
QY	461	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrPoiYser	480
Db	1381	GTTTACGGTTTGGTTCGTGCTTGGCTTGGCGTGGTTCGTTCCGGCGGGGTCTGCGGGGCTTC	1440
QY	481	ArgHisAsnGluArgArgPheLeuArgArgAsnThrLysIleSerLeuGlyLysHis	500
Db	1441	CGTCAACAAAGACGTCGTTCTCGGGTAAACACAAATAATCATCTCCCTGGGTAAACAC	1500
QY	501	AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu	520
Db	1501	GCTAAACTCTCCCTCAGGAACTGACCTGGAAATAGTCCGTTCTGGACCTCCGGCTGGCTG	1560
QY	521	ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnLysIle	540
Db	1561	CGTCCCTTCCCGGGGTGGTGGTCCCTTCCGCTCTGTAAACACCGCTCTCGTGAAGAATTC	1620
QY	541	LeuAlaLysPheLeuHisTyrLeuMetSerValTyrValValGlnLeuLeuArgSerPhe	560
Db	1621	CTGGCTAATTCCTTCACTGGCTGATAGTCGTTTACGTTTGAACCTGCGTGGTCTTC	1680
QY	561	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
Db	1681	TTCTACGTTACCGAAACACCACTTCAGAAATAACCGCTGTTCTTCTTACGTAATTCGGT	1740
QY	581	TyrSerLysLeuGlnSerLleGlyLysLeuGlnHisLeuLysArgValGlnLeuArgLys	600
Db	1741	TGGTCCAACTGCACTCCATCGTATCGGTACGACCTGAAACCGTTTCACTGCGTGA	1800
QY	601	LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg	620
Db	1801	CTGTCCGAAGCTGAAGTTGCTAGACCCGTAAAGCTGCTCCGGCTCTGCTAATCTCCCGT	1860
QY	621	LeuArgPheLleProLysPheProAspGlyLeuArgProLleValAsnMetAspTyrValVal	640
Db	1861	CTGCCTTTCATCCCAAAACCGACCGCTCTCGCTCCGATCGTTTACATGACCTACAGCTTGGT	1920
QY	641	GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuLeuThrSerArgValLysAla	660
Db	1921	GGTGCTCGTACTCTCCGTGCTGTAATAAGTCTGAACCTCTGACCTCCCGCTTAAAGCT	1980
QY	661	LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyLysSerVal	680
Db	1981	CTGTTCTCCGTTCTAACACTAACAAAGTCTCGTCTCGGGCTCTGCTGGGTGCTTCGGTT	2040
QY	681	LeuGlyLeuAspAspLleHisArgAlaTyrPheArgThrPheValLeuArgValArgAlaGln	700
Db	2041	CTGGGCTCGAGACATCACCGGACCTGGGGTACCTTCTTCCGCGTTCCGGCTCAG	2100
QY	701	AspProProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrLle	720
Db	2101	GACCCGCGCGGAGACTGTAAGTCTTAAAGTTAGCGTTACCGGGCTTACGACACATC	2160
QY	721	ProGlnAspArgLeuThrGluValIleAlaSerLleLysProGlnAsnThrTyrCys	740
Db	2161	CCGCGAGACCGCTGACCGAAGTTATCCTTCCATCATCAACACGCGAACAACCTACATGC	2220
QY	741	ValArgArgTyrZalValValGlnLysAlaAlaHisGlyHisValArgLysValPheLys	760
Db	2221	GTTGCTCCTTACGCTGTTGTTCAGAACCTGCTACGGGTACCGTTCGTAAGACTTTCAAA	2280

QY	761	SeRHSVA1SeRThLeuThAspLeuGlnProLYrMeCArGGInPheValAlaHisLeu	780
Db	2261	TCcCAcGTTTCACcCCTCAcCGACcCTGCAGcCGTACATGcGTCAgTTcGTTCcTCAcCTG	2344
QY	761	GInGInThrSerProLeuAArgAspAlaValIleGInSerSerSerLeuAsnGln	800
Db	2341	CAGGAACcCTCCcCGcCTcCGTGAcGcCTGTGTATCGAAcAGcCTcCTcCTCGAAcGAA	2400
QY	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle	820
Db	2401	GcTTcCTcCGGcCTGcTTCGAGcGTTTcCTcGcGTTcCATGTCcACcACAGcGcTTCGATcC	2460
QY	821	ArgGlyYSerTYrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThLeu	840
Db	2461	cGTGTAATcCTACGTTCAcGTCAGcGCAcAGGATcCCcGcAGGcGTTcCATcCTcCTCAcCCTG	2520
QY	841	LeuCYSerLeuCYrTYrGlyAspMetGlnAsnLYsLeuPheAlaGlyIleArgArgAsp	860
Db	2521	cTGcGcTcCCcGTGcTGAcGTGAcATGAAACAAAcGTTCcGTGcATcCCcTGcGAC	2580
QY	861	GlyLeuLeuLeuAArgLeuValAspAspPheLeuLeuValThrProHisLeuThHisAla	880
Db	2581	GcTcGcTcGcTcGcGcTcGTTGAcGAcTcCTcCTcGTTAcCCcCGAcCTGAcCCAcCCT	2640
QY	881	LYsThrPheLeuAArgThrLeuValArgGlyValProGlnTYrGlyCYsValValAsnLeu	900
Db	2641	AAAcCTTCcCGcGTAcCCcCTGcTTCcGTTCcGGAATcCGGAAATcCGcTTCGcTGTAAcCTG	2700
QY	901	ArgLYsThrValValAsnPheProValGlnAspGlnAlaLeuGlyGlyThrValAPheVal	920
Db	2701	cGTAAACcCGTTGTTAAcTTCcCGcGTTGAACAGAcGCTcTGcGGTGAcCCcCTTCGTT	2760
QY	921	GlnMetProAlaHisGlyLeuPheProTYrCysGlyLeuLeuLeuAspThrArgThLeu	940
Db	2761	CAGATcCGcGcTCAcCGcTcGTTCcCGGcGcGcGcGTcGcTcGcTGAcACcCGTAcCCTG	2820
QY	941	GlnValGlnSerAspTYrSerSerTYrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
Db	2821	GAAcGTcAGTCcCGAcTAcTcCTcCTAGcCTGTAcCTCAACcCGcTTCcCTCAcCCTTC	2880
QY	961	AsnArgGlyPheLYsAlaGlyArgAsnMetArgArgLYsLeuPheGlyValLeuArgLeu	980
Db	2881	AAcCGcGcTTCAAAGcCGcGcTcGTACATGcGTcGTGAACcGTTcCGcTTCcGcTcCTG	2940
QY	981	LYsCYsHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCYsThrAsn	1000
Db	2941	AAATcGCCAcTcCCcGTTCcCTGAcCTcGAcCTGAcCTACcCTCGcAGAcCGcGTTGAcCAAC	3000
QY	1001	IleTYrLYsIleLeuLeuLeuGlnAlaTYrArgPheHisAlaCYsValLeuGlnLeuPro	1020
Db	3001	ATcTACAAACAcCTcGcTcCTcGAcGcCTTACcGcTTCACAcGcTTCcGTTcTcGAcCTcCG	3060
QY	1021	PheHisGlnGlnValITrPLYsAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
Db	3061	TTTCACcAGAcGcGTTTGGAACAAACcCGAcCTTCCTTCcGcGTATcCTCGAcCAcCGcT	3120
QY	1041	SerLeuCYsTYrSerIleLeuLYsAlaLYsAsnAlaGlyMetSerLeuGlnLYsAlaLYsGly	1060
Db	3121	TCcCTcGcTcACTAcCTAcCTCGAAAGcCTPAACAcCTcGTATcCTCGcGGcGTAAAGcT	3180
QY	1061	AlaAlaGlyProLeuProSerGlnAlaValGlnTrpLeuCYsHisGlnAlaPheLeuLeu	1080
Db	3181	GcTcGcTcGcTcCGcTcCGcTcCGAGcGTTCAGcGcTcGcTcCCAcCGAcGcTTCcTcCTG	3240
QY	1081	LYsLeuThrArgHisArgValThrTYrValProLeuLeuGlySerLeuAArgThralGln	1100
Db	3241	AAAcTGAcCCcCTCAcCGcGTTAcCTAcGTTCCcGTcGTGGcGTTCCcTGAcCGcCTAG	3300
QY	1101	ThrGlnLeuSerArgLYsLeuProGlyIThrThrThleuThralaLeuGlyAlaAlaAsn	1120
Db	3301	AcCGAcGcTcTcCGTAAAcTcGcCGGGATCAcCAcCTGAcCGcTcTGAAGcGTcGTAcAC	3360
QY	1121	ProAlaLeuProSerAspPheLYsThrIleLeuAsp	1132

Db 3361 CGGCTGCGCTCGACTCAAAACATCTCGAC 3396

RESULT 8

US-09-721-456-640
Sequence 640, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-Nov. 6617110-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 640:

SEQUENCE CHARACTERISTICS:

LENGTH: 3396 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: 1..3396

OTHER INFORMATION: /note="HYRT-encoding sequence employing
alternative codon distributions for
yeast (all genes)"

SEQUENCE DESCRIPTION: SEQ ID NO: 640:

US-09-721-456-640

Alignment Scores:

Pred. No.: 0

Score: 5961.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 4

Gaps: 0

US-10-044-692-2 (1-1132) x US-09-721-456-640 (1-3396)

QY 1 MetProAlaAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTryArgGlu 20
DB 1 ATGCCAAGAGCTCCAAAGATGTAGACTGTAGATCTTGTGAGATCTCATATAGAGA 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheLeuValGln 40
DB 61 GTTTCCTAGTGGCTACTTGTGTAGAGATGGGTCCAAAGTTGGAGATTGGTTCA 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 AAGAGTGATCCAGCTGCTTTAGACTTGGTGGCTCAATGTTGGTTGTGTCATGG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGluLeu 80
DB 181 GATGCTAGACCCACACAGCTCCTCATCTTTTAAACAAGTTCTTGTGAAGAATTG 240
QY 81 ValAlaArgValLeuGlnArgLeuGlyGluArgGlyAlaValAspValLeuAlaPheGly 100
DB 241 GTTGCTAGAGTTTGCAGAAAGATTGTGTGAAGAAGTCTAAAGATTTTGGCTTTGGT 300
QY 101 PheAlaLeuLeuAspGlyValAlaArgGlyGlyProGlnGlyAlaPheThrSerValArg 120
DB 301 TTGCTTGTGTTGAGATGTGTCTAGAGTGTCCACCAAGACTTTACTTCTGTTTAA 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
DB 361 TCTTATTTGCCAAATACGTCTCTGATGCTTGAAGAGTTCGTGGCTTGGGTTTGTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 TTGAGAAAGTTGTGATGATGTTTGTGTTCAATTTGTGGCTAGAGTGTCTTGTGTT 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 TTGGTTGCTCCATCTTGTGCTTATCAAGTTGTGTGCCACATTTGATCAATGGGTGCT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCTACTCAAGCTAGACCAACCAACCATGCTTGTGGTCCAAAGAAATGGGTTGTGAA 600
QY 201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 AAGCTTGGAATCATTTGTTAGAGAACTGTGTTCATTTGGTTTGGCTAGCTCAGGT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCTAGAAAGAGGTGCTTCTGCTTCTAGATCTTTTCCATTTGCCAAAAGACCAAGAA 720
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 721 GGTGCTGCTCCAGAACCAAGAAAGAACTCCAGTTGGTCAAGTTCTTGGCTCATCAGGT 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 AAGACTAGAGGTCCATGTGATAGAGTTTGTGTGTTTCCACGTAGACCAAGCTGAA 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300

```
Db      841 GAAGTACTCTTGGAGAGGTGCTTGTCTGTAAGTACATTCATTCATCTGTTGGT 900
Qy      301 ARGHNIHSIAAGLYPRPProSerThrArgProProArgProTTPabPThrPro 320
Db      901 AGAACATATATCTGCTCCACATCTACTCTAGACACACAGACCATGGGATCTCCA 960
Qy      321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
Db      961 TGCCACCACTTATGCTGAAGTAACTAAATTTTGTGATCTTCTGGTGATTAAGAACAA 1020
Qy      341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db      1021 TTGAGACCACTTTTGTGTTGCTCTTGTGAGACCACTTTGAGCTGGTGTGAGAAATTTG 1080
Qy      361 ValGluThrLlePheLeuGlySerArgProTTrMetProGlyThrProArgArgLeuPro 380
Db      1081 GTTGAAACTATTTTGTGGTCTAGACATGAGATGCGACAGTACTCCAGAAAGATTGGCA 1140
Qy      381 ArgLeuProGluArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400
Db      1141 AGATTGCCAACAAAGATATTTGGCAATGAGACCATTTGTTTGGAAATTTGGGTATCAT 1200
Qy      401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaValThr 420
Db      1201 GCTCAATGTCCAATATGCTGTTTGTGAAGAACTCATTTGTCATTTGAGAGCTGCTTACT 1260
Qy      421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGln 440
Db      1261 CCAAGCTGCTGCTTGTGCTGTAAGAAACCAAGATTCGTCTGCTGCTCCAGAGAA 1320
Qy      441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db      1321 GAAGATATCGATCCAGAAAGATTGTTCAATTTGTGAGAACAACTCTTCTCATGGCAA 1380
Qy      461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db      1381 GTTATAGTTGTTGTAGACCTGTTTGAAGAAATGTTGTTCCACAGGTTTGCGGTTCT 1440
Qy      481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheLleSerLeuGlyLysHis 500
Db      1441 AGCATTAAGAAAGAAAGATTTTGGAGAAATCTAAATAATTTTCTTGGGTAAACAT 1500
Qy      501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db      1501 GCTAAATTTCTTTGCAGAAATTTGACTGGAATAATGCTGTAGAGATTGCTGCTGGT 1560
Qy      521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLle 540
Db      1561 AGAAGATCTCCAGAGTGTGTTGTTGTTCCAGCTGTCGAAACATAGATTGAGAGAGAAAT 1620
Qy      541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
Db      1621 TTGGCTAAATTTTGGATTTGGTTGATGCTGTTTAAATTTGTTGATTTGTTGATCTTT 1680
Qy      561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db      1681 TTTTATGTTACGAAACTACTTTTCAAAAAATAGATGTTTATTTTATGAAAAATCTGTT 1740
Qy      581 TrpSerLysLeuGlnSerLleGlyLleArgGlnHisLeuLysArgValGlnLeuArgGln 600
Db      1741 TGCTCTAAATTTGCAATCTATTGGTATTAGACAAACATTTGAAAGAGTTCAATTTGAGAGA 1800
Qy      601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db      1801 TTGTCGAAGCTGAGATTAGACAAACATAGAGAGCTAGACCAAGCTTTGTTGCTCTAGA 1860
Qy      621 LeuArgPheLleProLysProAspGlyLeuArgProLleValAsnMetCaspTyrValVal 640
Db      1861 TTGAAGTTTATTCCAAAACCAATGATGTTTGAACCAATTTGTTAAATATGATTAATGTTGT 1920
Qy      641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660

Db      1921 GGTGCTAGAACTTTTAGAAGAGAAAAAGAGCTGAAGATGACTTCTAGATTAAAGCT 1980
Qy      661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db      1981 TTGTTTCTGTTTGTGAATATGAAAGAGCTAGAAAGACCAAGTTTGTGGGCTCTTGCT 2040
Qy      681 LeuGlyLeuAspAspLleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
Db      2041 TTGGGTTTGAATGATTTATAGAGCTTGAGAACTTTTGTGTTTGTGAGCTTGAAGCTCAA 2100
Qy      701 AspProProGluGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrLle 720
Db      2101 GATCCACCAACCAAGATTTGATTTGTTAAAGTTGATGTTAGCTGGTCTTATGATCTAAT 2160
Qy      721 ProGlnAspArgLeuThrGluValLleAlaSerLleLleLysProGlnAsnThrTyrCys 740
Db      2161 CCACAGATAGATGACTGAAAGTTATGCTTATATTAATTAACCAACAAATCTTAATGCT 2220
Qy      741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db      2221 GTTAGAAGATATGCTGTTCTCAAAAAGCTGCTCATGTCATGTTAGAAAAGCTTTTAA 2280
Qy      761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db      2281 TCTCATGTTCTAATTTGACTGATTTGCCAACATATATAGACAAATTTGCTCATTTTG 2340
Qy      781 GlnGluThrSerProLeuArgAspAlaValLleGluGlnSerSerSerLeuAsnGln 800
Db      2341 CAAGAACTCTCCATGAGATGCTGTTGTTATTAAGAAATCTTCTTTTGAATGA 2400
Qy      801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLle 820
Db      2401 GCTTCTTGCTGTTGTTGTTGATGTTTGTGAGATTTATGTCATCAACAGCTGTTGATTT 2460
Qy      821 ArgGlyLysSerTyrValGlnCysGlnGlyLleProGlnGlySerLleLeuSerThrLeu 840
Db      2461 AGAGGTAAATCTTAATGTTCAATGTCAGAGTATTCACAAAGGTTCTAATTTGCTACTTTG 2520
Qy      841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyLleArgArgAsp 860
Db      2521 TTGTGTTCTTGTGTTAGTGATATGAGAAATTAATGTTGCTGGATTAAGAAAGAT 2580
Qy      861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db      2581 GGTGTTGTTGAGATTTGTTGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2640
Qy      881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db      2641 AAAACTTTTGTGAGAACTTTGTTGAGAGTGTTCAGAAATATGCTTGTGTTGTTAATTTG 2700
Qy      901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db      2701 AGAAATCTGTTGTTAAATTTTCCAGTTGAGATGAGATGAGCTTTGGGGTGAAGCTTTGTT 2760
Qy      921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db      2761 CAATGTCAGCTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2820
Qy      941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerLleArgAlaSerLeuThrPhe 960
Db      2821 GAAGTTCAATCTGATTAATCTTTATGCTAGAACTTCTATTAAGCTTCTTTGACTTTT 2880
Qy      961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db      2881 AATAGAGCTTTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
Qy      981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db      2941 AAATGTCATCTTTGTTGTTGTTGATTTGCAAGTAACTTCTTGCACAACTGTTGACTAAT 3000
Qy      1001 IleTyrLysLleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db      3001 AATTATAAATTTTGTGTTGCAAGCTTAATGATTTCAAGCTTGTGTTGTTGCAATGCA 3060
```

QY 1021 PheHISGLNGLNValTRPlySAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
DB 3061 TTTCATCAACAAGATTGGAAAAATCCAACTTTTITTTGAGAGTATTCTATCTACTGCT 3120
QY 1041 SerLeuCySYrSerIleLeuLYSAlaLYSAsnAlaGlyMetSerLeuGlyValAlaYsgly 1060
DB 3121 TCTTTGTGTATTCTATTGTAAGCTAAATGCTGGATCTCTTTGGGCTCTAAAGGT 3180
QY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTRPLeuCyHISGLNAlaPheLeuLeu 1080
DB 3181 GCTGCTGGTCCATTCGCACTCAAGCTGTTCATAGTGTGTCTCATCAAGCTTTTGTGTG 3240
QY 1081 LysLeuThrArgHISArgValThrTrpValProLeuLeuGlySerLeuArgThrAlaGln 1100
DB 3241 AAATTGACAGACATAGAGTACTTATGTTCCATGTTGGGTTCTTTGGAAGCTGCTCAA 3300
QY 1101 ThrGlnLeuSerArgLYSLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
DB 3301 ACTCAATTGTCTAGAAATATGCGAGGTACTACTTGTGACTGCTTGGAACTGCTGTAT 3360
QY 1121 ProAlaLeuProSerAspPheLYSThrIleLeuAsp 1132
DB 3361 CCAGCTTGCCATCTGATTTTAACTATTGTGAT 3396
RESULT 9
US-09-721-456-641
; Sequence 641, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 641:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note="hTERT-encoding sequence employing
alternative codon distributions for
Yeast (high expressing genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 641:
US-09-721-456-641
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-044-692-2 (1-1132) x US-09-721-456-641 (1-3396)
QY 1 MetProAlaGAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTrpArgGlu 20
DB 1 ATGCCAAGAGCTCCCAAGATGAGAGCTGTAGATCTTGTAGATCTCAGACAGAGA 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
DB 61 GTTTGGCCATTGGCTACTCTTCTGTTAGAACTTGGCTCCACAAAGTTGAGATTGGTCAA 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
DB 121 AGAGTGAACCCAGCTGCTTTCAGAGCTTGGTGTCTCAATGTTGGTTGCTTCATGG 180
QY 61 AspAlaArgProProProProAlaAlaProSerPheArgGlnValSerCysLeuLYSGLuLeu 80
DB 181 GACGCTAGACCAACCAACGAGCTGCTCCATCTTTCACAAAGTTCTGTTGAAGAAATTG 240
QY 81 ValAlaArgValLeuGluArgLeuCysGluArgGlyAlaLYSAsnValLeuAlaPheGly 100
DB 241 GTTGTCTAGAGTTTTCAGAAAGATTGTGTGAAGAGGTCTAGAAAGCTTTGGCTTCGT 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThiSerValArg 120
DB 301 TTCGCTTGTGTGAGCGGTGCTAGAGTGGTCCACCAAGAGCTTTCACACTCTCTGTAGA 360
QY 121 SerTrpLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrpGlyLeuLeu 140
DB 361 TCTTACTGCGCAACACGTTTACTGACCGTTTGAAGAGTTCTGCGTGGGCTTGGTGG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 TTGAGAAAGTTGGTGAACGACGCTTTGGTCTCACTTGGCTAGATGCTCTTGTTCGTT 480
QY 161 LeuValAlaProSerCysAlaTrpGlnValCysGlyProProLeuTrpGlnLeuGlyAla 180
DB 481 TTGGTGTGCTCATCTTGTGCTTACCAAGTTGTGTGCTCCACATGTATACCAATTTGGTGT 540

QY 181 AlaThrGlnAlaArgProProHISAlaSerGlyProAlaArgArgLeuGlyCysGlu 200
Db 541 GCAACTCAAGCTGACCAACCAACCAACGCTTCGCTCCAAAGAAAGATTGGGTGTGAA 600
QY 201 ArgAlaTrpAlaMetHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 601 AGAGCTTGGAAACCACTGTTAGAGAGCTGGTGTTCATTGGGGTTGCGAGCTCCAGGT 660
QY 221 AlaArgArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProAlaArg 240
Db 661 GCTAGAAAGAGAGGTGTTCTGCTTCAATTCCTTGCAATTCGCAAGAACAGCAAGAGA 720
QY 241 GylAlaAlaProGluProGluArgTrpProValGlyGlnGlySerTrpAlaHisProGly 260
Db 721 GGTGCTGCTCCAGAACCAAGAAAGAACTCCAGTTGGTCAAGTTCTGGGCTCACCAAGT 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
Db 781 AGAAGTAAGAGGTCCATCTGACAGAGGTTCTGTGTGTCTCCAGCTAGACAGCTGAA 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 841 GAAGCTACTCTTGGAGAGGTGCTTGTCTGTAGTACTAGACACTCTCACCATCTGTGGT 900
QY 301 ArgGlnHisHisAlaGlyProProSerTrpSerArgProProArgProTrpAspTrpPro 320
Db 901 AGACAACACCAACGCTGGTCCACCATCTTCTTAGACCAACCAAGCAATGGGACATCCCA 960
QY 321 CysProProValArgAlaGluTrpLysHisPheLeuTrpSerSerGlyLysAllyGlnGln 340
Db 961 TGTCACCAAGTATTAAGCTGAAGCACTTCTTACTCTTCTGTGTAACAAGAAACAA 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1021 TTGAGACCAATCTTCTTGTGTCTTCTTGGACCACTTTGACTGTGCTGTAAGATTG 1080
QY 361 ValGluTrpLysPheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
Db 1081 GTTGAACATATTTCTTGGGTCTAGACCATGATCCAGGTACTCCAGAAAGATTGCCA 1140
QY 381 ArgLeuProGlnArgTrpTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyLysHis 400
Db 1141 AGATTCCCAAGAAAGTAAGTGGCAAAAGAACATGTTCTTGGAAATGTTGGGTAAACCA 1200
QY 401 AlaGlnCysProTrpGlyValLeuLeuLysTrpHisCysProLeuArgAlaAlaValThr 420
Db 1201 GCTCAATGTCATTAAGGTGTTTGTGAAAGCTCACTGTCCATTTAGAGACTGCTGTACT 1260
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
Db 1261 CCAGCTGCTGGTGTGTGCTAGAGAAAGCAACAAGGTTCTGTGCTCTCCAGAGAA 1320
QY 441 GluAspTrpAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1321 GAAGACACTGACCCCAAGAAAGATTGTTCAATGTTGAGCAACAACCTTCTCCATGGCAA 1380
QY 461 ValTrpGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db 1381 GTTTACGGTTCGTAGAGCTTGTGTAAGAGTTGGTTCCACCAAGTTTGTGGGGTTCT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnTrpLysPheLeuSerLeuGlyLysHis 500
Db 1441 AACAACAAGAAAGAAAGATTCTTGAGAAACACTTAAGAGTTCAATTTCTTTGGGTAAAGAC 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db 1501 GCTAAGTTCTCTTGGAAAGATTGACTTGAAGAGTCTGTTAGAGACTGTCTGGGTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLe 540
Db 1561 AGAAGATCTCCAGAGTGTGTGTGTCTCAGCTGCTGAACACAGATTGAGAGAAAGAAATT 1620

QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTrpValValGluLeuLeuArgSerPhe 560
Db 1621 TTGGCTAAGTTCTTGCACCTGGTTGAGTGTCTGTACGTGTGGAATGTGTGAACTTTC 1680
QY 561 PheTrpValThrGluThrTrpPheGlnLysAsnArgLeuPhePheTrpArgLysSerVal 580
Db 1681 TTCTACGTACTGAACACTCTTCCAAAAGAACAGATTGTTCTTCAAGAAAGCTGTGT 1740
QY 581 TrpSerLysLeuGlnSerLysGlyTrpLeuArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db 1741 TGATCTAAGTTCAATCTAATGGTATTTAGACAACCTTGAAGAGATTCAATTGAGAGAA 1800
QY 601 LeuSerGluAlaGlyValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 TTGTCTGAAGCTGAAGTTRAGACACACAGAGACTTAACCAAGCTTGTGTGACTTCTAGA 1860
QY 621 LeuArgPheLeuProLysProAspGlyLeuArgProAlaValAsnMetAspTrpValVal 640
Db 1861 TTGAGATTCAATCCAAAGCCAGACGGTTGAGACCAATTTGATGACATGAGACTGTTGT 1920
QY 641 GylAlaArgTrpPheArgArgGlyLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1921 GGTGCTAGAAGCTTTCAGAGAGAAAGAGAGCTGAAGATTGACTTCAAGAGTTAAGCTT 1980
QY 661 LeuPheSerValLeuAsnTrpGluArgAlaArgArgProGlyLysLeuGlyValaSerVal 680
Db 1981 TTGTTCTCTGTTTAACTTACGAAGAAAGACTAGAGACCAAGTTTGTGGGTCTTCTGTT 2040
QY 681 LeuGlyLeuAspAspLysHisArgAlaTrpArgTrpPheValLeuArgValArgAlaGln 700
Db 2041 TTGGGTTTGGACGACATTCACAGAGCTTGAGAACTTTCGTTTGGAGGTTAGAGCTCA 2100
QY 701 AspProProProGluLeuTrpPheValLysValAspValThrGlyAlaTrpAspThrLys 720
Db 2101 GACCCACACCAAGAAATGTACTCTGTTAAGTTGACGTACTGCGGTAGACACTATTT 2160
QY 721 ProGlnAspArgLeuThrGluValLysAlaSerLysLeuLysProGlnAsnThrTrpCys 740
Db 2161 CCACAAGACAGATTGACTGAAGTTATTGCTTCTATTTAAGCCACAACCACTTACGT 2220
QY 741 ValArgArgTrpAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2221 GTTAAAGATACGCTGTTGTTCAAAAGGCTGCTCACGGTCAAGTTAAGAGGCTTCAAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTrpMetArgGlnPheValAlaHisLeu 780
Db 2281 TCTCAGCTTCTACTTGAACGACTGACCAACCAATGAGCAAAATTCGTGCTCACTTG 2340
QY 781 GlnGluTrpSerProLeuArgAspAlaValLysGlnGlnSerSerSerLeuAsnGlu 800
Db 2341 CAAGAACTTCTCATTTGAGAGACGCTGTTGTATTGAAACAATCTTCTTTGAAGAA 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLys 820
Db 2401 GCTTCTTGTGTTGTGTCAGAGTTCCTTGAATTCATGTCACCAAGCTGTAGAAATT 2460
QY 821 ArgGlyLysSerTrpValGlnCysGlnGlyLysProGlnGlySerTrpLeuSerThrLeu 840
Db 2461 AGAGGTAAAGTTCATGCTTCAATGTCAGAGTATTCACAAAGGTTTATTTGTCTACTTTG 2520
QY 841 LeuCysSerLeuCysTrpGlyAspMetGluAsnLysLeuPheAlaGlyLysArgArgAsp 860
Db 2521 TTGTGTTCTTGTGTACGGTGATGAGAAACAAGTTGTCGTGTGATTTAGAAAGAGAC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGTGTGTGTGAGATTTGTGAGACTTCTGTGTGTACTCCACACTGAGCTCAAGCT 2640
QY 881 LysThrPheLeuArgTrpLeuValArgGlyValProGluTrpGlyCysValAlaAsnLeu 900
Db 2641 AAGACTTCTTGAAGAACTTTGGTTAGAGGTGTTCCAAATACGGTTGTCTGTTAACTTG 2700
QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920

181 GATGCCCGTCACACCAACGCCGCCCATCTTCCGTCAGATTCTTGTGGAAGAATTG 240
QY
DB 81 VALAIAArgValIleuGlnArgLeuCysGluArgGlyValAlaIleAsnValIleuAlaPheGly 100
241 GTTGCCTCGTGTTCGACAGTTTGTGTGAACGTGGGCCAAAACGTTTGGCCTTCGT 300
QY 101 PheAlaLeuLeuAspGlyValIleArgGlyGlyProProGluAlaPheThrThrSerValArg 120
DB 301 TTGCCTGTGTGAGTGTCCCGTGGTGTGCACCAAGACCTTCAACACCTCTGTTCGT 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrpGlyLeuLeu 140
DB 361 TCTTACTTGCACAAACCCGTTACCGATGCCGTGCGGTTCGTGGTCCGCGGTGGTGG 420
QY 141 LeuArgArgValGlyAspAspValIleuValIleLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 TTGCGCTCGTGTGTGATATGTTTGTGTTCACTTGTGGCCGTTGTGCTTGTTCGT 480
QY 161 LeuValAlaIleProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 TTGGTGGCCCATCTTGTGCTTACCAAGTTTGTGTGCACCAATTGACCAATTGGGTGCC 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGly 200
DB 541 GGCACCCAAAGCCCGTCACACCAACAGCCCTGTGTGCACAGTCGTGTTGGGTGTGA 600
QY 201 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGTGCCTGGAACCACTCTTGTGTGTAAGCCGCTGTTCATTGGGTTGGCAGCCCAAGT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCCCGTCGTGTGTGTCTGTGCTCTGCTTCTGTTCCATTGCAAAACGTCACGTCGT 720
QY 241 GlyAlaAlaIleProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
DB 721 GGTCGCCGCCCAAGAACCAACAGTACCCAGTTGTGCAAGTTCTTGGGCCCAACCAAGT 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValIleSerProAlaTrpProAlaGlu 280
DB 781 CGTACCCGTCGTGTGATCTGATCGGTCTTGTGTGTTCCTCCAGCCCGTCACGCCGA 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAAGCCACCTCTTGGAAAGTGCCTGTGTGTAACCGTCACCTCAACCACTGTGTGT 900
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspTrpPro 320
DB 901 CGTCAACACACGCGCGGTCCACATCTACCTCTGTGTCAACAGTCCATGGAGATACCCA 960
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyValAspLysGluGln 340
DB 961 TGTCCACAGTTTATGCCCGAAACCAACACTTCTTGTACTCTTGTGTATTAAGAACAA 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1021 TTGCGTCATCTTCTTGTGTCTTGTTCGTCATCTTGAACCGGTCCGCTGTGTG 1080
QY 361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
DB 1081 GTTGAACCAATTTCTTGGGTCTCGTCCATGATGCCAGGTACCCACGTCGTGGCCA 1140
QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1141 CGTTTGCACAAAGTTACTGGCAATGCGTCATGTCTTGGAAATTGTGGTTAACCA 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysTrpHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCCCATGTCCATAGCGGTGTGTGAAACCAACCACTGTCATGTGTCGCGCGCTTAC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
DB 1261 CCAGCGCGCGGTGTGTGTGCGGTGAACCAACAGGTTCTGTGTGCCCGCCAGAAAGA 1320

441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
DB 1321 GAAGATACCGATCCACGTCGTGTGTTCAATTGTGGCGTCACACCTCTTCCATGGCA 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
DB 1381 GTTTACGGTTTCGTTCGCGCGGTGTGGTCCGTTGTGTCCACAGGTTTGGGGGTCT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
DB 1441 CGTCAACAAAGCGTCGTTTCTTGCCTAACACCAAAAATTCATTTCTTGGGTAAAC 1500
QY 501 AlaLysLeuSerLeuGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
DB 1501 GCCAATTTGCTTTCAGAAATGACCTGGAATAATGTCTGTTGCGATGTCCTGCTGTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540
DB 1561 CGTCGTTCTCCAGGTGTGTGTGTGTCCAGCCGCCGAACACCGTTTGGTGAAAGAAAT 1620
QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValIleGluLeuLeuArgSerPhe 560
DB 1621 TTGCGCAAAATTTTGCACCTGATGATGTCGTTTACGTTGTGAATTGTGCGTCTTTC 1680
QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1681 TTCTACGTTACCGAAACCAACCTCCAAAACCGTTTGTCTTCAACGTAATCTGTT 1740
QY 581 TrpSerLysLeuGlnSerIleGlyTlleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB 1741 TGGTCTAAATTGCATCTATGGTATGTCGTCAACCTTGAAACGTTGTCATTTGGGTGA 1800
QY 601 LeuSerGluAlaGlnValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
DB 1801 TTGTCTGAAGCCGAAGTGTGAACACGTGAAGCCGTCACGCTTGTGTACCTCTGCT 1860
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAlaSerMetAspTyrValVal 640
DB 1861 TTGCGTTTCATTCAAAACCAAGATGTTGGCTCCAAATTGTTAACATGATTAACGTTGT 1920
QY 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGluArgLeuThrSerArgValLysAla 660
DB 1921 GGTCGCCGTCATCTTCCGTGTGAACCAAGTGCAGACGTTGACCTCGTGTAAAGCC 1980
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgAspProGlyLeuLeuGlyValAsnSerVal 680
DB 1981 TTGTTCTCTGTTTAACTACGACGTCGCGCTCGTCCAGTTTGTGGGTGCTCTGTT 2040
QY 681 LeuGlyLeuAspAspIleHisAlaArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
DB 2041 TTGGGTGTGATGATTAACCGTCGTCGCTACCTTCGTTTGGTGTGTCGCCAA 2100
QY 701 AspProProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
DB 2101 GATCCACCAACCAAGATTAATCTCGTTAAAGTTGATGTATCCGCGCTCAACATACAT 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
DB 2161 CCACAAAGTCGTTACCGAAATGATGCTTATATTAACCAACAAACCTTACGT 2220
QY 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
DB 2221 GTTGTGTCGTTACGCGGTGTTCAAAAGCCGCCCAACGTCACGTTGTTAAACCTTCAA 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
DB 2281 TCTCACGTTTTCATCTTGCACATTTGCAACATACATACGTCATCTGTTGCCCATTTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValAlaIleGluGlnSerSerLeuLeuGln 800
DB 2341 CAAGAAACCTTCATCTGATGATGCGGTGTTATTTGAACAATCTTCTTTTGAACGA 2400

QY	80	Alse	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	Ala	Val	Arg	1	820			
Db	2401	GCC	TCT	TGG	TTG	TGC	ATG	TTT	CTT	GCG	TTC	ATG	TGC	ACC	GCG	CTT	CG	ATT		2460			
QY	821	Arg	Gly	Leu	Ser	Val	Gln	Cys	Gln	Gly	Val	Leu	Pro	Gln	Ser	Ile	Leu	Ser	Thr	Leu	840		
Db	2461	CGT	GTT	AAAT	CTT	CA	GTT	CA	TGC	AA	GAT	TTC	CA	CA	AGG	TTT	CT	ATT	GT	CT	2520		
QY	841	Leu	Cys	Ser	Leu	Cys	Val	Arg	Met	Gln	Asn	Leu	Phe	Ala	Gly	Ile	Arg	Asp		860			
Db	2521	TTG	GTT	CTT	TGT	CTT	ACG	GAT	ATG	AA	AA	CAA	TTT	GTC	GCG	GAT	TCG	TCG	AT		2580		
QY	861	Gly	Leu	Leu	Leu	Asp	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Ala		880			
Db	2581	GGT	TGT	TGT	GCG	TTT	GAT	GAT	ATT	CTT	TGT	TGT	ATC	CA	CA	CTT	AT	CA	CTT	2640			
QY	881	Leu	Thr	Phe	Leu	Asp	Thr	Leu	Val	Arg	Gly	Val	Pro	Gln	Val	Cys	Val	Ile	Asn	Leu	900		
Db	2641	AAA	CTT	CTT	TGG	TAC	CTT	CGT	TTC	CGT	TGC	TTC	CA	AA	TAC	CGG	TGT	GT	TTA	CTT	2700		
QY	901	Arg	Gly	Thr	Val	Val	Asn	Phe	Pro	Val	Gln	Asp	Gln	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	920	
Db	2701	CGT	AAA	CCG	GTG	TAA	CTT	CCG	ATG	GAT	GAA	GAT	AAG	CGT	TGG	TGG	TAC	CGC	CTT	CGT	2760		
QY	921	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	Thr	Cys	Gly	Leu	Leu	Asp	Thr	Arg	Thr	Leu	940		
Db	2761	CAA	TG	CCG	CA	CGC	CGT	TGT	TTC	CA	GAT	GAT	GAT	GAT	GAT	GAT	GAT	GAT	GAT	2820			
QY	941	Gln	Val	Gln	Ser	Asp	Arg	Val	Ser	Ser	Val	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	960	
Db	2821	GAA	GT	CA	AT	GT	CA	T	CT	CTT	CTT	CA	CGC	CGT	CA	CT	TA	TT	CG	T	CTT	2880	
QY	961	Asn	Arg	Gly	Phe	Val	Arg	Asn	Met	Arg	Arg	Gly	Leu	Phe	Gly	Val	Ileu	Arg	Leu		980		
Db	2881	AAC	CGT	GAT	TTC	CA	AGC	CGC	CGT	CA	TAC	GAT	GAT	GAT	GAT	GAT	GAT	GAT	GAT	2940			
QY	981	Leu	Gly	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	1000
Db	2941	AAA	GT	CA	CT	TTT	GTT	CTT	GAT	TTT	GCA	ATT	TA	CTT	TTG	CA	AA	CCG	TTT	GT	TA	CA	1000
QY	1001	Ile	Thr	Val	Ser	Ile	Leu	Leu	Gln	Ala	Val	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	1020	
Db	3001	ATT	TAC	CA	AAA	TTT	TGT	TTG	TTC	CA	AGC	CTT	CA	CGC	CTG	TGT	TTG	CA	ATT	GC	CA	1040	
QY	1021	Phe	His	Gln	Gln	Val	Trp	Leu	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile	Ser	Asp	Thr	Ala	1040	
Db	3061	TTC	CA	CA	CA	CA	AGT	TTG	GA	AAAA	CC	CA	CTT	CTT	CGG	TAT	TT	CG	AT	CA	CGC	3120	
QY	1041	Ser	Leu	Cys	Val	Ser	Ile	Leu	Val	Ala	Val	Asn	Ala	Gly	Met	Ser	Leu	Gly	Val	Arg	Gly	1060	
Db	3121	TCT	TGT	TGT	ACT	CT	AT	TTT	TA	AA	AGC	CA	AA	AA	CCG	GAT	TGT	TGG	GCC	AAA	AGT	3180	
QY	1061	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Gln	Ala	Val	Gln	Thr	Phe	Cys	His	Gln	Ala	Phe	Leu	Leu	1080	
Db	3181	GCG	CGC	CGG	TC	AT	TGC	AT	CA	T	GA												

661 LeuPheSerValIleuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerVal 680
2008 CTGTTCTCCGTTCTTAAGTACGACGCTGCTGCTCCGGTCTGCTGCTCCGTT 2067
661 LeuGlyLeuAspAspIleHisArgAlaTPrArgThrPheValIleuArgValArgAlaGln 700
2068 CTGGGTCTGAGACATCCACCGTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2127
701 AspProPheProGlnLeuTyrPheValIleuValAspValThrGlyAlaTyrAspThrIle 720
2128 GACCCGCGCGCGGAACTGTAAGTTCGTTAAAGTTGACGTTACCGCGCGCGTACACACATC 2187
721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleAspProGlnAsnThrTyrCys 740
2188 CCGCGAGACCGTCTACCGAAGTATCGCTTCATCATCAACCGAAGACCTTACCTG 2247
741 ValArgArgTyrAlaValAlaGlnIleValAlaHisGlyHisValArgIleValPheLeu 760
2248 GTTCGTCGTTACGCTGTTGTTGAGAAAGCTGCTCACGGTTCGTTAAAGCATTTCAA 2307
761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
2308 TCCCAAGTTTCCACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 2367
781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGlu 800
2368 CAGGAAACCTCCCGCTGCTGACCGTGTGTTATCGAACATCTCTCCCTCCGTAAGCA 2427
801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
2428 GCTTCCTCCGCTGCTGTTGAGAGTTTCCGCTTCAATGCAACAGCTGTTGTTATC 2487
821 ArgGlyIleSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
2488 CGTGGTAATCCTACGTTACAGTGCAGAGGATATCCCGCAGGGTTCATCTGTCACCCCTG 2547
841 LeuCysSerLeuCysTyrGlyAspMetGluAsnIleValPheAlaGlyIleArgArgAsp 860
2548 CTGTCTCTCCCTGTGCTACGCTGACGTAAGAAACATCTGCTGCTGCTGCTGCTG 2607
861 GlyLeuLeuLeuArgIleValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
2608 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2667
881 LysThrPheLeuArgThrIleuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
2668 AAAACCTTCTCGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2727
901 ArgIleThrValValAspPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
2728 CGTAACACCGTGTAACTTCCCGGTGAAGACGAAAGCTCTGAGGTGACCCCTTTCGTT 2787
921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
2788 CAGATGCGCGCTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2847
941 GlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
2848 GAAATTCAGTCCGACTACTCTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2907
961 AsnArgGlyPheLeuAlaGlyArgAsnMetArgArgIleValPheGlyValIleuArgLeu 980
2908 AACCGGTGTTTAAAGCTGCTGTAACAGCTGCTGTAACAGCTGCTGCTGCTGCTG 2967
981 LysCysHisSerLeuPheLeuAspLeuGlnValAspSerLeuGlnThrValCysThrAsn 1000
2968 AATGCGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3027
1001 IleTyrIleValIleLeuLeuGlnAlaTyrArgPheHisAlaCysValIleuGlnLeuPro 1020
3028 ATCTACAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3087

1021 PheHisGlnGlnValTPrIleAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
3088 TTCCACCGACGAGTTGGAAAAACCGACCTTCTTCTGCGGTATATCTCCGACACCGCT 3147
1041 SerLeuCysTyrSerIleLeuIleValAlaValAsnAlaGlyMetSerLeuGlyAlaValGly 1060
3148 TCCCTGCTCTACTCATCTTAAGTAAAGCTTAAAGCTGATATGCTCTGGGTCTAAAGCT 3207
1061 AlaAlaGlyProLeuProSerGlnAlaValGlnThrLeuCysHisGlnAlaPheLeuLeu 1080
3208 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3267
1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
3268 AATCTGACCGCTGACCGGTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3327
1101 ThrGlnLeuSerArgIleLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
3328 ACCCAGCTGCTCCGTAACCTGCGGGTACCACTGACCGCTGCTGGAAGCTGCTGCTG 3387
1121 ProAlaLeuProSerAspPheLeuThrIleLeuAsp 1132
3388 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3423

RESULT 12
US-09-721-456-721
Sequence 721, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997.

QY	541	LeuNlaIysPheIeuNhIeTProIeMeSeSerValTYrValValGIuIeuLeuAysSePhe	560
Db	1648	CTGGCTAAATTCCTGCACACTGGCTAGTATGCTCGTAATACGTTGTGAACGTCTCGTTCCTTC	1707
QY	561	PheTYrValIThrGIuIThrThrPheGIuIySaAsnAArgLeuPhePheTYrArgIySeSerVal	580
Db	1708	TTCTTACGTTCACGAACACCACTTCCAGAAAAACGTCCTGTTCTTCTACCGTAATTCGTT	1767
QY	581	TrpSerIySLeuGIuInSerIleGIyITLeArgGIuHIsleuIyPaRgValGIuIeuAysGIu	600
Db	1768	TGTCCTCAAACTGCAGTCCATCGGTATTCGGTCAGACACTGAACACGTGTTCACTCGGTGTA	1827
QY	601	LeuSeRgIuAIGluValArgGIuHIsArgGIuIlaaAgPProAlaIeuLeuThSeRyG	620
Db	1828	CTGTCCGAAGCTGAAGTTCGTACAGACCGTAAGCTGTCCGGCTCTGTCTACCTCCCGT	1887
QY	621	LeuArgPheIleProIyPProAspGIyLeuArgPProIleValAsnMeIAspTYrValVal	640
Db	1888	CTGCCTTTCATCCGAACCCGACCGGTCTGCCTCCGATCGTAAACATGATCACTGTTCTT	1947
QY	641	GIyAlaArgIThrPheArgArgGIuIyAArgIaIGluArgLeuThSeRyArgValIySaA	660
Db	1948	GGTGTCTGTAACCTTCCTCGTAAGAAAAAGTGTGAGCTCTGAACCTCCCGTGTAAACT	2007
QY	661	LeuPheSeRValIleuAsnTYrGIuAArgIaArgaAgPProGIyIleuLeuGIyAlaSeSerVal	680
Db	2008	CTGTCTTCCTCCGTTCTGAACATCGAAAGTGTCTGTCTCCGGGTCTGTGAGGTCTTCCTT	2067
QY	681	LeuGIyIleuAspAspIleHIsaRgAlaTTrpArgTrpPheValIleuAysValArgIaGIu	700
Db	2068	CTGGGTCTGGAGACATCCACCGTCTTGGCGTACCTTCGTTCTGCGTTCGTCTCAG	2127
QY	701	AspProProGIuIeuTYrPheValIySaIaAspValIThrGIyAlaTYrAspThrIle	720
Db	2128	GACCCGCCGCCGAACGTAGTACTGTTAAAGTTGACGTACCGCGCGGAGAACACACATC	2187
QY	721	ProGIuAspAArgLeuThrGIuValIleAlaSeRilleIeIySProGIuAsnThrTYrCys	740
Db	2188	CCGACGAGACCGCTCAGACGAATGTTCGTTCCATCATCAACACCGACAAACCTCACTGC	2247
QY	741	ValArgaSGTYrAlaValaGIuIySaIaAlaHIsGIyHIsaValArgIySaIaPheIyS	760
Db	2248	GTTTCGTCGTACGCTGTTGTTCAAAAGCTGCTACGGTACAGTTCTGTAAAGCATTCAA	2307
QY	761	SeRHisValSeRThrLeuThrAspLeuGIuProTYrMeIArgGIuPheValaIaHIsIleu	780
Db	2308	TCCACGTTTCCACCTCGACCGAACCTGACGCGGTACATCGTCAAGTTCGTTCTCACTG	2367
QY	781	GIuGIuIThrSeRProIeuAysAspAlaValIleGIuGIuInSeSeSerIeuAsnGIu	800
Db	2368	CAGGAACCTCCCCCTGCTGTCACCTGTGTATTCGAACAATCTCTCTCTCGAACGA	2427
QY	801	AlaSeSerGIyLeuPheAspValPheIeuAysPheMeCYsHIsaIaValArgIle	820
Db	2428	GCTTCTCCGGTCTGTTCGACGTTTCTCGCGTTTCATGTGCCACACACGCTGTTGTA	2487
QY	821	ArgGIyIySeSerTYrValGIuIyCysGIuGIyIleProGIuGIySeRilleuSeRThrIeu	840
Db	2488	CGTGTAAATCTTAAGTTCAAGTCCAGAGGTATCCCGACAGGTTCCATCTGTGCCACCTG	2547
QY	841	LeuCYSeSerIeuCYeTYrGIyAspMeTCIuAsnIyIleuPheAlaGIyITLeArgaAsp	860
Db	2548	CTGTCTCTCCCTGTGCTACCGTACATGTGAACAAACCTGTTGCTGTGATTCGTGTGAC	2607
QY	861	GIyIleuLeuLeuAysLeuValaAspAspPheIeuLeuValIThrProHIsIeuThrHIsaIa	880
Db	2608	GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2667
QY	881	IySThrThrPheIeuAysTrpIleuValaArgGIyValaProGIuTYrGIyCYeSaValaAsnIeu	900
Db	2668	AAACACTTCTCTCGTACCTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2727
QY	901	ArgIySThrThrValaAsnPheProValGIuAspGIuAlaIeuGIyGIyThrAlaPheVal	920

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
OTHER INFORMATION: /note= "human telomerase reverse
OTHER INFORMATION: transcriptase (hTERT) catalytic protein
component"
US-08-851-843A-224

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-044-692-2 (1-1132) x US-08-851-843A-224 (1-4015)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 56 ATGCCCGCGGCTCCCGCTGCCAGCGCGTCCCTGCGGAGCCACTACCGCGAG 115
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPargLeuValGln 40
DB 116 GTGCTGCGCCCTGCGCCAGTTCGTGCGCGCCCTGGGGCCCAAGGCGTGGCGCTGGAG 175
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 176 CCGCGGGAGCCCGCGGCTTCCCGCGCGTGGTGGCCCAAGTGGTGTGCTGCTGCTG 235
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB 236 GAGCGACGCGCGCCCGCCCGCCCTTCCTCCGCAAGTGTCTGCAAGAGAGCTG 295
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaAlaGlnValLeuAlaPheGly 100
DB 296 GTGGCCCGAGTCTGCAAGGCTGTGCGAGCGGGGCGCAAGAACCTGTGCGCTTCCGCG 355
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
DB 356 TTGCGCGCTCTGAGCGGGGCGCGGGGGCCCCCGGAGGCTTTCACCAACGAGCTGCG 415

QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
DB 416 AGCTACCTGCCCAACACGGGTGACCGACCTGCCGGGGAGCGGGCGTGGGGGCTGCTG 475
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 476 CTGCGCGCGGGGCGACACAGCTGTGCTTCACTGCTGTGACAGGCTGCGCGCTCTTTGG 535
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 536 CTGTGTGCTCCAGCTGCGCCCTTACAGAGTGTGCGGGCCCGCCCTGTACCACTCGCGCT 595
QY 181 AlaThrGlnAlaArgProProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 596 GCCACTCAGGCCCGGGCCCGCCGACACGCTAGTGACCCCGAAGGGGTCTGGGATGCGAA 655
QY 201 ArgAlaTTPAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 656 CCGGCTTGAAACCAAGCTCAGGAGGCGGGGCTCCCTGGGCTGCGACCCCGGGGT 715
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 716 GCGAGAGGCGCGGGGCGACGTGCCAGCCCAAGTCTGCTTCCCAAGAGGCCACAGGCT 775
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 776 GCGGCTGCCCTGAGCGGAGCGAGCGCCGTGTGGGAGGGGTCTCGGGCCACCGCGGC 835
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 836 AGACGCGGTGACCAAGTACCGTGTCTGTGTGTCTCACTGCGACCGCCGCGAA 895
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyTyrArgHisSerHisProSerValGly 300
DB 896 GAAGCACTCTTTGAGGGGTGCGCTCTGTGCAAGCGCCACTCCACCACTCCGTGGGC 955
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
DB 956 CGCCAGACACACGCGGGCCCCCATCCATCGCGGCGCCACAGTCCCTGGGACACGCTT 1015
QY 321 CysProProValTyrAlaGluThrIleHisPheLeuTyrSerSerGlyAspIleGluGln 340
DB 1016 TGTCCCCGCTGTACGCCGACCAAGCACTTCTCTCTCTCAGGCGACCAAGAGACAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1076 CTGCGGCTCTCTCTACTACGCTCTGTAGGCCCAAGCTACTGCGCTCGAGGCTC 1135
QY 361 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyTyrProArgArgLeuPro 380
DB 1136 GTGAGACCATCTTCTGGGTTCAGGCCCTGTGATGCCAGGGACTCCCGCAGTTGCCC 1195
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyHis 400
DB 1196 CGCTGCGCCCAAGCTACTCGCAATGCGGCCCTGTGTGTGCACTGTGTGGAAACAC 1255
QY 401 AlaGlnCysProTyrGlyValLeuLeuTyrHisCysProLeuArgAlaAlaValThr 420
DB 1256 GCGAGTGCCTTACGGGGGTCTCTCAAGAGCACTGCGCGCTCGAGCTCGGCTAC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaProGluGlu 440
DB 1316 CCAGCAGCGGAGTGTGTGCGCGGAGAAAGCCCAAGGCTGTGTGGCGGCCCGAGAG 1375
QY 441 GluAspThrAspProArgArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1376 GAGGACACAGACCCCGTGTGCTGTGACGCTGCTCCGCAAGACAGAGCCCTTGGGAG 1435
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB 1436 GTGTGCGCTTGTGCGGAGCTGTGCGCGGCTGTGGTCCCCCAGGCTCTGGGGGCTCC 1495
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrIleLysPheHisSerLeuGlyLysHis 500


```

1496 AGGCACACGAGCGCGCTTCTCCAGAGAACCAAGATTATCTCTCCGGGAGGACAT 1555
1501 AAlaylsuSerLeuGlnGluLeuThrTPrlyMetSerValArgAspCyValaTrpleu 520
1556 GCCAAGCTCTCCCTGAGAGCTGACGTGAAGATGAGGTGGGAGCTGCGCTTGGCTG 1615
521 ArgAspSerProGluValaGlyCyValaProAlaAGLHHisArgLeuArgGluGlu 540
1616 CGCAGAGAGCCAGGGGTTGGCTGTGTCCGGCCGAGAGACGCTGTGTGAGAGAGATC 1675
541 LeuAlaLysPheLeuHisTrpleuMetSerValTyrValValGluLeuLeuArgPhe 560
1676 CTGGCCAAAGTTCTCTCAGCTGAGTGTGATGATGCTGCTGAGAGTGTCTTCTTC 1735
561 PheTyrValaTrpleuThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
1736 TTTTATGTACGGAGAACACAGTTTCAAAAGAACAGGCTTTTCTTACCGGAAAGATGT 1795
581 TrpSerLysLeuGlnSerLysLeuGlyLeuArgGlnHisLeuLysArgValaGlnLeuArgGlu 600
1796 TGGACCAAGTTCCAAAGCATTTGGAATCCAGACAGCATTTGAAGAGGTGACGCTGGGAG 1855
601 LeuSerGluValaGluValaArgGlnHisArgGluValaArgProAlaLeuLeuThrSerArg 620
1856 CTGTGCGAAGCAGAGGTGACGAGCATCGGAGAACGAGCCGCGCTGTGACGTCCAGA 1915
621 LeuArgPheLeuProLysProAspGlyLeuArgProLysLeuAsnMetSerPyrValaVal 640
1916 CTCCCTTCATCTCCCAAGCTGACGGCTGCGCGCATTTGTGAACATGTGACATCACTGCGTG 1975
641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValaLysAla 660
1976 GGAGCCAGAACCTTCCGACGAGAAAGAGGCGCGAGCGCTCACTCCAGGGTGAAGGA 2035
661 LeuPheSerValLeuAsnTyrGluValaArgArgProGlyLeuLeuGluValaSerVal 680
2036 CTGTTCAACGCTCTCAACTACAGAGCGGCGCGCGCGCTCTGAGGCGCTCTGTG 2095
681 LeuGlyLeuAspAspAlaHisArgAlaTrpArgThrPheValLeuArgValaArgAlaGln 700
2096 CTGGGCTCGAGAGATATCCACAGGCGCTGGCGCACCTTGTGTCTGCTGTGGGCGCCAG 2155
701 AspProProGlnLeuTyrPheValLysValAspValaThrGlyValaTyrAspThrIle 720
2156 GACCGCGCGCTGAGCTGACTTTGTCCAGAGTGAATGTACAGCGGCGCGTACACACATC 2215
721 ProGlnAspArgLeuThrGluValaIleAsnIleLysArgProGlnAsnThrTyrCys 740
2216 CCCCAGGACAGGCTCAGGAGGTATCGCCAGCATCATCAACCCAGAACAGATATGTC 2275
741 ValaArgArgTyrAlaValaGlnLysAlaAlaHisArgHisValaArgValaLysPhe 760
2276 GTGCTCGGTATGCGGTGTCCAGAGGCGCGCCATGGGACAGTCCGCAAGGCGCTTCAAG 2335
761 SerHisValaSerThrLeuThrAspLeuGlnProTyrMetArgGluPheValaHisLeu 780
2336 AGCCACGCTCTCACTTGAAGACCTCCAGCCGTACATGCGACAGTTGCTGCTAAGCTG 2395
781 GlnGlnThrSerProLeuArgAspAlaValaValaIleGlnGlnSerSerSerLeuAsnGln 800
2396 CAGGAGACAGGCGCGCTGAGGATCGCGTCCATCCAGACAGAGCTCCCTCGATGATAG 2455
801 AlaSerSerGlyLeuPheAspValaPheLeuArgPheMetCysHisHisAlaValaArgIle 820
2456 GCCACAGAGGCTCTTGCACGCTTCTCAACCTTCAATGTGACACACCCGCTGGCGATC 2515
821 ArgGlyLysSerTyrValaGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
2516 AGGGCAAGCTCTACGTCCAGTGCAGGGGATCCCGAGAGGCTTCATCTCTCCAGCTG 2575
841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

```

```

2576 CTCTGACAGCTGTGCTTACGGGACATGAGAACAAAGCTTTTGGGGGATTCGGCGGAGC 2635
861 GlyLeuLeuLeuValaAspAspPheLeuLeuValaThrProHisLeuThrHisAla 880
2636 GGGCTGCTCTCCGCTTTGTGGATGATTTCTTTGTGGTGAACCTCACCCTCACAGCGG 2695
881 LysThrPheLeuArgThrLeuValaArgGlyValaProGluTyrGlyCysValaValaAsnLeu 900
2696 AAAACCTTCTCAGAGACCTGGTCCGAGGTGCTCCGTGATATGCTGCTGGTGAACCTG 2755
901 ArgLysThrValaValaAsnPheProValaGlnAspGluValaLeuGlyValaThrAlaPheVal 920
2756 CGGAAGACAGGTGAACCTTCTGTGAAGACAGAGGCGCTGGGAGCAGCGCTTTTGT 2815
921 GlnMetProAlaHisGlyLeuPheProTyrPyrGlyLeuLeuLeuAspThrArgThrLeu 940
2816 CAGATGCGGCGCCAGCGCTTATCTCCCTGTGCGGCTGCTGCTGATATCCCGAGACCTG 2875
941 GlnValaGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
2876 GAGGTGACAGAGGACTACTCCAGCTATGCGCGACCTTCATCAGAGCCAGTCTACCTTC 2935
961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValaLeuArgLeu 980
2936 AACCGCGCTTCAAGGCTGGAGAACATGCGTCCCAACTTTTGGGTCTTGGCGGCTG 2995
981 LysCysHisSerLeuPheLeuAspLeuGlnValaAsnSerLeuGlnThrValaCysThrAsn 1000
2996 AAGTGTCAAGCTTTTGTGATTTGACAGGTGAACAGCTTCCAGACGGTGTGCACCAAC 3055
1001 IleTyrLysLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValaLeuGlnLeuPro 1020
3056 ATCTCAAGATCTCTCTGTCAGAGCGTAAAGTTTCAAGCATGTGTGCTGACAGCTCCA 3115
1021 PheHisGlnGlnValaTrpLysAsnProThrPhePheLeuArgValaIleSerAspThrAla 1040
3116 TTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGGTATCTTCAACAGCGGC 3175
1041 SerLeuCysTyrSerLysLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
3176 TCCCTCTGCTACTCATCTGTAAGCCAGAACCGAGGAGATGCTGCGGGCGCAAGGGC 3235
1061 AlaAlaGlyProLeuProSerGlnAlaValaGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
3236 GCGCGCGCGCTCTGCTGCTCCAGGCGCTGAGGTGCTGTGCAACAAAGATCTCTGCTC 3295
1081 LysLeuThrArgHisArgValaThrTyrValaProLeuLeuGlySerLeuArgThrAlaGln 1100
3296 AAGCTGACTCGACACCGTGTCACTTACGTGCCACTCTGGGGGTCACTCAGAGCACGCCAG 3355
1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
3356 ACGCAGCTGAGTGGAGACTCCGGGAGACGAGCTGAGCTGCGCTGTGAGGCGCAGCAGAAC 3415
1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
3416 CCGGACATGCTCTCAGACTTCAAGACATCTCGAAC 3451

```

RESULT 14
 US-08-974-549A-1
 Sequence 1, Application US/08974549A
 Patent No. 6166178
 GENERAL INFORMATION:
 APPLICANT: Czech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56..3454
 OTHER INFORMATION: /product= "hTERT"
 OTHER INFORMATION: /note= "human telomerase reverse
 OTHER INFORMATION: transcriptase (hTERT) catalytic protein
 OTHER INFORMATION: component"
 US-08-974-549A-1

Alignment Scores:
 Pred. No.: 0
 Score: 5961.00
 Percent Similarity: 100.008
 Best Local Similarity: 100.008

Length: 4015
 Matches: 1132
 Conservative: 0
 Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-044-692-2 (1-1132) x US-08-974-549A-1 (1-4015)

1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 56 ATGCCGCCGCTCCCGCTGCCGAGCCGTGGCTCTCCCTGCGCAGACCTACCCGAG 115
 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
 116 GTGTCGCGCTGGCCACGTTGTCGCGCGCTGGAGGCCCCAGAGCTGGCGCTGTGAG 175
 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 176 CGCGGGAGACCGCGGCTTTCCGCGCGCTGGTGGCCAGTGGCTGTGTGCGCTGGC 235
 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLeuGluLeu 80
 236 GACGACCGCGCCCGCCCGCGCCCTTCCTCCGACGAGTGTCTGTGCTGAAGAGCTG 295
 81 ValAlaArgValLeuGlnArgLeuGlyArgGlyValAlaValAspValLeuAlaPheGly 100
 296 GTGCGCCGAGTGTCTGAGAGCTGTGCAAGCGCGGAGAGACCTGTGCTTCCGCG 355
 101 PheAlaLeuLeuAspGlyValaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 356 TTGCGCTGTGAGAGGGGCGCGGGGCGCCCGCGAGGCTTACACACAGCTGCGC 415
 121 SerTyrLeuProAlaThrValThrAspAlaLeuArgGlySerGlyValaTyrGlyLeuLeu 140
 416 ACCTACCTGCGCCACGAGTGTGACGACGACGCGGGAGCGGGGCGTGGGCGCTGCG 475
 141 LeuArgArgValaGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 476 CTGCGCGCGCTGGCGGACGACGTGCTGTCACTGTGCGACGCTGCGCGCTTTGG 535
 161 LeuValaAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 536 CTGGTGGCTCCAGCTGCGGCTTACGAGGTGCGGGGCGCGCTGTACAGCTCGGCGCT 595
 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 596 GCACCTCAGCGCCCGCCCGCCGACACGCTATGTGACCCGAGGCGTCTGGAGATCGGA 655
 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValaProLeuGlyLeuProAlaProGly 220
 656 CGGGCTGGAACCAAGCGTCAGGAGCGCGGGGTCCCTGGGCTGTGCACGCCGCGGT 715
 221 AlaArgArgArgGlyGlySerAlaSerAlaSerArgSerLeuProLeuProGlyArgArgArg 240
 716 GCGAGGAGCGCGGGGCGAGTCCAGCGAAGTGTGCGCTTCCCAAGAGCGCCGCGCT 775
 241 GlyAlaAlaProGlnProGlnArgThrProValaGlyGlnGlySerThrAlaHisProGly 260
 776 GGCGCTGCCCTGAGCGGAGCGAGCGCGCTTGGGAGGGGTCTTGGGCCACCCGGGCG 835
 261 ArgThrArgGlyProSerAspArgGlyPheCysValaValSerProAlaArgProAlaGln 280
 836 AGGACCCGTGACCAAGTACCTGTGTTCTGTGTGTCTACCTGCCAGACCCGCGGAA 895
 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValaGly 300
 896 GAAGCCACTCTTTGAGGGGTGCGCTCTGTGACGCGCACTCCACCACTCCGTGGGCG 955
 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
 956 CGCCAGCACCGCGGCGCCCATTCACATCGCGGCAACAGTCCCTGGGACACGCGCT 1015
 321 CysProProValTyrAlaGlnThrTyrHisPheLeuTyrSerSerGlyAspLysGlnGln 340
 1016 TGTCCCCCGGTATACCGGAGACCAAGCACTTCTCTACTCTTCAAGCGGACCAAGAGGAG 1075

341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgLeu 360
Db CTGGGCCCCCTCTTCTACTAGCTCTCTGAGGCCAGCTGACCTGGCGCTCGAGGCTC 1135
361 ValGluThrIlePheLeuGlySerArgProThrMetProGlyThrProArgArgLeuPro 380
Db GTGGAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCGAGTTGGCC 1195
381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400
Db GCGCTGCCCGACGCTGAGGAAATGCGGCCCTGTTTCTGGAGCTGCTTGGAAACAC 1255
401 AlaGlnCysProTyrGlyValLeuLeuGlyThrHisCysProLeuArgAlaAlaValThr 420
Db GCGGAGTGGCCCTTACGGGGTGTCTCTCAAGACGACTGCCCTGGAGCTGGGCTGAC 1315
421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGlnGlu 440
Db CCAGACGCGGTGTCTGTCCCGGAGAAAGCCCGAGGGCTGTGTGGCGGCCCGCGAG 1375
441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProThrGln 460
Db GAGGACACAGACCCCGTGGCTGTGGTGTCTCGCCAGACAGACAGACCCCTGGCAG 1435
461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrProGlySer 480
Db GTGTACGGCTTGTGTGGGGCTGTGCTGCCCGGTGTGTCTCCCGACGCTCTGGGGCTC 1495
481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
Db AGGCAACAGAACGCGCTTCTCTCAGAGAACACCAAGAACTCATCTCCCTGGGAGAGCAT 1555
501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db GCGAAGCTCTCCCTGAGGAGCTGACGTGAAGATAGCGTGGGAGCTGCGTGGCTG 1615
521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLe 540
Db CCCAGAGGCCCAAGGGTGTGTGTGTCCGGCCGAGACACCGCTGTGGTGAAGAGATC 1675
541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db CTGGCCAAAGTCTCTGACTGGCTGATGTGTATGATGATGATGATGATGATGATGATG 1735
561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db TTTTATGTACCGAGACCAAGCTTTCAAAAGAAACAGGCTCTTTTTCACCGGAAAGATGTC 1795
581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db TGGAGCAAGTTCGAAAGCATTTGGAAATCAACAGCACTTGAAGAGGATGAGCTGGGGAG 1855
601 LeuSerGlnAlaGluValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db CTGTCCGAAGACGAGAGTCAAGGAGCATCGGAAAGCAAGGCCCGCTGTGATGCACA 1915
621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db CTCCTGCTTATCTCCCAAGCCTGACGGGCTGCGGCTCATTTGTGAACATGACATCACTG 1975
641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db GAGGCCAAGACGTTCCGAGAGAAAGAGAGGCCGAGCTGTCACTTCAGAGGATGAGAGGA 2035
661 LeuPheSerValLeuAsnTyrGlnAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db CTGTTCAAGCTGCTCACTACAGAGCGGGCGGGCGCCGCTCTCGGAGCGCTCTGAG 2095
681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
Db CTGGGCTGAGACATATCCACAGAGGCTGAGCACTTCTGTGTGTGTGTGTGTGTGTGTGT 2155
701 AspProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720

2156 GACCCCGCCGCTGACCTACTTGTCAAGGTGATGTGACGGGGCGCTGACACACCATC 2215
721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db CCCCAGAGAGGCTACAGAGGTATCGCCAGCATATCAAAACCCAGAACAGATATGC 2275
741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db GTGGCTCGGTATGCCGTGTGTCCAGAGGCCGCCCATGGGCAAGCTCCGCAAGGCTTCAAG 2335
761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db AGCCACGCTCTTACCTTGACAGACCTCCAGCGGTATATGCAAGTTCGTGCTGACCTG 2395
781 GlnGluThrSerProLeuArgAspAlaValAlaIleGlnGlnSerSerSerLeuAsnGlu 800
Db CAGGAGACCAAGCCCGTGAAGGATCGCTGTATCGACAGACAGCTCTCTCTGAATAG 2455
801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db GCCACAGTGGCTCTTTCGACGCTTTCCTACGCTTATGTGCAACACCGCGTGGCATC 2515
821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db AGGGCAAGTCTTACGTCAGATGCCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTG 2575
841 LeuCysSerLeuCysTyrGlyLysPheMetGluAsnLysPheAlaGlyIleArgArgAsp 860
Db CTCTGACGCTGTGTGTACCGGCACATGAGAACAGAGCTGTGTGGCGGATTTGGCGGGAC 2635
861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db GGGCTGTCTCTCGT 2695
881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db AAACCTTCTCAGAGACCTGTGTCCGAGGTGTCCCTGATATGAGCTGTGTGTGAACCTG 2755
901 ArgLysThrValValAsnPheProValGluAspGlnAlaLeuGlyGlyThrAlaPheVal 920
Db CGAAGACAGTGTGTGAACCTTCTGTGAGAAAGCAGAGCCCTGGTGGCAAGCTTTTGT 2815
921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db CAGATGCGGCCCAAGGCTTATTCCTGTGAGAGAGAGGCTGTGTGTGTGTGTGTGTGTGT 2875
941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db GAGGTGCAAGAGGACTACTCCAGCTATGCGGACCTCATCAGAGCCAGTCTCACCTTC 2935
961 AsnArgGlyPheLysAlaGlyValArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db AACCCCGGCTCTCAAGGCTGGAGAGAACATGCTCCGAAACTTTTGGGGTCTTTCGCGCTG 2995
981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db AAGTGTCAAGCTGTTTGTGATTTGACAGGTGAACAGCTCCAGACGATGTGCACCAAC 3055
1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db ACTCAAGATCTCTCTGTCAGAGGCTACAGTTTCAAGCATGTGTGTGTGTGTGTGTGTGT 3115
1021 PheHisGlnGlnValITrpyAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db TTTTCATCAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGGTATCTCTACACCGGGC 3175
1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
Db TCCCTGTCTACTCATCTTGAAGCCAGAACGAGGATTCGCTGGGGGCGCAAGGC 3235
1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080

Db 3236 GCCGCCGCCCTCTGCTCCGAGCCGTGACGTGTCACCAAGACATTCCTGCTC 3295
 QY 1081 LysLeuThrArgHisArgValThrIYValProLeuLeuGlySerLeuArgThrIaGln 1100
 Db 3296 AACGTACTGACACCGCTGTCACTTACGTCCACTCTCTGGGTCATCTACGACAGCCCGAG 3355
 QY 1101 ThrGlnLeuSerArgIYsLeuProGlyThrThrLeuThrAlaLeuIuaIaIaIaasn 1120
 Db 3356 ACCGACGTGAGTGGAGAGCTCCGGGGAGACGACGCTGACTGCTCTGGAGGCCGACGCCAAC 3415
 QY 1121 ProAlaLeuProSerApphelysThrIleLeuAsp 1132
 Db 3416 CGGGCACTGCGCTCAAGACTTCAAGACCATCTGGAC 3451
 RESULT 15
 US-08-854-050-224
 Sequence 224, Application US/08854050
 Patent No. 6261836
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Hatley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6261836el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 224:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

/ MOLECULE TYPE: cDNA
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 56..3454
 / OTHER INFORMATION: /product= "hTRT"
 / OTHER INFORMATION: /note= "human telomerase reverse
 / OTHER INFORMATION: transcriptase (hTRT) catalytic protein
 / OTHER INFORMATION: component"
 US-08-854-050-224
 Alignment Scores:
 Pred. No.: 0 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-044-692-2 (1-1132) x US-08-854-050-224 (1-4015)
 QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisIYrArgIu 20
 Db 56 ATGCGCGGCTCCCGCTGCCAGCGGTGCGCTCTGCTGCGACGACCTACCGCGAG 115
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 Db 116 GTGCTGCGCGCTGCCACCGTGTGCGGCGCTGGGGGCCACAGGCTGGGCGCTGTGCGAG 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTTP 60
 Db 176 CCGGGGAGACCCGCGCGCTTTCGCGCGCTGTGCGCGCGAGTGTGCTGTGTGCTGTGCG 235
 QY 61 AspAlaArgProProProAlaAlaPheSerPheArgGlnValSerCysLeuIYsGluLeu 80
 Db 236 GACGACG 295
 QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaIYsAsnValLeuAlaPheGly 100
 Db 296 GTGGCGCGAGTCTGCAAGGCTGTGCGAGCGCGCGCGAGAAAGTGTGCTGTGCGCG 355
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyIYsProProGluAlaPheThrThrSerValArg 120
 Db 356 TTCGCGCTGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgIYsSerGlyAlaTTPGlyLeuLeu 140
 Db 416 AGCTACCTGCCAACAACGCTGACCGACGACGCGCGGAGCGCGCGCGCGCGCGCGCTG 475
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 476 CTGGCGCGCGTGGCGGACGACGCTGTGCTTCACTGTGCGACGCTGCGCGCTTTTGTG 535
 QY 161 LeuValAlaPheProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 536 CTGTGTGCTCCAGCTGTGCTTACCGAGGTGTGCGGCGCGCGCTGTACAGCTTGGCGCT 595
 QY 181 AlaThrGlnAlaArgProProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 Db 596 GCCATCAGCGGT 655
 QY 201 ArgAlaTTPAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 656 CGGGCTGTGAACATAGCGTCAAGGAGCGCGGGGTCCCTGTGGCGCTCCAGCGCGGGT 715
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProIYsArgProArgArg 240
 Db 716 GCGAGAGCGCGCGGCGGAGTGCAGCGCAAGTGTGCGGTGCCCAAGAGCGCGCGGT 775
 QY 241 GlyAlaAlaPheProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
 Db 776 GCGCGTGCCTCTGAGCGCGAGCGAGCGCGCGCTTGTGGAGGCGGCTCTTGGGCCACCGCGG 835
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280

```
Db      836 AGAAGCGGTGGACCGAGTGAACGTGTTCTGTGTGATGCTGACCTGCCAGACCCGCCGAA 895
Qy      281 GUAUATThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db      896 GAAGCACCTCTTGGAGGGTGGCTCTCTGGCAGCGCCACTCCACCCTATCCCTGGGC 955
Qy      301 ArgGlnHisAlaGlyProProSerThrSerArgProArgProThrAspThrPro 320
Db      956 CGCCAGCACAGCGGGCCCCCATTCACATGCGGACACAGCTCCCTGGAGACGGCTT 1015
Qy      321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
Db      1016 TGTCCCCGGGTGTAGCGCGAGACCAAGCACTTCTCTACTCTCTCAGGGGAGCAAGAGCAG 1075
Qy      341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db      1076 CTGCGGCGCTCTCTCTACTAGCTCTCTGAGCGCCAGCTGACTGCGGCTTGGAGGCTC 1135
Qy      361 ValGluThrIlePheLeuGlySerArgProThrMetProGlyThrProArgArgLeuPro 380
Db      1136 GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAACTCCCGCAGGTTGCC 1195
Qy      381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGluLeuLysHis 400
Db      1196 CGCCTGCCCGCCAGCGCTACTGCGCAATGGCGCCCTGTTTCTGGAGCTGTTGGAAACAC 1255
Qy      401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db      1256 GCGCGAGTCCCTTACGGGGTGTCTCTCAAGACGACTGCCCGCTCGAGCTCGCGTCAAC 1315
Qy      421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGlnGlu 440
Db      1316 CCAAGACGCGGGTGTGTGCCCCGAGAGAGCCCGAGGCTGTGTGGCGCCCGCAGAGAG 1375
Qy      441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
Db      1376 GAGGACACAGACCCCGCTGCTGCTGTCAGCTGCTCCGCGACACAGACGCCCTGGCAG 1435
Qy      461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrGlySer 480
Db      1436 GTGTTCGCGCTTCTGTCGGGGCTGCTGCGCGCCGCTGTGTCGCCCGAGGCTCTGGGGCTCC 1495
Qy      481 ArgHisAsnGluArgArgPheLeuArgHisThrLysPheIleSerLeuGlyLysHis 500
Db      1496 AGGCAACAAGAACGCCGCTTCTCAAGAACACCAAGAGTTATCTCCCTGGGGAAAGCAT 1555
Qy      501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaThrLeu 520
Db      1556 GCCAAGCTCTGCTGCTGACGAGAGCTGACGTGAGATGAGCGTCCGGGACTGCCCTTGGCTG 1615
Qy      521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGluIle 540
Db      1616 CGCAGAGACCCCGGGGTTGGCTGTGTCCGCGCGCAGAGCACCGTCTGCTGATGAGAGATC 1675
Qy      541 LeuAlaLysPheLeuHisThrLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db      1676 CTGGGCAAGTTCTCTCACTGCTGATGAGTGTGATGCTGCTGACTGCTGAGGCTTTC 1735
Qy      561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db      1736 TTTTATGTCACGAGAACCAACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGC 1795
Qy      581 TrpSerLysLeuGlnSerIleGlyTyrLeuArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db      1796 TGGACAAGAGTTGCAAGATCGAATCGACAGCACTTGAAAGAGGTTGACGCTGGCGGAG 1855
Qy      601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db      1856 CTGTGGAAAGAGAGGTGAGGAGCTCGGGAAAGCCGCGCCCTGTGTGACGTCCAGA 1915
Qy      621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db      1916 CTCGCGTTTCATCCCAAGCTGACGGGCTGGCGCGGATTTGTGAACATGACTACGTCGTG 1975
Qy      641 GUAUATThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db      1976 GAGCGAAGAGTTCCGAGAGAAAGAGGCCCGAGGCTCTCACTCAAGGGTGAAGCA 2035
Qy      661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db      2036 CTGTTTACGCTGTCAACTACAGAGCGGGCGCGGCCCGGCGCTCTGGGGCTCTGTG 2095
Qy      681 LeuGlyLeuAspAspIleHisArgAlaThrArgThrPheValLeuArgValArgAlaGln 700
Db      2096 CTGGGCGCTGAGAGATATCCACAGGCGCTGGCGCACCTTCTGCTGCTGCTGGCGGCCAG 2155
Qy      701 AspProProProGluLeuTyrPheValLysValAspValThrGlyValTyrAspThrIle 720
Db      2156 GACCGCGCGCTGAGCTTACTTGTCAAGGTGATGAGGAGGGCGGCGTACACACACTC 2215
Qy      721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db      2216 CCCCAGACAGGCTTACCGAGAGTCAATGCCCAAGCATCAAAACCCAGAACACGTAATCC 2275
Qy      741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db      2276 GTGCGCTCGGTATGCGCTGTGTCAGAAAGCCGCCCATGCGGCAAGCTCCGCAAGGCTTCAAG 2335
Qy      761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db      2336 AGCCAGTCTTACTTACAGAACCTCCAGCGGTACAGCAAGTTGTGTGCTCACTG 2395
Qy      781 GlnGluThrSerProLeuArgAspAlaValAlaIleGlnGlnSerSerSerLeuAsnGlu 800
Db      2396 CAGAGACACAGCCCGCTAGAGGATCCCTGCTCATGACAGAGACTCTCTCTGATAG 2455
Qy      801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
Db      2456 GCACAGATGAGCTCTTGTGAGTGTCTTCAAGCTTCAAGTCCACCAAGCGGTGGCATTC 2515
Qy      821 ArgGlyLysSerTyrValGlnCysGlnLysIleProGlnGlySerIleLeuSerThrLeu 840
Db      2516 AGGGCAAGTCTTACGTCACAGTCCAGGGAGTCCGAGGGCTTCATCTTCCACGCTG 2575
Qy      841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db      2576 CTCTGACAGCTGTGCTAGCGGACATGAGAAACAAGCTTTTGGCGGATTTGGCGGAGAC 2635
Qy      861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db      2636 GGGCTGCTCCGTGGTGTGGATGATTTCTTGTGTGAGACCTCACTCACCCACGCG 2695
Qy      881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db      2696 AAAACCTTCTCAGAGACCTGCTGCGAGGTGCTCCGTGAGTATGCTGTGGTGAACCTTG 2755
Qy      901 ArgLysThrValAlaAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db      2756 CGAAGAGATGTGTAACTTCCCTTAAAGACAGAGGCCCTGGGTGGACAGGCTTTGT 2815
Qy      921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db      2816 CAGATGCGGGCCACAGGCTTATTCCTCTGTGGGCTGTGCTGTGATACCGGACCTTG 2875
Qy      941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db      2876 GAGGTGACAGAGACTTACTTCAAGCTATGCCCCGAGCTTCATCAAGGCAAGTTCACCTTC 2935
Qy      961 AsnArgGlyPheLysAlaGlyArgHisMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db      2936 AACCGGCTTCAAGGCTGCGAGAGAACATGCTGTGCAAACTTTTGGGGCTCTGGGGCTG 2995
Qy      981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db      2996 AAGTGTCAAGGCTGTCTTGTGATTTGACAGGTGAACACCTTCAAGACGGTGTGACCAAC 3055
```

```
Qy 1001 11eTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTACAGAGATCTCTCTGCGAGGCGTACAGGTTTCACGACATGTGTCTGCAGCTCCCA 3115
Qy 1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCATCAGCAGATTGGAGAAGACCCACATTTTCTCTGCGGTCACTCTGACAGGCC 3175
Qy 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
Db 3176 TCCCTCTGCTACTCCATCTGAAAGCCAAAGACGACGAGATGCGCTGCGGGCCAAAGGGC 3235
Qy 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCCGCGGCGCTCTGCGCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC 3295
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTGACACCCGTGTCACTTACGTGCCACTCTGGGGTCACTCAGACAGCCAG 3355
Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTGGAGAGCTCCGCGGAGACGACGCTGACTGCGCTGGAGGCCGCGAGCCAAAC 3415
Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGCACTGCGCTCAGACTTCAAGACCACTCTGGAC 3451
```

Search completed: October 28, 2004, 15:24:24
Job time : 432 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 09:37:01 : Search time 11351 Seconds
(without alignments)
4716.055 Million cell updates/sec

Title: US-10-044-692-2
Perfect score: 5961
Sequence: 1 MPRAACRAVMSLRSHYRE.....TALBAANPALPSDEKTLID 1132

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n.model -DEV=xlh
-O=/cgn2.1/USPTO_spool/US10044692/runat_28102004_103654_1358/app_query.fasta_1.1287
-DB=GenEmbl1 -QFMT=fastap -SUFFIX=xrge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCT -NOM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044692@cgn2.1_1.6972@runat_28102004_103654_1358 -NCPU=6 -ICPU=3
-NO_WMAP -LARGECUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl1.*
1: gb_ba.*
2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_srs.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	3396	6 AR393358	Sequence
2	5961	100.0	3396	6 AR393359	Sequence
3	5961	100.0	3396	6 AR393360	Sequence
4	5961	100.0	3396	6 AR393361	Sequence

5	5961	100.0	3396	6 AR393362	Sequence
6	5961	100.0	3396	6 AX957656	Sequence
7	5961	100.0	3396	6 BD091553	Adult bon
8	5961	100.0	3396	6 BD094749	The cell
9	5961	100.0	3396	6 BD096291	Cells cap
10	5961	100.0	3399	6 AX481414	Sequence
11	5961	100.0	3451	6 AR393441	Sequence
12	5961	100.0	4015	6 AR104587	Sequence
13	5961	100.0	4015	6 AR175848	Sequence
14	5961	100.0	4015	6 BD178834	Method an
15	5961	100.0	4015	6 E36793	Human telom
16	5961	100.0	4015	6 AR182221	Sequence
17	5961	100.0	4015	6 AR224455	Sequence
18	5961	100.0	4015	6 AR226390	Sequence
19	5961	100.0	4015	6 AR243328	Sequence
20	5961	100.0	4015	6 AR263555	Sequence
21	5961	100.0	4015	6 AR265996	Sequence
22	5961	100.0	4015	6 AR390470	Sequence
23	5961	100.0	4015	6 AR393084	Sequence
24	5961	100.0	4015	6 AR404030	Sequence
25	5961	100.0	4015	6 AR438403	Sequence
26	5961	100.0	4015	6 AX019310	Sequence
27	5961	100.0	4015	6 AX133979	Sequence
28	5961	100.0	4015	6 AX552695	Sequence
29	5961	100.0	4015	6 AX810036	Sequence
30	5961	100.0	4015	6 BD011044	Human tel
31	5961	100.0	4015	6 BD011583	Quantitat
32	5961	100.0	4015	6 BD082985	Method fo
33	5961	100.0	4015	6 BD131727	Method fo
34	5961	100.0	4015	6 AF015950	Homo sapi
35	5961	100.0	4042	6 AX001446	Sequence
36	5961	100.0	4042	6 AX003121	Sequence
37	5961	100.0	4042	6 BD136185	Human tel
38	5961	100.0	4070	6 AX391946	Sequence
39	5961	100.0	4015	6 CQ717133	Sequence
40	5961	99.9	3396	6 BD196290	Vertebral
41	5961	99.9	3396	6 BD196267	Vertebral
42	5961	99.9	4027	6 BD233924	Method an
43	5961	99.9	4027	6 AF018167	Homo sapi
44	5961	99.9	8860	12 AR043739	Synthetic
45	5961	99.8	4037	6 E36819	Human telom

ALIGNMENTS

RESULT 1
LOCUS AR393358 3396 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 638 from patent US 6617110.
ACCESSION AR393358
VERSION AR393358.1 GI:40118784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3396)
AUTHORS Cech,T.R., Lingner,U., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL Patent: US 6617110-A 638 09-SEP-2003;
FEATURES
source Location/Qualifiers
1..3396
/organism="Unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 6.73e-151
Score: 5961.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 3396
Matches: 1132
Conservative: 0
Mismatch: 0
Indels: 0

DB: 6 Gaps: 0
US-10-044-692-2 (1-1132) x AR393358 (1-3396)

QY 1 MetProAlaGlaProAlaGlyCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
Db 1 ArgCGCGCGCGCGCGCGCTGCGCGCGGTGCGAGCCGTGCGCCAGCATTTATCGCGAA 60

QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPAArgLeuValGln 40
Db 61 GTGCTGCGCGCTGCGAGCACTTTGTGCGCGCTGAGCCGCGAGGCTGAGCGCTGTGCGAG 120

QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 121 CGCGCGCGATCGCGCGCGCTTTCGCGCGCTGTGCGCGAGTCCCTGAGTGTGCTGCGCTGG 180

QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGluLeu 80
Db 181 GATCGCGCGCGCGCGCGCGCGCGCGAGCTTTTGGCCAGGTGAGCTCCGTAAGAAAGAACTG 240

QY 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyValAlaValAsnValLeuAlaPheGly 100
Db 241 GTGCGCGCGCGCTGCGAGCACTTGTGCGCGCTGCGAGCGCGCGCGAAAGAGTGTGCGCTGGC 300

QY 101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
Db 301 TTTGCGCTGCTGATGCGCGCGCGCGCGCGCGCGCGCGAGCGTTTACCAACAGGTGCGC 360

QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATTPGlyLeuLeu 140
Db 361 AGCTATCTGCGCAACACGTGACCGATGCGCTGCGCGCGCGCGCGCGGTGAGGCTGTGCTG 420

QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 421 CTGCGCGCGCGCGCGATGATGTCGTGTCATCTGTCGCGCGCGCGCTGCTGTTGTCG 480

QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 481 CTGCTGCGCGCGAGCTGCGGTACAGTGTGCGCGCGCGCGCGCTGTATCATCGTGTGCGCG 540

QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
Db 541 GCGAGCCAGCGCGCGCGCGCGCGCATGCGAGCGCGCGCGCGCGCGCTGTGAGTGGAA 600

QY 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 601 CGCGCGTGAACCAATAGCTGCGCGAGCGCGCGTGTGCGCTGCGCGCGCGCGCGCGG 660

QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProAlaArg 240
Db 661 GCGCGCGCGCGCGCGCGCGCGAGCGCGCGCTGCGCTGCGCGAAACCGCGCGCGCG 720

QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
Db 721 GCGCGCGCGCGCGAGAACCGAACCGCGGTGCGCGAGCGAGCTGTGCGCATCCGGGG 780

QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
Db 781 CGGACCGCGCGCGCGCGATCGCGCTTTGCGTGTGAGCGCGCGCGCGCGCGCGAGAA 840

QY 281 GlyAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 841 GAAGGCAACGCTGGAAGCGCGCTGAGCGGCAACCGCGCATGCGATCGGAGCGTGGGC 900

QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
Db 901 CGGCACATCATATCGCGCGCGCGAGCAACAGCGCGCGCGCGCGCGTGTGGATACCCG 960

QY 321 CysProProValTyrAlaGlnTyrHisPheLeuTyrSerSerGlyValAspGlnGln 340
Db 961 TGCCTGCGCGGTATGCGGAAACAAATTTCTGTATAGCAGCGCGCATTAAGAAACAG 1020

QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360

Db 1021 CTCGCCCGAGCTTTCTGCTGAGCACTGCGCCGAGCTGACCGCGCGCGCGCGCTG 1080

QY 361 ValGlnThrIlePheLeuGlnGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380

Db 1081 GTGAAACCATTTTTCTGGGAGCGCGCGCGGTGATCGGGAGCAACCGCGCGCGCTGCGCG 1140

QY 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuLeuGlnHis 400

Db 1141 CGCTCCCGAGCGCTATTTGGCAGATGCGCGCTGTCTGTGAACTGCTGGGCAACAT 1200

QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420

Db 1201 GCGCACTGCCCGATGCGCTGCTGCGAAACCATATGCCCTGCGCGCGCGCGGTGAC 1260

QY 421 ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGln 440

Db 1261 CGCGCGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAA 1320

QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460

Db 1321 GAAGATACGATCCGCGCGCTGTGTCAGCTGTGCGCGCGCATAGCAGCCGTGCGAG 1380

QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrGlySer 480

Db 1381 GTGTATGCTTTGTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440

QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysPheIleSerLeuGlyLysHis 500

Db 1441 CGCATTAACGAACGCGCGCTTTCTGTGCGCAACCAAAATTTATTAAGCTGTGGCAACAT 1500

QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrrLysMetSerValArgAspCysAlaThrLeu 520

Db 1501 GCGAAACTAGCTGCTGCGAGAACTGACCTGGAAGAAAGAGGTGCGGATTTGCGGTGGCTG 1560

QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGln 540

Db 1561 CGCCCGAGCGCGCGGTGGCTGCTGCGCGCGCGCGAGCAATCGCTGCGCGAGAAATTT 1620

QY 541 LeuAlaLysPheLeuHisThrLeuMetSerValTyrValValGlnLeuLeuArgSerHe 560

Db 1621 CTGGGAAATTTCTCATTTGCTGATGAGCGTGTATGTGTGGAATCTGCTGCGAGCTTT 1680

QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerVal 580

Db 1681 TTTTATGTGACCGGAACCACTTTTCAAAAAACCGCTTTTATTCGAAAAAGCTG 1740

QY 581 TrpSerLysLeuGlnSerIleGlyTlleArgGlnHisLeuLysArgValGlnLeuArgGln 600

Db 1741 TGGAGCAACCTGCAAGCATTTGGCATTCGCAACATCTGAACCGGTGCACTGCGCGAA 1800

QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620

Db 1801 CTGAGCGAAGCGGAAGTGGCGAGCATGCGAAGCGCGCGCGCGCTGTACCAAGCGCG 1860

QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640

Db 1861 CTGCGCTTTATTCGGAACCGGATGCGCTGCGCGCGATTTGGAACATGATATGTGTG 1920

QY 641 GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660

Db 1921 GCGCGCGCGACCTTTGCGCGGAAAGCGCGCGAAACCGCTGACAGCGCGGTGAAAGCG 1980

QY 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlnAlaSerVal 680

Db 1981 CTGTTTACGCTGCTCAATTATGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGTG 2040

QY 681 LeuGlyLeuAspAspIleHisArgAlaTrrPargThrPheValLeuArgValArgAlaGln 700

Db 2041 CTGGGCGCTGATGATATCATCGCGGTGCGCACTTTGTGCTGCGCGGTGCGCGCGAG 2100

QY 701 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720

```

Db      2101 GATCCGCCGCCGGAACGTATTGTTGTAAGTGAATGACCGCGCGTATGATCACTT 2160
Qy      721 ProGlnaPArgLeuThrGluValIleAserIleIleValProGlnaPThrArg 740
Db      2161 CCGCAGAGATCGCTACCGAAGTGAATGAGACATTATTAACCGAGAACCTATATGC 2220
Qy      741 ValATGATGTATValValGlnIleValAsnIleAsnIleValArgIleValPhe 760
Db      2221 GTGCCCGCTATGCGGTGTGTGAGAAAGCGGCATGCGCATGTGGCAACGTTTAA 2280
Qy      761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValIle 780
Db      2281 AGCCATGTAGACACCTGACCATCTGCAGCGGTATATGCGCAGTTTGTGGCGCATCTG 2340
Qy      781 GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerLeuGln 800
Db      2341 CAGGAACACCGCCGCTGCGCATGCGGTGATTGAACAAGCAGCGCTGAACGA 2400
Qy      801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisIleValArg 820
Db      2401 GCGACAGCGCGCTGTTGATGTGTTCTGCGCTTATGTGCATCATCGGTGGCAT 2460
Qy      821 ArgGlyLeuSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSer 840
Db      2461 CCGCGCAAAAGCTATGTGACAGTGCAGCGCATTCGACAGGACATTCGACACCTG 2520
Qy      841 LeuCysSerLeuCysTyrGlyAspMetGluIleValLeuPheAlaGlyIleArg 860
Db      2521 CTGTCAAGCTGTGCTATGCGCATATGAAACAACTTTGGCGGCATTCGCCCGAT 2580
Qy      861 GlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHis 880
Db      2581 GCGCTGCTGCTGCGCTGCTGATGATTTCTGCTGCTGATCCCGCATCTGACCTG 2640
Qy      881 LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrGlyCysValVal 900
Db      2641 AAAACCTTTCTGCGCACCTGCGTGGCGCGCGCATATATGCTGCTGCGTGAAC 2700
Qy      901 ArgGlyThrValValAsnProValGluAspGluAlaLeuGlyValThrAlaPhe 920
Db      2701 CGCAAAACCGGTGTGAACCTTTCCGTGGAAGATGAAGCGCTGGCGGCACCG 2760
Qy      921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArg 940
Db      2761 CAGATGCGCGCGCATGCGCTGTTCCGTGCTGCGCTGCTGCTGATACCGCACCT 2820
Qy      941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeu 960
Db      2821 GAAGTGCAGAGCATATATGACATATGCGCGCACCATTCGCGCAGCTGACCTTT 2880
Qy      961 AsnArgGlyPheLeuValArgIleAsnMetArgGlyLeuPheGlyValLeuArg 980
Db      2881 AACCGCGGCTTTAAAGCGGCGCGCAATGCGCGCAAACTTTTGGCGTGTGCGCT 2940
Qy      981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValC 1000
Db      2941 AATGTCATAGCTGTTCTGATCTGACAGTGAACGCTGACAGCCGTGTGCACCA 3000
Qy      1001 IleTyrIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGln 1020
Db      3001 ATTTATTAATAATCTGCTGCTGCGAGCGGTATCGCTTCAAGCGGTGTGCGCG 3060
Qy      1021 PheHisGlnGlnValTyrPheAsnProThrPhePheLeuArgValIleSerAs 1040
Db      3061 TTTTCATCAGAGTGTGAAAAACCGACCTTTTCTGCGCGTGTATGCGCATAC 3120
Qy      1041 SerLeuCysTyrSerIleLeuValAlaValAsnAlaGlyMetSerLeuGlyAla 1060
Db      3121 AGCTCTGCTATAGCATTTCTGAAGCGAAAGCGCGCATAGCTTGGCGCGAAAG 3180
Qy      1061 AlaAlaGlyProLeuProSerGluAlaValGlnThrLeuCysHisGlnAlaPhe 1080
Db      3181 GCGCGCGGCGCGCTGCGAGCGAAGCGGTGCACTGCTGTCATAGGCGTTTCTG 3240

```

```

Qy      1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAla 1100
Db      3241 AACTGACCCCGCATCGCGTACCTATGTGCGGTGCGGAGCGCTGGCAACCGCG 3300
Qy      1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAla 1120
Db      3301 ACCCAGCTGAGCGCAAACTGCGCGGCACACCTGACCGCGCTGGAAGCGCG 3360
Qy      1121 ProAlaLeuProSerAspPheLeuThrIleLeuAsp 1132
Db      3361 CCGGCGCTGCGCAGCATTTTAAACCATCTCGAT 3396

RESULT 2
AR393359 3396 bp DNA linear PAT 18-DEC-2003
LOCUS AR393359
DEFINITION Sequence 639 from patent US 6617110.
ACCESSION AR393359
VERSION AR393359.1 GI:40118786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3396)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL Patent: US 6617110-A 639 09-SEP-2003;
FEATURES
source Location/Qualifiers
1..3396
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6,73e-151 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-044-692-2 (1-1132) x AR393359 (1-3396)
Qy      1 MetProAlaAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArg 20
Db      1 ATGCGCGCTGCTCCGCGTGTGCGGTGCTGTCGTTCCCTGCTGCGTCCCATACG 60
Qy      21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuVal 40
Db      61 GTTCTGCGCTGCTACCTTCTGTTGCTGTGCGGTGCGGTGCGGTGCGGTGCGGT 120
Qy      41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValPro 60
Db      121 CGTGTGACCGCGGTCTTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy      61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlu 80
Db      181 GACGCTGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy      81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyValAlaValAsnValLeuAla 100
Db      241 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy      101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrSerValArg 120
Db      301 TTGCTGCTGCTGAGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy      121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrpGly 140
Db      361 TCTTACTGCTGCAACACCGTTACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

```

QY	141	LeuAARGARValG1YASpASpValIleuVal1H1sIleuVal1AARGCysAlaIleuPheVal	160
Db	421	CTGCCTCGGTGGTGGAGCAGCTTCGGTTCACCTGCTGAGCTGGTGGCTGTGGT	480
QY	161	IleuValAlaPProSerCysAlaTyrGlnValCYsGlyProProLeuTyrGlnIleuGlyAla	180
Db	481	CTGGTGGCTCCGCTCGGGCTTACAGGTTTCGGGTCGGCCGCTGTACAGTGGGTGT	540
QY	181	AlaThrGlnAlaARGProProProHiSa1AserylProARGARGLeuG1CYsGlu	200
Db	541	GCTACCCAGGCTGTCGCCGCCGACGACCTTCGGGTCGGCTGCTGGTGGTGGCA	600
QY	201	ARGAlaTPASHiSeserValARGGValAG1ValProLeuG1LeuProAlaProGly	220
Db	601	CGTCTGTGAAACACTCCGTGTGAAGCTGGTGTCCGTGAGTCTGGCGGCTCGGAT	660
QY	221	AlaARGARGG1YGLYSerAlaSerAGSerLeuProLeuProLYsARGProARGARG	240
Db	661	GCTCGCGGTGGTGGTGGTTCGGCTTCGGTCCGTGCCGCTCCAAAGTCCGGGTGT	720
QY	241	G1YAlaAlaPProGluProGluARGThrProValG1YGlnGlySerTTPAlaHiSProGly	260
Db	721	GGTGTGCTCCGGAACCGGAACGTACCCGGTGTGACAGGTTCTCGGGCTCACCCGGAT	780
QY	261	ARGThrARGLYProSerASPARGLYPheCYsValValSerProAlaARGProAlaGlu	280
Db	781	CGTACCCGGTGGCCCTCCAGCCGTGGTTCGGTGTGTTCCCGGCTGTCCGGCTGA	840
QY	281	GluAlaThrSerLeuG1G1YAlaLeuSerG1YThrARGHiSesHiSProSerValGly	300
Db	841	GAAGTACTCTCCCTGGAGAGTCTCTGTCCGGTACCTGACTCCACCCGTCCTTGGT	900
QY	301	ArgGlnHiSHiSa1GlyProProSerThrSerARGProProARGProTTPASPThrPro	320
Db	901	CGTCAGACACAGCGTGGTCCGCCGTCCACTCCCGTCGGCGGCTCCGGAGGACACCCG	960
QY	321	CysPProPovalTyrAlaGluThrTyrHiSPheLeuTyrSerSerGlyAspLyseGluGln	340
Db	961	TGCCCGCGGTTAGCGTGAACCAAAACATTCCTGTACTCTCCGGTGAACAAAMAAG	1020
QY	341	LeuARGProSerPheLeuLeuSerSerLeuARGProSerLeuThG1YAlaARGARGLeu	360
Db	1021	CTGGCTCGGCTCTTCTGTGTCTCTCCCTGGCTCCGTCCCTGAACGGGTGCTGTCTG	1080
QY	361	ValGluThr1IephLeuG1YSerARGProTTPMetProG1YThrProARGARGLeuPro	380
Db	1081	GTTGAAACCATCTTCCTGGGTTCCCGTCGTGAAGCCGGGATCCCGCGTGTCTGCG	1140
QY	381	ArgLeuPProGlnARGTyrTTPGlnMetARGProLeuPheLeuGluLeuLeuGlyAsnHiS	400
Db	1141	CGTCTCCGCAAGCTTACTCGGAGATGGTCCGCTGTTCTGGAACTGCTGGTAACAC	1200
QY	401	AlaGlnCYsProTyrG1YValLeuLeuLYsThrHiSProLeuARGAlaAlaValThr	420
Db	1201	GCTCAGTCCCGTACGGGTGTCTGTGAACCACTGCGCGCTCGTGTGTGTACC	1260
QY	421	ProAlaAlaG1YValCYsAlaARGG1YLYsProGlnGlySerValAlaAlaPProGluGlu	440
Db	1261	CCGGCTGCTGGTGGTGGCTGTGAATAAACCGCAGGGTCCGTTGCTGCTCCGGAATA	1320
QY	441	GluAspThrARPProARGARGLeuValGlnLeuLeuARGlnHiSPeserSerProTTPGln	460
Db	1321	GAAGCAGACGACCCCGCTGTCTGGTTCAGCGCTGTACACTCTCTCCCGGCGAG	1380
QY	461	ValTyrG1YPheValARGAlaCYsLeuARGARGLeuValProProG1YLeuTTPG1YSer	480
Db	1381	GTTTACGGTTCCTTCCTGCTTGCCTGCGGTGTCTGGTTCGGCCGGGCTGTGTGGGATTC	1440
QY	481	ARGHiSaENG1UARGARGPheLeuARGAsnThrLYsPheIleSerLeuG1YLYsHiS	500
Db	1441	CGTCACAAACGACGCTTCTCTCGGTGAACACCAAAAATTCATCTCCCTGGTGAACAC	1500
QY	501	AlaLYsLeuSerLeuGlnGluLeuThrTriPLYsMetSerValARGAspCYsAlaTriPLeu	520

Db	1501	GCTAACTCTCCCTCCAGGAACTGACCTGGAAAATGTCCTTCGACTGGCGCTTG	1566
Qy	521	ACGATGSeerProglValGlyCyserValProAlaIaGlnHisArgLeuArgGluGlnIle	540
Db	1561	CGTCCTCCCGCGGCTGGTGGCTTCGGCTGTGAACACCGCTCCGGAGAAATC	1622
Qy	541	LeuAlaIysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
Db	1621	CTGGCTAAATTCCTGCACCTGGCTGATGTCCTGTTCAGTTGTGTGAACCTGCTCGTTCCTTC	1680
Qy	561	PheTyrValThrGluThrThrPheGlnIysAsnArgLeuPhePheTyrArgIysSerVal	580
Db	1681	TTCTACGTTACCGGAAACCACTTCCAGAAAAACCGTCGTTCTCTTACCGTAAATTCGGTT	1740
Qy	581	TrpSerIysLeuGlnSerIleGlyIleArgGlnHisLeuIysArgValGlnLeuArgGlu	600
Db	1741	TGGTCCAACTGCACATCCATCGGATTCCTGTACAGACCTCGAAACGTTTCAGCTCGTGA	1800
Qy	601	LeuSerGlnValGlnIleValArgGlnHisArgGlnIlaArgProAlaLeuLeuThrSerArg	620
Db	1801	CTGTCCGAACTGGAAGTTGCTCAGACCGGTGAAGCTGTCGGGCTGCTGACTCCCGGT	1860
Qy	621	LeuArgPheIleProIysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
Db	1861	CTGCGTTTCATCCCGAAACCGGACGGCTGGGTCGGACGTTAACATGACATACGATGGTTT	1920
Qy	641	GlyAlaArgThrPheArgArgGluIlyAsArgIaGlnArgLeuThrSerArgValIlyAla	660
Db	1921	GGTGCTCTCACTTCCGTCGTGAAAACGTCCTGAACGCTTGACCTCCCGTGTTAAAGCT	1980
Qy	661	LeuPheSerValLeuAsnTyrGluArgIlaArgArgProGlyLeuLeuGlyIleSerVal	680
Db	1981	CTGTTCTCGTTCTGAACATACGAAAGTCTGCTGTCGGGCTGCTGGGCTTCCTGCT	2040
Qy	681	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
Db	2041	CTGGGTCGAGCAACATCCACCGGCTGGAGTACCTTCGTCGCTGGTTCGGTCCAG	2100
Qy	701	AspProProGlnLeuTyrPheValIlyValAspValThrGlyAlaTyrAspThrIle	720
Db	2101	GACCCGCGCGGAACTGATCTTGGTTAAATTACCTTACCGGTCCTTACGACACCATC	2160
Qy	721	ProGlnAspArgLeuThrGlnValIleAlaSerIleIleIysProGlnAsnThrTyrCys	740
Db	2161	CCGCGAGACCGTCTGAACGAAAGTTATCGCTTCATCATCAACCGCAGAACACTTACCTGC	2220
Qy	741	ValArgAspGlyTyrAlaValGlnIlyAlaAlaHisGlyIlyIleValaGlyAlaPheIys	760
Db	2221	GTTCTCTCTTAACGCTGGTGGTTCACAAAAGCTGCTACGCTACGTTCTGTAAAGCTTTCAA	2280
Qy	761	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu	780
Db	2281	TCCACAGTTTCAACCTTCAGCCGACCTGACGCCGATACGCTCAGTTCTGTTCTCACCTG	2340
Qy	781	GlnGlnThrSerProLeuArgAspAlaValValIleGlnGlnIserSerSerLeuAsnGln	800
Db	2341	CAGGAACCTCCCGCGCTGCGTGAAGCTGTTTATCAACAGTCTCTCTCCCTGAACGAA	2400
Qy	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
Db	2401	GCTTCCTCCGCTGCTGTCAGAGTTTCTCTGCTGTTTCAATGTCGCCACACGCGTGTCTATC	2460
Qy	821	ArgGlyIysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
Db	2461	CGGTGTAAATCTTAACGTTCAGTGCACAGAGTATCCGACAGGAGTTCACCTGTCACACCTG	2520
Qy	841	LeuCysSerLeuCysTyrGlyAspMetGluAsnIysLeuPheAlaGlyIleArgAsp	860
Db	2521	CTTGCTCTCCCTGCTGCTACGGTGACATGAAAAACAAATGTTTCCGTGTATCCGTCGAC	2580
Qy	861	GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880

Db	2581	GGTGTGCTGGCTGGCTGTGTGTGAAGACTTCTGCTGGTTACCCGCACTGACCCAGCT	2640		
Qy	881	LysThrPheLeuAlaGThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900		
Db	2641	AAACCTTCTCGCTACCTCCGTGGTTCGGTGGTTCGGAAATACGGTGTGGTTAACTGG	2700		
Qy	901	ArgGlyThrValValAsnPheProValGlnAspGlnAlaLeuGlyGlyTyrAlaPheVal	920		
Db	2701	CGTAAACCGGTGTGTTAACTTCCCGGTGGAGACGAACTCTGGGTGGTACCGCTTGGTT	2760		
Qy	921	GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu	940		
Db	2761	CAGATGCGGGTCACGGTCTGTTCCCGGGTGGCGGTGTGCTGCTGGACACCCGTAACCTGG	2820		
Qy	941	GluValGlnSerArgPyrSerSerTyrAlaArgThrSerIleAlaGlnAspLeuThrPhe	960		
Db	2821	GAACTTCAGTCCGACTACTCTCTCTACGCTGTGACTCCATCCGTGGCTTCCCTACCTTC	2880		
Qy	961	AsnArgGlyPheLeuValGlyValArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu	980		
Db	2881	AACGGTGGTTCAAAGCTGGTGTGTAACTGGGTGTGTAACCTGTTCGGTGTCTGGCTGG	2940		
Qy	981	LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000		
Db	2941	AAAGGCCACTCCCTGTTCTCTGGACTGTGAGTTAACTCCCTGCAAGACCGTTTGACACGAC	3000		
Qy	1001	IleTyrIysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020		
Db	3001	ATCTACAAAATCCCTGCTGTGACAGGCTTACCGTTCACCGCTTCGTTCTGCACTGGCG	3060		
Qy	1021	PheHisGlnGlnValIleTyrPheAsnProThrPhePheLeuArgValIleSerAspThrAla	1040		
Db	3061	TTCCACACAGCAGGTTTGGAAAAACCCGACCTTCTTCGCTGTGTATCTCCGACACCGCT	3120		
Qy	1041	SerLeuCysTyrSerIleLeuIysAlaIysAsnAlaGlyMetSerLeuGlyValIysGly	1060		
Db	3121	TCCCTGTGCTACTCACTCTGTAAGACTTAAACCGCTGTATGCTCCCTGGGTGCTTAAAGCT	3180		
Qy	1061	AlaAlaGlyProLeuProSerGlnAlaValGlnTyrLeuCysHisGlnAlaPheLeuLeu	1080		
Db	3181	GCTGCTGGTCCGCTGCGCTCGAAGCTGTTCAGTGGCTGTCCACACAGGCTTTCCTGCTG	3240		
Qy	1081	LysLeuThrArgHisArgValIleTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100		
Db	3241	AAACTGACCCCTCACCGCTGTACTTACCTTCCGCTGGGTTCCTGCGTACCGCTCAG	3300		
Qy	1101	ThrGlnLeuSerArgIysLeuProGlyTyrThrThrLeuThrAlaLeuGlnAlaAlaAsn	1120		
Db	3301	ACCAAGCTGTCCCGTAACTCCCGGGTACCACTTGACCCGCTCTGGAAAGCTGTGCTTAC	3360		
Qy	1121	ProAlaLeuProSerAspPheIysThrIleLeuAsp	1132		
Db	3361	CCGGCTGTGCGCTCGAATTCAAAACATCTGTGAC	3396		
RESULT 3	AR393360	3396 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	AR393360	Sequence 640 from patent US 6617110.			
ACCESSION	AR393360				
KEYWORDS	AR393360.1	GI:40118788			
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 3396)				
AUTHORS	Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,				
TITLE	Hailey,C.B. and Andrews,W.H.				
JOURNAL	Cells immortalized with telomerase reverse transcriptase for use in				
FEATURES	Patent: US 6617110--A 640 09-SEP-2003;				
SOURCE	Location/Qualifiers				
	1..3396				
	/organism="unknown"				

ORIGIN	/mol_type="genomic DNA"
Alignment Scores:	
Prod. No.:	6.73e-151
Score:	5961.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
US-10-044-692-2 (1-1132) x AR393360 (1-3396)	
QY	1 MetProAArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTryArgGlu 20
DB	1 ATGCCAAGAGCTCCCAAGATGTAGAGCTGTAGATCTTTGTGAGATCTCATTTATAGAA 60
QY	21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
DB	61 GTTTTGCCATTGGCTACTTTTGTGTAGAGATTGGGCCACAGTTGAGATTGGTTCAA 120
QY	41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProThr 60
DB	121 AGAGGTGATCCAGCGCTTTTAGACCTTTGGTGCATAGTTGGTTGGTTGTTCCATGG 180
QY	61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB	181 GATGCTAAGCACCAACCAAGCTGCTCATCTTTTATAGCAAGTTCTTTGTGAAAGATTG 240
QY	81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaAlaValAsnValLeuAlaPheGly 100
DB	241 GTTGCTTAGAGTTTTCCAAGATGTGTGAAAGAGGCTAAATAATGTTTGGCTTTGGT 300
QY	101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGluAlaPheThrThrSerValArg 120
DB	301 TTGCTTTGTTGGAGGTGTCTAGAGGTGCTCACCAAGAGCTTTTACTCTTGTTTAGA 360
QY	121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValaTTPGlyLeuLeu 140
DB	361 TCTTATTTGCCAATAACTGTTCATGATGCTTTGAGAGGTTCTGGTGGCTTTGGTTG 420
QY	141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB	421 TTGAGAAAGATTGGATGATGTTTGGTTCATTTGTTGGCTAGAGTGGCTTTGGTTG 480
QY	161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuLysGlnLeuGlyAla 180
DB	481 TTGGTTGCTCCATCTTGCTTATCAAGATTGTGTGCCACATGTATCAATTTGGGTCT 540
QY	181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB	541 GCTACTCAAGCTAGACCAACCAACACATGCTTCTGGTCCAAAGAAAGATTGGGTGAA 600
QY	201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB	601 AGAGCTTGAATCATCTGTGTAGAAAGCTGTGTCCATTGGGTTTGGCAGCTCCAGGT 660
QY	221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB	661 GCTAATAAAGAGAGGTGCTTGCCTTCAGATCTTGGCCATTGGCCAAAGAACCAAGAGA 720
QY	241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
DB	721 GGTGCTGCTCCAGAACCAAGAAAGAACTCCAGTTGGTCAAGGTTCTTGGGTATCCAGGT 780
QY	261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB	781 AGAATCAAGGCTCATCTGATAGAGGTTTTTGTGTGTTTCCCACTGACCAAGCTGAA 840
QY	281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyLysThrArgHisSerHisProSerValGly 300
DB	841 GAGGCTACTCTTTTGAAGAGGCTTGTGTGTGACTAGACATTTCTATCATCTGTGGT 900

QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrPheThrPro 320
Db 901 AGACAACATCATGCTGGTCCACCATCTACTTACAGACCAACAGACCATGGCATCTCCA 960
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
Db 961 TGCACCAACAGTTATGCTGAACTCAACATTTTGTGATTTCTGCTGTGTAAGAACA 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1021 TTGAGACCATCTTTTGTGTCTCTTTAGAACCATCTTGTGACTGGTGTAGAGATTG 1080
QY 361 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
Db 1081 GTTGAACATATTTTGGGTCTAGACCATGATGTCAGGTCTCCAAAGAGTTGCCA 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400
Db 1141 AGATTGCCAAGATATGTCGAATGACCAATGTTTGGATTTGGATTTGGGTAAATCAT 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db 1201 GCTCAATGTCATATGATGATGTTGTGAAACATCATTTGTCATTTGAGAGCTGCTTACT 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
Db 1261 CCAGCTGCTGCTGTTGCTGTAGGAAAAACCAAGGTTCTGTGTGCTCCAGAA 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
Db 1321 GAAGATACGATCCAGAAAGATTTGGTTCATTTGTAGACACATCTTCTCATGGCAA 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
Db 1381 GTTTATGCTTTTGTAGAGCTGTTTGAGAAAGATTGGTTCACAGGTTTGTGGGTTCT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
Db 1441 AGACATATATGAAGAATTTTGGAAATATCTAAATAATTTATTTCTTGGGTAAACAT 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaTyrPhe 520
Db 1501 GCTAAATGCTCTTGGCAAGAAATGACTGGAATAATGCTGTGAGAAATGTGTGGTTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540
Db 1561 AGAAGATCTCCAGGTGTGTGTGTGTCCAGCTGCTGAACATGATTGAGAGAAAGAAAT 1620
QY 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
Db 1621 TTGGCTAAATTTTGGCATTTGGTGTGATGCTGTTATGTTGTAATTTGTAAGATCTTTT 1680
QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1681 TTTTATGTTACTGAACACTCTTTTCAAAAAATGAAATGTTTATTTATGAATAATCTGTT 1740
QY 581 TrpSerLysLeuGlnSerIleGlyLysArgGlnHisIleLeuLysArgValGlnLeuArgGlu 600
Db 1741 TGGTCTAAATTTGCAATCTATTTGTTATTAAGCAACATTTTGAAGAAGTTCAATTGAAGAA 1800
QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 TTGTCTGAAGCTGAAGTTAGAACACATAGAGAGCTAGACCACTTTGTTGACTTCTAG 1860
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db 1861 TTGAGATTATTCAAAAACAGATGGTTGAGACCAATGTTAATAGATTATTTGTTT 1920
QY 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1921 GGGGCTAGAACTTTTGAAGAGAAAAAAGAGCTGAAGAGATTGACTTCTAGAGTTAAAGCT 1980
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680

Db 1981 TTGTTTCTGTTTGAATTATGAAGAGCTAGAGACCAAGTTTGTGTGGTCTTCTGTT 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrPheThrPheValLeuArgValArgAlaGln 700
Db 2041 TTGGGTTTGATGATATTCATAGAGCTTGAGAACTTTTGTGTTGAGCTTGAAGCTCAA 2100
QY 701 AspProProProGluLeuThrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
Db 2101 GATCCACCAACCAATTTGATTTTGTAAAGTTGATGATTACTGGTCTTATGATCTAATT 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db 2161 CCACAAGATAGATGACTGAAAGTATGCTTCTATATTATTAACCAACAAATATCTTAATG 2220
QY 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2221 GTTAGAAGATATGCTGTTGTTCAAAAAGCTGCTCATGTCATGTTAGAAACCTTTTAA 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2281 TCTCATGTTTCTACTTGTGACTGATTTGCCAACATATATAGACAAATTTGTCTCATTTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu 800
Db 2341 CAAGAAACTTCTCCATTGAGAGATGCTGTTGTTATTAAGAACATCTTCTTTGAATGAA 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2401 GCTTCTTCTGTTGTTGTTGATGTTTGTGAAATTAATGTCATCATCTCTTGTGAAT 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGAGGTAATCTTATCTTCAATGTCAGGATATTCACAAAGTTCTATTTTGTCTACTTTG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2521 TTGTGTTCTTGTGTTATGATGATAGAAATTAATTTGTTGCTGTGATAGAAAGAT 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGTGTGTGTAGATGATGATGATGATTTTGTGTGTGTACTCCAAATTTGACTCATAGCT 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2641 AAAACTTTTTTGAAGACTTTGTTAGAGGTGTTCCAGAAATATGTTGTGTCTTATATTG 2700
QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2701 AGAAAAACGTGTGTAATTTTCCAGTTGAAGATGAAGCTTTGGGTGACTCTCTTTGTT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAAATGCCAGCTCAAGTGTGTGTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2800
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2821 GAAGTCAATCGATTATTTCTTATGCTAAGATTTCAATTAAGAGCTTCTTTGACTTTT 2880
QY 961 AsnArgGlyPheLysAlaGlyValArgAsnMetArgGlyLysLeuPheGlyValLeuArgLeu 980
Db 2881 AATAGAGGTTTAAAGCTGTGTGAATAATGAGAAATAATGTTGTGTGTGTGTGTGTGTG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2941 AATGTCATCTTGTGTTTGTGATTTGCAAGTTAATCTTTGCAACAGTTGTGTCTAAT 3000
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATTATTAATAATTTTGTGTGTGCAAGCTTATGATTTCAATGCTTGTGCTTTGCAATTGCC 3060
QY 1021 PheHisGlnGlnValIleTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040

Db 3061 TTTCATCAACAGTTGGAAAAATCCAACTTTTTTTTGAGATTATTTCTGATACTGCT 3120
 QY SerLeuCyATySerTlleuLeuYsAlaYsAsnAglYMeSerLeuGlyAlaYsGly 1060
 Db 3121 TCTTTGTGTTATCTATTTTGAAGCTAAATAATGCTGATGCTTTGGGCTGAAGGT 3180
 QY 1061 AlaAglYProLeuProSerGluAlaValGlnTrpLeuCySHIseGlnAlaPheLeuLeu 1080
 Db 3181 GGTGTGGTCCATTCGTCAGTCAAGCTGTTCAATGGTTGTCATCAACGCTTTTGTG 3240
 QY 1081 LysLeuThrArgHISArgValThrTyValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3241 AAATGACATGACATAGACTTCTTATGTTCCATGTTGGTCTTTGGAACGCTGCA 3300
 QY 1101 ThrGlnLeuSerArgYsLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
 Db 3301 ACTCAATGTCTAGAAATAATGCCAGGTACTACTTGTGACTGCTTGGAACTGCTGAAT 3360
 QY 1121 ProAlaLeuProSerAspPheYsThrIleLeuAsp 1132
 Db 3361 CCAGCTTTCCTCATCTGATTTTAAACTATTTGGAT 3396
 RESULT 4
 AR393361 3396 bp DNA linear PAT 18-DEC-2003
 LOCUS AR393361
 DEFINITION Sequence 641 from patent US 6617110.
 ACCESSION AR393361
 VERSION AR393361.1 GI:40118790
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3396)
 AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
 Harley,C.B. and Andrews,W.H.
 TITLE Cells immortalized with telomerase reverse transcriptase for use in
 drug screening
 JOURNAL Patent: US 6617110-A 641 09-SEP-2003;
 FEATURES Location/Qualifiers
 source 1..3396
 ORIGIN /organism="Unknown"
 /mol_type="genomic DNA"
 Alignment Scores:
 Pred. No.: 6,73e-151 Length: 3396
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-044-692-2 (1-1132) x AR393361 (1-3396)
 QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyArgGlu 20
 Db 1 ATGCCAAGAGCTCCAAAGATGTAGAGCTGTTGATCTTTGTGAGATCTCACTACAGAGA 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 Db 61 GTTTGGCCATTGGCTCTTTCGTTAGAGATTGGGCCAACAGGTGGAGATTGGTTCAA 120
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
 Db 121 AAGAGTGACCCAGCTGCTTCAGAGCTTGTGCTCAATGTTGGTGTTCATG 180
 QY 61 AspAlaArgProProProAlaAlaPProSerPheArgGlnValSerCysLeuYsGluLeu 80
 Db 181 GACGCTAGACCAACCACTGCTCATCTTTCAAGCAAGTTCTTTGTAAGGAATG 240
 QY 81 ValAlaArgValLeuGlnArgLeuCySgluArgYsAlaYsAsnValLeuAlaPheGly 100
 Db 241 GTTGCTAGAGTTTGGCAAGATGTGTGAAAGAGGTGCTAAGAACGTTTGGCTTCGGT 300

QY 101 PheAlaLeuLeuAspGlyValaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
 Db 301 TTCGCTTTGTTGAGAGGTGCTAGAGGTGTCACCAAGAAAGCTTTCACACTCTGTTTAA 360
 QY 121 SerTyLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValaTTPGlyLeuLeu 140
 Db 361 TCTTACTGTCNAACACTGTTACTGACGCTTGAAGAGGTTCTGAGCTTGGGTTGTG 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 421 TTGAAGAAGTTGGTGAACGACGTTTGTTCACCTTGTGGCTAGAGATGCTTGTTCGT 480
 QY 161 LeuValAlaProSerCysAlaTyrcGlnValCysGlyProProLeuTyrcGlnLeuGlyAla 180
 Db 481 TTGGTTCCTCATCTTGTGCTTACCAAGTTTGTGTCACCATTTGACCAATTTGGTGT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 Db 541 GCTACTCAAGCTAGAACCAACCAACACGCTTCTGGTCCAAAGAAAGATTGGGTTGTGA 600
 QY 201 ArgAlaTTPAsnHisSerValaArgGluAlaGlyValaProLeuGlyLeuProAlaProGly 220
 Db 601 AAGCTTGGAAACCTGCTGTTAGAGAGCTGGTGTCCATTGGGTTGTCACCTCCAGGT 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db 661 GCTAGAGAGAGGTGTTCTGCTTCTAGATCTTTGCCATTCCTCAAGAGACCAAGAA 720
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
 Db 721 GGTGCTGCTCCAGAACCAAGAAAGAACTCCAGTTGGCAAGTTCTGGGCTCACCCAGGT 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 Db 781 AAGACTAGAGGTCCATCTGACAGAGGTTCTGTGTTTCCACGATGACCAAGCTGAA 840
 QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAACTACTCTTTTGGAGAGTCTTGTCTGTTACTAGACATCTCAACCATCTGTGGT 960
 QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro 320
 Db 901 AAGCAACACCAACGCTGCTCAACATCTACTTCTAGACCAACCAAGACATGGACATCCA 960
 QY 321 CysProProValTyrcAlaGlnThrIlyshIsPheLeuTyrcSerGlyAspYsGluGln 340
 Db 961 TGTCAACCACTTAAAGCTGAACTAAGCACTTCTGTACTCTTGTGTGTAACAAGAACAA 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThcGlyAlaArgArgLeu 360
 Db 1021 TTGAAGCAACTTCTTGTGTTCTTCTTTGAAACATCTTTTACTGCTGCTAGAGATTG 1080
 QY 361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
 Db 1081 GTTGAACATATTTCTGAGGTTCTAGACCATGAGGCCAGTACTCAAGAAAGATTGCCA 1140
 QY 381 ArgLeuProGlnArgTyrcTTPGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 Db 1141 AAGATTGCCAAGAAAGATACGCAATGAGACCATGTTCTTGGAAATGTTGGGTAAACAC 1200
 QY 401 AlaGlnCysProTyrcGlyValLeuLeuLeuYsThrHisCysProLeuArgAlaAlaValThr 420
 Db 1201 GCTCAATGTCATAGAGTGTGTTGTTGAAGACTCACTGTCCATTGAGAGCTGCTTAACT 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGluYsProGlnGlySerValAlaAlaProGluGlu 440
 Db 1261 CCAGCTGCTGAGTGTGCTAGAGAAAGCCAAAGGTTCTGTGCTGCTCCAGAAAGAA 1320
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
 Db 1321 GAAGACACTGACCAAGAAAGATTGTTCAATTGTGAGCAACACTTCTTCATGGCAA 1380

Qy	461	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer	480
Db	1381	GTTTACGGTTTCGTAGAGCTTGTGTAGAAAGATTGGTCCACACAGTTTGTGGGGTTCT	1440
Qy	481	ArgHisAsnGluArgArgPheLeuArgAsnThrIleValPheIleSerLeuGlyIleHis	500
Db	1441	AGACACAAACAAAGAAATCTTGAGAAACATGAAGAGTTCAATTTCTTGGGTAAAGCAC	1500
Qy	501	AlaIleuSerLeuGlnGlnIleuThrTrpIleuMetSerValArgArgPheValIleu	520
Db	1501	GCTAAGTGTCTTGGCAAGAAATGACTGGAAGATGTCTGTAGAGACTGTGCTTGGTTG	1560
Qy	521	ArgArgSerProGlyValGlyCysValProAlaIleuHisArgLeuArgGluGluIle	540
Db	1561	AGAAGATCTCAAGGTGTGGTGTGTTCAGCTGCTGACACAGATTGAGAGAAAGAAAT	1620
Qy	541	LeuAlaIlePheLeuHisIleTrpLeuMetSerValTyrValIleGluLeuLeuArgSerPhe	560
Db	1621	TTGGCTAAGTCTTGACCTGGTGAATGTCTGTTTACCTTGATGATTTGATGATCTTTC	1680
Qy	561	PheTyrValThrGluThrPheGlnIleValAsnArgPhePheTyrArgIleSerVal	580
Db	1681	TTTCTACCTTCTGAAACTTACTTTCACAAAGAACAGATTGTTCTTACAGAAAGTCTGTT	1740
Qy	581	TrpSerIleuLeuGlnSerIleGlyIleArgGlnHisIleuIleArgValGlnLeuArgGlu	600
Db	1741	TGGCTTAAGTTCACATCTATTGGTATTAGCAACACTGGAAGAGTTCATTTGAGAGAA	1800
Qy	601	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
Db	1801	TTGTCTGAAGCTGAAGTTAGAACACACAGAAAGCTAGACACACTTGTGTGACTTACGA	1860
Qy	621	LeuArgPheIleProIleProIleValArgProIleValAsnMetAspTyrValIle	640
Db	1861	TTTGAAGTTCATTCAAAGCCAGACCGTTTGAACACATTTTAACTGACATACGTTGTT	1920
Qy	641	GlyAlaArgThrPheArgArgGlyIleValArgAlaGluArgLeuThrSerArgValIle	660
Db	1921	GGTGTCTAAGAACTTTCAGAAAGAAAGAGAGCTGAAGATTGACTTGAAGTTAAGGCT	1980
Qy	661	LeuPheSerValIleuSerTyrGluValArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
Db	1981	TTGTCTCTGTTTGAACCTACGAAAGAGCTGAAGACACAGTTTGTGGTGTCTTGTGTT	2040
Qy	681	LeuGlyLeuAspAspIleHisIleArgAlaIleArgArgThrPheValLeuArgValArgAlaGln	700
Db	2041	TTGGGTTTGGACACATTCACAGACTTGGAGAACTTTCGTTTGAAGTTAAGCTCA	2100
Qy	701	AspProProGluLeuTyrPheValIleValAspValThrGlyAlaTyrAspThrIle	720
Db	2101	GACCCACCAACCAAAATTTGACTTCGTTAAGGTTGAGGTTACTGTGCTTACGACACTATT	2160
Qy	721	ProGlnAspArgLeuThrGluValIleIleAspIleGlyLeuProGlnIleuSerTyrCys	740
Db	2161	CCACAGACAGATTGACTGAAGTTATTGCTTCTATTATTAGCCACAAACACTTACTGT	2220
Qy	741	ValArgArgTyrAlaValAlaGlnIleValAlaHisGlyHisIleValArgIleValPheIle	760
Db	2221	GTTAAGAAATACGCTGTGTTCAAAAGGCTGTCAAGCTCAAGCTTGAAGAAAGCTTCAAG	2280
Qy	761	SerHisIleValSerThrIleuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu	780
Db	2281	TTCTCAGGTTTCACTTGTGACTGACCTTGCAACCATATGAGCAAAATTCGTGCTCACTTG	2340
Qy	781	GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGlu	800
Db	2341	CAAGAAACTTCTTCATTGAGACAGCGCTTGTATTGAACATCTTCTTCTTGAACGAA	2400
Qy	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisIleValArgIle	820
Db	2401	GCTTCTTCTGTTGTTGTTGACAGCTTTCTTGAGATCATGTCACACACCGCTGTGAAT	2460
Qy	821	ArgGlyIleuSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
Db	2461	AGAGGTAAGTCTTACCTTAATCTCAAGGTAATTCACAAAGTTCTTATTGTTGCTACTTGG	2520
Qy	841	LeuCysSerLeuCysTyrGlyAspMetGluAsnIleuPheAlaGlyIleArgArgAsp	860
Db	2521	TTGTGTCTTGTGTTGTTGACTGACATGGAACAAAGTTGTTGCTGTGTTATGAAGAGAC	2580
Qy	861	GlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisIleuThrHisAla	880
Db	2581	GTTTGTGTGTGAGATGGTGTGACGACTTGTGTGTGTTACTTCCACACTTGACACGCT	2640
Qy	881	IleThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
Db	2641	AGAATCTTCTTGAAGAACTTGTGTAGAGGTCTTCCAGAAATACGTTGTGTGTAACTTG	2700
Qy	901	ArgIleThrValIleAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	920
Db	2701	AGAAAGACTGTGTAACTTCCAGTTGAAGACAGAAAGCTTGGGTGTACTGCTTTCGTT	2760
Qy	921	GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuAspThrArgThrLeu	940
Db	2761	CAAAATCCAGCTCAGGTTGTGTTCCATGCTGTGTGTGTGTGTGACACTGAACTTGG	2820
Qy	941	GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
Db	2821	GAAATTCATCTGACTACTCTTCTTACGCTAAGACTTCATTAAGAGCTTCTTGACTTTC	2880
Qy	961	AsnArgGlyPheLeuAlaGlyArgAsnMetArgGlyIleuPheGlyValLeuArgLeu	980
Db	2881	AACAGAGGTTTCAAGCTGTGTGAAGAAACATGAAGAAAGTTGTTGCTGTGTGTGATTTG	2940
Qy	981	IleCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
Db	2941	AAGTGTCACTCTTGTGTCTTGTGACCTTGAAGTTAACTCTTTCGAAACCTGTTGTACTAC	3000
Qy	1001	IleTyrIleValLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
Db	3001	ATTACAAAGATTTTGTGTGTGCAAGCTTACAGATTCCAGCTGTGTTGTGCAATTTGCCA	3060
Qy	1021	PheHisGlnGlnValThrIleAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
Db	3061	TTCCACCAACCAAGTTTGAAGAAACCAACTTCTTCTTGAAGTTATTCTGACACTGCT	3120
Qy	1041	SerLeuCysTyrSerIleLeuIleValIleValAsnAlaGlyMetSerLeuGlyAlaIleGly	1060
Db	3121	TCTTGTGTGTTACTTATTGTAAGCTTAAGAACCTGTGATGTCTTGGGTCTTAAGGCT	3180
Qy	1061	AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
Db	3181	GCTGCTGGTCCATTCATCTGAACCTGTCAATGTTGTGTGCAACAAGCTTCTTGTGTTG	3240
Qy	1081	IleLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
Db	3241	AAGTTGACTAGACACAGATTACTTAAGCTCAATGTGTGGTCTTTGAGAACTGCTCA	3300
Qy	1101	ThrGlnLeuSerArgIleLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaIleAsn	1120
Db	3301	ACTCAATTGTCTAAGAAATGTCAGATCTACTTGAAGCTGTTGGAAGCTGCTCTAAC	3360
Qy	1121	ProAlaLeuProSerAspPheIleThrIleLeuAsp	1132
Db	3361	CCAGCTTGGCCATCTGACTTCAAGACTATTTTGGAC	3396
RESULT 5			
AR393362			
LOCUS AR393362 3396 bp DNA linear PAT 18-DEC-2003			
DEFINITION Sequence 642 from patent US 6617110.			
ACCESSION AR393362			
VERSION AR393362.1 GI:40118792			
KEYWORDS			
SOURCE Unknown.			
ORGANISM Unknown.			
Unclassified.			

REFERENCE 1 (bases 1 to 3396)
AUTHORS Cecchi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,
Harley, C.B. and Andrews, W.H.

TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening

JOURNAL Patent: US 6617110-A 642 09-SEP-2003;

FEATURES Location/Qualifiers

source 1..3396
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Score, No.:	6,73e-151	Length:	3396
Percent Similarity:	5961.00	Matches:	1132
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	6	Indels:	0
		Gaps:	0

US-10-044-692-2 (1-1132) x AR393362 (1-3396)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
DB 1 ATGCCACGCGCCCAAGTGTGCGTCCGTTCTTGTGCGTTCTCATTACCGTGA 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheLeuValGln 40
DB 61 GTTTGGCCATTGGCCCACTTCGTCGTTGGGTCACAAAGTGGCGTTGGTCAA 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGTGGGATCCAGCCGCCCTTCCTGCTGCTGGTCCCAATGTTGGTTGTGTTCATGG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuGlyLeu 80
DB 181 GATGCCCGTCCACACACCGCCCGCCATCTTCCTGCAAGTTCTGTTGAAGAATTG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyValAlaValAsnValLeuAlaPheGly 100
DB 241 GTTGGCCCGTGTGGCAACGTTGTGTGAACGTGGGCCAATAACCTTTGGCTTCGGT 300
QY 101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGCGCTTGTGGATGTGTCGCCGTGTGTGTCCACGAAGCTTTCACACCTCTGTTCT 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeu 140
DB 361 TCTTACTTGCACAAACACCGTTACCGATGCTTCGTGGTTCGTGGGTTGTTG 420
QY 141 LeuAlaArgValAlaGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 TTGCGTCGTGTGGTATGATGTTGTGTGTTCACCTTGTGGCCGTGTGTGCTT 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 TTGGTTGGCCCATCTTGTGCTTACCAAGTTGTGGTCCACATTGACCAATGGGTGCC 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCCACCCAAAGCCGTCACACACACGCTCTGTGTCCACGTGTGTTGGGTTGTGA 600
QY 201 ArgAlaTyrAsnHisSerValArgGlyValGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGTGCTGGAACACCTCTGTTCGTGAAGCCGTGTTCACATGGGTTGGCCAGCCAGG 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProIlyAsArgProArgArg 240
DB 661 GCCCGTCGT 720
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrPheAlaHisProGly 260
DB 721 GGTGGCGCCCGCAAGAACGTAACCCAGTTGTGTCAAGTTCTTGGGCGCCACCGAGG 780

QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 CGTACCGCGTGGTCATCTGATGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 281 GluAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAAGCCACCTCTTGTGAAGTGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
DB 901 CGTCAACACACGCGGTCCACATCTCTCTGTCCACACGTCATGGGATACCCCA 960
QY 321 CysProProValTyrAlaGlyThrLysHisPheLeuTyrSerSerGlyAspGlyGln 340
DB 961 TGTCCACAGTTTACGCCGAAACCAACACTTCTGTACTCTTCTGTGTGTGTGTGTGTGT 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1021 TTGCGTCCATCTTCTTGTGTCTTCTTGTGTCTTCTTGTGTGTGTGTGTGTGTGTGT 1080
QY 361 ValGluThrThrIlePheLeuGlySerArgProTyrMetProGlyTyrProArgArgLeuPro 380
DB 1081 GTTGAACCACTTCTTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlyLeuLeuHis 400
DB 1141 CGTTTGCACACAGCTTACGTGAATGCGTCCATTGTTGTGTGTGTGTGTGTGTGTGT 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuValAlaValThr 420
DB 1201 GCCCAATGCCATACGAGT 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
DB 1261 CCAGCGCGCGGT 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1321 GAAGATCCGATCCACAGT 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB 1381 GTTTACGGT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
DB 1441 CGTCAACAAACGTCGTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
DB 1501 GCCAATTTCTTGTGCAGAAATTCGACCTGGAATAATGTCGTGTGTGTGTGTGTGTGT 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlu 540
DB 1561 CGTGTGTCCAGAGT 1620
QY 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
DB 1621 TTGGCCAAATTTGTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1681 TTCTACGTTACCAACCAACCTTCCAAATAACCGTTTCTTCTACCGTAAATCTGT 1740
QY 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB 1741 TGTCTTAATTCATATCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800
QY 601 LeuSerGlnAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
DB 1801 TTGTCTGAAGCCGAAAGTTGTCAACACCGTGAAGCCCGTCCAGCTTGTGTACCTCTCGT 1860

```

QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal
Db 1861 TTGGGTTTCATTCCAAAACGAGATGTTGGCTCAATTGTTAAACATGATTAAGTTGTT 1320
QY 641 G1ValArgThrPheArgArgGlyValArgAlaGluArgLeuThrSerArgValValVal
Db 1921 GGGGCCGATACCTTCCTCGTGAAGAAACGTCGCAAGGTTGACCTTCGTTGAAGCC 1980
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal
Db 1981 TTGTTCTCTGTTTGAACACGAGACGTCGCTGCTCAAGTTGTTGGTGCTCTGTT 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTTrpArgThrPheValLeuArgValAlaArgAlaGln
Db 2041 TTGGGTTGGATGATATTCACCGGTCGCGTACCTTCGTTTGGCTGTTGCGGCCAA 2100
QY 701 AspProProProGluLeuTyrPheValValAspValAspValAlaTyrAspThrIle
Db 2101 GATCCACACACGAGATGATCTTCGTTGAAGTTGATTCACCGTGCTACGATACCAAT 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys
Db 2161 CCACAAAGATGTTGACCGAAGTTATTCCTCTATTATTAACACAAACACCTACTGT 2220
QY 741 ValArgArgTyrAlaValValGlnLysValAlaHisGlyHisValArgLysAlaPheLys
Db 2221 GTTCGTGTTACCGCGTTGTTCAAAAACGCGCCACCGTCCGTAAGCCTTCAAA 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu
Db 2281 TTTCACTTTCTACCTTTCGACCGATTCGACACCATACATGCGTCAATTCGTTGCCACTTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValValIleGlnGlnSerSerLeuAsnGlu
Db 2341 CAGAAACCTCTCCATTCGCGTATGCGCGTTGTTATTGAACAATCTTCTTTGAACGA 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValAlaGlyIle
Db 2401 GCTCTCTTCTGTTGTTGATGATGTTTCTTCGCTTCAATGTCACACACGCGTTCGTAAT 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrIleu
Db 2461 CGTGGTAACTTACCTTCATATGTCATGATGATTCACACAGGTTCTATTGTTGTTACTTG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp
Db 2521 TTGTTGTTCTTGTGTTACGCTGATGATGAAACAAATGTTGCGCGTATTCGTCGAT 2580
QY 861 GlyLeuLeuLeuArgLeuValAlaAspPheLeuLeuValThrProHisIleuThrHisAla
Db 2581 GATTTGTTGTTGCGTTGTTGATGATGATTTCTGTTGTTAACCCCAACCTTGACCCGCG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu
Db 2641 AAAACCTTCTTGGCTACCTTGGTTGCTGCTTCGAAATACGCTTGTTGTTAACTTG 2700
QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheVal
Db 2701 CGTAAACCGCTGTAACTTCCAGTTGAAGATGAAGCCTTGCGTACCGCTTCGTT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTTrpCysGlyLeuLeuLeuAspThrArgThrLeu
Db 2761 CAATATGCCAGCCACGATGTTGTTCCATGATGTTGTTGTTGTTGATACCCCTACCTTG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe
Db 2821 GAAGTTCAATCTGATTACTTCTTACGCCGCTTCACTCACTCACTTCTTGAACCTTC 2880
QY 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu
Db 2881 AACCGGTGTTTCAAAACCGGTCGTAAACATGCGTCGTAAATGTTGCGTTGCGCTTGG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn

```

```

Db 2941 AATGTCACCTTGTGTTCTTGATTTGCAAGTTACTCTTTCGAAACCGTTGTACCAAC 3000
QY 1001 IleTyrIleIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro
Db 3001 ATTTACAAAATTTGTTGTTGCAAGCTTACCGTTTCCAGCGCTGTTGTTGCAATTGCCA 3060
QY 1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla
Db 3061 TTCCACCAACAAGTTTGAAAAACCAACCTTCTTTCGCTGTTATTTCTGATACCGCC 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaGly
Db 3121 TCTTGTGTTACTCTATTTTGAAGCAAAACCGCGTATGTTGTTGGTGCCAAAGGT 3180
QY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu
Db 3181 GCGCGCGTCCATGTCATCTGACCTGACAGCGTTCAATGTTGTCACCAACCTTCTGTTG 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln
Db 3241 AATTTACCCGTCACCGCTTACCTTACCTTCAATGTTGGTTCTTTGGGTACCGCCCA 3300
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn
Db 3301 ACCCAATTGTCGTAAATTCACAGGTACCACTTGACCGCTTGGAAGCCGCCCAAC 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp
Db 3361 CCAGCTTCCATCTGATTTCAAAACCATTTGGAT 3396

RESULT 6
AX957656 3396 bp DNA linear PAT 08-JAN-2004
LOCUS AX957656
DEFINITION Sequence 3 from Patent WO03095605.
ACCESSION AX957656
VERSION AX957656.1 GI:40785528
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Moll,J., Schunichel,A. and Stouten,P.
TITLE A chimeric reverse transcriptase and methods for identifying
JOURNAL Patent: WO 03095605-A 3 20-NOV-2003;
Pharmacia Italia S.p.A. (IT)
FEATURES
source
1. 3396
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 6,73e-151 Length: 3396
Score: 5961.00 Matches: 1132
Best Local Similarity: 100.00% Conservative: 0
Percent Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-044-692-2 (1-1132) x AX957656 (1-3396)
QY 1 MetProAlaGlnAlaProArgCysArgAlaValArgSerLeuLeuAspSerHisTyrArgGlu 20
Db 1 ATGCGCGCGCTCCCGCTGCGAGCCGTCGCTCCCTGCGCGACGACCTACCGCGCAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTrpArgLeuValGln 40
Db 61 GTGTCGCGCGCTGCGACATTCGTGCGCGCTTGCGGCGCCCAAGGCTGCGGCTGTCAG 120

```

QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
 DB CGCGGGAGACCGCGGGCTTTCGCGCGCTGGTGGCCAGATGCTGTGGTGGCCCTGG 180
 QY 61 AspAlaArgProProProAlaAlaPheSerPheArgGlnValSerCysLeuValSerGlnLeu 80
 DB GACGACAGCG 240
 QY 81 ValAlaArgValLeuGlnArgLeuValArgGlnValAlaValAsnValLeuAlaPheGly 100
 DB GTGGCGCCAGTCTCTGACAGAGCTGTGCGAGCGCGCGCGAGAAAGCTGTGGCTTCGCG 300
 QY 101 PheAlaLeuLeuAspGlyValAlaArgGlyGlyProProGlnValAlaPheThrThrSerValArg 120
 DB TTGCGGCTGTGAGCGGGGCGCGCGGGGGCGCGCGAGAGCTTCACACAGCGTGGCGC 360
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrpGlyLeuLeu 140
 DB AGCTACCTGCGCCAAACAGGTGACGACGCTGCGGGGAGCGGGGCGGTGGGGGCTGCTG 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 DB CTGCGCGCGGTGGGAGACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 DB CTGGTGGCTCCACAGCTGCGCTTACAGGTCGTGCGGGCGCGCTGTACAGCTCGCGCT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
 DB GGCACCTACGGCG 600
 QY 201 ArgAlaTrpAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB CGGGGCTGAGACATAGCTTACAGAGAGCGCGGGGCTCCCTGGGCTTGCACGCCCGGG 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB GCGAGAGAGCGCGGGGGGAGTGCACGACGAGTCTGCTGCTGCCAAGAGCGCGAGCGT 720
 QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
 DB GGCGGTGCGCTGAGCGCGAGCGAGCGCGCGGTGGGCGAGGGGCTCGGGCGCACCGGG 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
 DB AGGACGCGTGAACCGAGTACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisAspSerValGly 300
 DB GAAGGCACTCTTTGGAGGGTGGCTCTGTGACGCGGCACTCCCACTCCATCCGTGGGG 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
 DB CCCGACGACACGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyValAspLysGln 340
 DB TGTCCCCCGGTGAACCGGACGACGACCTTCTGTACTCTCCAGGCGCAAGAGGACAG 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 DB CTGCGCGCGCTCTCTTACTACTAGCTCTGTAGGCGCCAGCTGACTGTGGCGCTCGAGG 1080
 QY 361 ValGlnThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
 DB GTGGAGACCATCTTTCTGGGTTCGAGGCTCGATCCAGGAGCTCCCGCGAGTTGGCC 1140
 QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlnValAsnHis 400
 DB CGCGTGGCGCGAGGCTACTGGCAAAATGGCGCGCGCTTGTGTGTGTGTGTGTGTGTGT 1200
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420

DB 1201 GCGCAGTCCCGCTTACGGGGTCTCTCAAGAGCATCCCGCTGCGAGCTCGGTCAAC 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGln 440
 DB CCAGACCGCGGT 1320
 QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
 DB GAGGACACAGACCCCGTCTGCTGTGACGTGCTCCCGACAGACAGCGCCCTGGGAG 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
 DB GTGTACGCTTCTGTGCGGGCGCTGCTGCGCGCGGTGTGCGCGCGCGCTTGTGGGCTTC 1440
 QY 481 ArgHisAsnGlyAspArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
 DB AGGCAACAGAACCGCGCTTCTTCAAGAACACCAAGAACTTCTTCTCTGGGGAAGCAT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
 DB GCCAAGCTCTGCTGACAGAGCTGACGTGAAGATGAGCGTGGGACTGCGCTTGGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGln 540
 DB CGCAGAGACCCAGGGGTTGGCTGTGTTCGCGCGGACAGCACCGTCTGTGTGAGAGATC 1620
 QY 541 LeuAlaLysPheLeuHisSerTrpLeuMetSerValTyrValAlaGlnLeuLeuArgSerPhe 560
 DB CTGGCGCAAGTCTCTCACTGAGGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
 QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerVal 580
 DB TTTTATGTACGGAACACACCGTTTCAAAAGAACAGCGCTTTTCTTACCGGAAGATGTC 1740
 QY 581 TrpSerLysLeuGlnSerIleGlyLleArgGlnHisLeuLysArgValGlnLeuArgGln 600
 DB TGGACCAAGTTGCAAGATGGAATGCAACAGCATTTGATGATGATGATGATGATGATG 1800
 QY 601 LeuSerGlnAlaGlnValArgGlnHisSerGlnAlaArgProAlaLeuLeuThrSerArg 620
 DB CTGTGGAAGAGAGAGTCAAGGACATGGAAGCCAGGCCCGCTGTGTGACGTCCAGA 1860
 QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 DB CTCCGCTTCACTCCCAAGCTGACGGGCTGGCGCGGATTTGTGAACATGACCTACGTCGT 1920
 QY 641 GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
 DB 1921 GGAGCCAGAACGTTCCGACAGAAAGAGGCGCGAGCGCTCTACCTCGAGGGTGAAGGCA 1980
 QY 661 LeuPheSerValLeuAsnThrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
 DB CTGTTCAGGTCTCACTACACGAGCGGGCGCGCGCGCGCGCGCGCTCTGTGGCGCTCTGTG 2040
 QY 681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
 DB CTGGGCTTGAAGATATCCACAGGCGCTGGCGCACCTTGTGTGTGTGTGTGTGTGTGT 2100
 QY 701 AspProProProGlnLeuTyrPheValLysValAspValThrGlyAlaTrpAspThrIle 720
 DB GACCGCGCGCTGAGCTGTACTTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
 QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 DB CCCGAGGACAGGCTCAAGAGGTATCGGCACATCATCAAAACCCCAAGAACAGTATGTC 2220
 QY 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
 DB GTGCGTGGTATGCGGTGTCCAGAAAGCGCGCCATGGGCAAGTCCGCAAGGCTTCAAG 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780

```

Db 2281 AGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTACAGCAGCTTCGTGCTCACCTG 2340
Qy 781 |||||ThSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
Db 2341 CAGGAGACAGCCCGCTGAGGAGATGCGTGTATGAGAGAGAGCTCCCTCGAATGAG 2400
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2401 GCACAGAGTGGCTCTTCGACGCTTCCTCACTGCTTATGTCACACAGCCGCGGCCATC 2460
Qy 821 ArgGlyLeuSerArgValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGGGGAGAGCTTACGCTCCAGTCCAGGGGATCCCGAGGGCTCCATCCCTCCACGCTG 2520
Qy 841 LeuCysSerLeuCysArgValAspMetGlnAsnLeuPheAlaGlyIleArgAspArg 860
Db 2521 CTCTGACGCTTGCTCAGCGCAGCAGAGAACAGAGCTGTTTCGGGGATTCGGCGGAGC 2580
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGGCTGCTCTGCGTTGGTGATGATTTCTGTGGTGACACCTCACCTCACCCAGCGG 2640
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGlnArgCysValValAsnLeu 900
Db 2641 AAAACCTTCTCAGAGACCTCGTCCAGGAGTGTCCCTGAGTATGCTGCGGTGAACCTTG 2700
Qy 901 ArgLysThrValAlaAspPheProValGlnAspGlnAlaLeuGlnGlyThrAlaPheVal 920
Db 2701 CGAAGACAGTGTGAATCTCCCTGTAAGAGACAGAGCCCTGGGTGGACAGGCTTTGTT 2760
Qy 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCCGGCCACAGGCTATTCCTCGGTGGCGGCTGCTGTGATACCCGAGCCCTG 2820
Qy 941 GluValGlnSerSerArgSerSerArgValArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2821 GAGGTGAGAGGACACTACCTCAGCTATGCGGAGCTCCATCAGACCACTCCACCTTC 2880
Qy 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGCGGCTTCAAGGCTGGAGAGAACATGCTCGCAAACTCTTGGGGCTTGGCGGCTG 2940
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2941 AAGTGTACAGGCTGTTCTGAGTTGCAAGTGAACAGCTCCAGACGGGTGCACCAAC 3000
Qy 1001 IleTyrIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTACAGATCTCTCTGCTGCAAGGCTGACAGGTTTCAAGCATGTGTGCTGCAAGCTCCA 3060
Qy 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3061 TTTCAATCAGAACTTTGGAGAACCCACATTTTCTGCGCTCATCTCTGACAGGCTC 3120
Qy 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlnAlaLysGly 1060
Db 3121 TCCCTCTGCTACTCCATCTCGAAGCCAGCAAGACGAGGATGTGCTGGGGGCAAGGAG 3180
Qy 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnThrLeuCysHisGlnAlaPheLeuLeu 1080
Db 3181 GCGCGGCGCTCTGCGCTCGAGGCGGTGACATGTGTGTCACCAAGCATCTCTGCTC 3240
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3241 AAGCTACTGACACCGTGTCACTACGTGCCACTCTGCGGTCACTCAGAGACGCCAG 3300
Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3301 ACCGACAGTGTGTGAGAGCTCCGCGGAGACGACGCTGACCTCTGAGAGCGGACGAC 3360
Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3361 CCGGCACTGCTCAGACTTCAAGACCATCTCTGAC 3396

```

```

RESULT 7
BD091553 3396 bp DNA linear PAT 27-AUG-2002
LOCUS BD091553
DEFINITION Adult Bone marrow-origin cell capable of differentiating into
myocardial cell.
ACCESSION BD091553
VERSION BD091553.1 GI:22637164
KEYWORDS MO 0148149-A/16.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 3396)
TITLE Umezawa,A., Hata,J., Fukuda,K., Satoshi, Ogawa and Sakurada,K.
Adult bone marrow-origin cell capable of differentiating into
myocardial cell
JOURNAL Patent: WO 0148149-A 16 05--JUL-2001;
KYOWA HAKKO KOGYO CO LTD,AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI
FUKUDA, SATOSHI OGAWA, KAZUHIRO SAKURADA
COMMENT OS Homo sapiens (human)
PN MO 0148149-A/16
PD 05-JUL-2001
PE 28-FEB-2000 WO 2000JP001148
PR 28-DEC-1999 JP 99P 372826
PI AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI FUKUDA, SATOSHI PI
OGAWA, KAZUHIRO SAKURADA
PC C12N5/06,C12N5/00,A61K35/28,A61P41/00,A61K48/00,C07K16/18 CC
FH Key (1) . (3399).
FT CDS
LOCATION/Qualifiers
source 1..3396
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 6,73e-151 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-044-692-2 (1-1132) x BD091553 (1-3396)
Qy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
Db 1 ATGCCGCGGCTCCCGCGCTGCCGAGCCGCGCTCCCTGCTGCGAGCCACTACCGCGAG 60
Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlnGlyProGlnGlyTyrArgLeuValGln 40
Db 61 GTGCTGCGCTGCGCCAGTTCGTGTGCGGCGCTGGGGCCCAAGGCTGGGGCTGTGTCAG 120
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 121 CGCGGGGAGCCGCGCGCTTTCGCGCGGTGTGGCCAGTGCTGTGTGTGCTGCTGCTGG 180
Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80
Db 181 GAGCAGCGGCGCGCGCGCGCGCGCGCTTCCTCCGCGAGGTGTCTGCTGAAAGAGCTG 240
Qy 81 ValAlaArgValLeuGlnArgLeuGlnCysGlyValArgGlyValLysAsnValLeuAlaPheGly 100
Db 241 GTGGCCCGAGTCTGAGAGGCTGTGTCAGAGCGCGGCGGAGAAAGTGTGCTGCTTGGC 300
Qy 101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
Db 301 TTGCGGCTCTGAGAGGCGGCGCGCGCGCGCGCGCTTCAACACAGCGCTGCGC 360
Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValTyrGlyLeuLeu 140

```


Db 361 AGCTACTGCGCAACGCGTACCGACGCTGCGGGGAGCGGGGCGTGGCGCTGCT 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 421 CTGCGCGCGCTGGGCGACGAGCTGCTGTTCACTCTGCGACGCTGCGGCTCTTTGG 480
 QY 161 LeuValAlaProSerCysAlaArgValGlyValGlyValProProLeuValGlyValAla 180
 Db 481 CTGGTGGCTCCGAGCTGCGCTTACAGTGTGGCGGGCGCGCTGTACAGCTCGCGCT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 Db 541 GGCACCTACAGCGCGCGCGCGCGCACCGCTAGTGAGCCCGAAGGGGCTGGGATCCGAA 600
 QY 201 ArgAlaTrpAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CCGGCTTGAAACCATAGCTGCGAGGAGCGGGGCTCCCTGGGCTTGCACGCGCGGGT 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db 661 GCGAGAGGCGCGGGGCGAGTGCACCGCAAGTCTGCGGTGCGCAAGAGCGCGAGCGT 720
 QY 241 GlyAlaAlaArgProGlyProGlyValThrProValGlyGlnGlySerTrpAlaHisProGly 260
 Db 721 GGGGCTGCGCTGAGCGCGGAGCGCGCGCTGGGCGAGGGGTCTGGGCGCCACCGGGG 780
 QY 261 ArgThrArgGlyProSerArgArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 Db 781 AGGACCGGTGAGACGAGTACCGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAAGCAGCTCTTTGAGGGGTGCGCTCTGCGCAGCGCGCACTCCACCATCCGTGGGG 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
 Db 901 CCGCAGACACACG 960
 QY 321 CysProProValTyrAlaGlyThrLysHisPheLeuThrSerSerGlyLysAspLysGluGln 340
 Db 961 TGTCCCCCGGTGTACCGCGAGACCAAGCACTTCTTACTCTCCAGCGCGCAAGAGACAG 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1021 CTGCGCGCGCTCTCTTCACTAGCTCTGAGGCGCAAGCTGACTGCGCGCGAGAGCTC 1080
 QY 361 ValGlyThrTlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
 Db 1081 GTGGAGACCATCTTTCTGGGTTCAGGCGCTGGATGCCAGGAGCTCCCGCAGGTTGGCC 1140
 QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 Db 1141 CGCTGCGCGCGCGCGCTGAGCAATGCGCGCGCTTTCTTGTGAGCTGTGGAAACAC 1200
 QY 401 AlaGlnCysProGlyGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
 Db 1201 GGGAGGTGCGCGCTACGCGGGGTCTCTCAAGACCACTGCGCGCGTGGAGCTGGCTCAC 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
 Db 1261 CCAGCAGCGCGGT 1320
 QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
 Db 1321 GAGGAGACAGACCGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
 Db 1381 GTGTACGGCTTGT 1440
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLeuPheHisSerLeuGlyLysHis 500
 Db 1441 AGGCAACAAAGAAAGCGCGCTTCTCAGGAACACCAAGAAAGTTATCTCCCTGGGGAAGCAT 1500

QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
 Db 1501 GCGAAGCTCTCCCTGCGAGAGCTGACGTGGAAGATGAGGTGCGGGACGCGCTGGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLe 540
 Db 1561 CCGAGAGAGCCAGGGGTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
 QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 Db 1621 CTGGCGCAAGTTCCTGACTGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
 QY 561 PheTyrValThrGlyThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
 Db 1681 TTTTATGTACACGAGACACACGTTTCAAAAGAAACAGGCTTTTCTACAGGAAGATGTC 1740
 QY 581 TrpSerLysLeuGlnSerIleGlyTlleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
 Db 1741 TGGAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAAGGGGTGACGCTGCGG 1800
 QY 601 LeuSerGlnAlaGlyValArgGlnHisArgGlyAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGTGGAAGCAGAGGTACAGCAGCATCGGAAAGCCAGGCGCGCTGTGTGACGTCCAG 1860
 QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 Db 1861 CTCCGCTTATCCCAAGCTGACCGGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
 QY 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGlnArgLeuThrSerArgValLysAla 660
 Db 1921 GGAGCCAGAAAGCTTCGCGAGAAAGAGGCGCGAGCGCTCACCTCGAGGGTGAAGGCA 1980
 QY 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyLysSerVal 680
 Db 1981 CTGTTACAGGTCTCAACCTACAGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCTGTG 2040
 QY 681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGGCTTGAAGATATCCAGAGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
 QY 2101 GACCGCGCGCTGAGGTGACTTTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
 QY 721 ProGlnAspArgLeuThrGlyValIleAlaSerIleIleLysArgProGlnAsnThrTyrCys 740
 Db 2161 CCCAGGACAGGCTCACGAGAGGTCACTGCGCACATCATCAAAACCCAGAAACAGTACTGC 2220
 QY 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
 Db 2221 GTGCGT 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 Db 2281 AGCAGCTTCTTACCTTGAACAACCTCAGCGCTACATGCAAGTTCGTGCTCACCTG 2340
 QY 781 GlnGlyThrSerProLeuArgAspAlaValValIleGlnGlnSerSerSerLeuLeuGln 800
 Db 2341 CAGGAGACCAAGCCGCTGAGGATGCGGTGTCATCGACAGCAAGCTCCCTCTGAATGAG 2400
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 Db 2401 GCCAGAGTGGCTCTTGCAGCTCTTCTTCAAGCTTATGTGCACACACCGCGTGGCAGTC 2460
 QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db 2461 AGGGGGAAGTCTTACGTCCAGTCCAGGGGATCCCGCAGAGGCTCATCTCTCCAGCGTG 2520
 QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyTlleArgArgAsp 860
 Db 2521 CTCTGAGCTGT 2580

QY 861 G1yleuLeuLeuValaAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 DB 2581 GGGGTGCTCTGGTGGTGGATGATTTCTTGTGTGTGACCTACCTACCCAGCG 2640
 QY 881 LyeThrPheLeuValArgGlyValProGlyTyrGlyCysValValAsnLeu 900
 DB 2641 AAAACCTTCTCCAGAGACCTGGTCCGGGTGTCTCCAGATGATGCTGGCGGAACTTG 2700
 QY 901 ArgLysThrValValAsnProValGlnAspGlnAlaLeuGlyGlyThrAlaPheVal 920
 DB 2701 CGAAGACAGTGTGAATCTCCCTGTAAGAGACAGGCGCTGGGTGGACAGGCTTTGTT 2760
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 DB 2761 CAGATGCGGCGCCACGCGCTATTCCCTGGTGGCGCTGCTGTGATACCCGAGCCCTG 2820
 QY 941 GlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 DB 2821 GAGGTGACAGGACACTACCTCAGCTATGCGGAGCTCCATCCAGAGCCAGCTCCACCTTC 2880
 QY 961 AsnArgGlyPheLeuValArgValAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
 DB 2881 AACCGCGGCTTCAAGGCTGGAGAGACATGCTGCGAACTCTTTGGGCTTGGCGGCTG 2940
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 DB 2941 AAGTGTACACAGCTGTTCTGGATTGGACGTGAACGCTTCCAGACGGTGTCCACCAAC 3000
 QY 1001 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 DB 3001 ATCTACAGAGATCTCTGCTGACGGGTACAGATTTTCCACGATGTGTGCGACGCTCCA 3060
 QY 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 DB 3061 TTTCATCAGCAATTTGGAGAACCCACATTTTCTGGCGCTCATCTGTGACAGGCC 3120
 QY 1041 SerLeuCysTyrSerIleLeuValAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
 DB 3121 TCCCTCTGCTACTCCATCTCGAAAGCCAGAAACGCGAGGATGTGCTGGGGGCGCAAGGGC 3180
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnThrLeuCysHisGlnAlaPheLeuLeu 1080
 DB 3181 GCGCGCGGCTCTGCTCCCTCGAGGCGGTGACGTGTGTGCCACCAAGATTTCTGCTC 3240
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 DB 3241 AAGCTGACTGACACGCTGTCACTAGTGCACCTCTGGGGTCACTCAGAGAGCCCAAG 3300
 QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 DB 3301 ACCGACCTGAGTGGAGGCTCCCGGGGACGACGCTGACTGCTCGGAGGGCGGAGCCAA 3360
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 DB 3361 CCGGCACTGCTCCAGACTTCAAGACATCTGAC 3396
 RESULT 8
 BD094749 3396 bp DNA linear PAT 27-AUG-2002
 LOCUS BD094749
 DEFINITION The cell having the potentiality of differentiation into
 cardiomycytes.
 ACCESSION BD094749
 VERSION BD094749.1 GI:22640337
 KEYWORDS WO 0148150-A/16.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
 1 (bases 1 to 3396)
 Umezawa,A., Hata,J., Fukuda,K., Ogawa,S., Sakurada,K., Gojo,S. and
 Yamada,Y.
 TITLE The cell having the potentiality of differentiation into
 JOURNAL Patent: WO 0148150-A 16 05-JUL-2001;

COMMENT KYOWA HAKKO KOGYO CO LTD, AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI
 FUKUDA, SATOSHI OGAWA, KAZUHIRO SAKURADA, SATOSHI GOJO, YOJI YAMADA
 OS Homo sapiens (human)
 PN WO 0148150-A/16
 PD 05-JUL-2001
 PF 02-NOV-2000 WO 2000JP007741
 PR 28-DEC-1999 JP 99P 372826, 28-FEB-2000 WO PCTJP0001448 PI
 AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI FUKUDA, SATOSHI OGAWA, PI
 KAZUHIRO SAKURADA, SATOSHI GOJO, YOJI YAMADA
 PC C12N5/06, C12N5/10, C12N15/09, A61K31/203, A61K35/28, A61K38/19, PC
 A61K38/39,
 PC A61K38/45, A61K48/00, A61P9/10, A61P41/00, C07K16/28, C12P21/08, PC
 C12O1/02,
 PC C12O1/48, G01N33/577
 CC The cell having the potentiality of differentiation into CC
 FH Key Location/Qualifiers
 FT CDS cardiomycytes (1) . (3399).
 FEATURES
 source Location/Qualifiers
 1. 3396
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Alignment Scores:
 Pred. No.: 6,736-151 Length: 3396
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 DB: 6
 US-10-044-692-2 (1-1132) x BD094749 (1-3396)
 QY 1 MetProAlaGlyAlaProArgCysArgAlaValaArgSerLeuLeuArgSerHisTyrArgGln 20
 DB 1 ATGCCGCGGCTCCCGCGCTGCGAGCCGCGCTCCCTGCTGCGAGCCACTACCGCGAG 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
 DB 61 GTGCTGCGCTGCGACCTGCTGCGCGCGCTGCGGCGCCCAAGGCTGCGCTGTGTGACG 120
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValaGlnCysLeuValCysValProTyr 60
 DB 121 CCGGGGAGCCCGCGGCTTTCGCGCGCTGTGTGCGGCTGTGTGTGTGTGTGTGTGTGT 180
 QY 61 AspAlaArgProProProAlaAlaPheSerPheArgGlnValSerCysLeuLysGlnLeu 80
 DB 181 GACGACCGGCG 240
 QY 81 ValAlaArgValLeuGlnArgLeuGlyCysGlyValArgGlyValaLysAsnValLeuAlaPheGly 100
 DB 241 GTGGCGCGAGTCTCAGAGGCTGTGCGAGCGCGCGCGAGAAAGTGTGTGTGTGTGTGTGT 300
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 DB 301 TTGGCGGTGTGAGAGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCG 360
 QY 121 SerTyrLeuProAlaThrValaThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
 DB 361 AGCTACCTGCGCCACACGAGTGCACGACCTGCGCGGGGAGCGGGGCGGGGCGGGGCG 420
 QY 141 LeuArgArgValaGlyAspAspValaLeuValaHisLeuLeuAlaArgCysAlaLeuPheVal 160
 DB 421 CTGGCGCGGTGGGAG 480
 QY 161 LeuValaAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 DB 481 CTGGGTGCTCCAGCTGTGCGCTACAGAGGTGTGTGGGCGCGCGCTGTACCACTGTGGCCT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200

Db 541 GCCACTCAGGCCCCGCCCCGACACGCTAGTGAACCCGGAAGGCTCTGGAGTCGGA 600
 QY ArgAlaTPasnhisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CGGGCTTGAAACCAhAGCTCAGGAGGCGGGGCTCCCTGGGCTGCAAGCCCCGGGT 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProGlyArgProArgArg 240
 Db 661 GCGAGAGAGCGCGGGGCGAGTGCACAGCCGAGCTGCGCTGCCAAGAGGCCAGGCGT 720
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerThrAlaHisProGly 260
 Db 721 GCGCGTGCCTTGAGCGGAGCGGAGCGCCGTTGGCGAGGGGCTCTGGGCCACCCGGGCG 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 Db 781 AGGAGCGGTGACCGAGTACCGGTGTTCTGTGTGTGTCTACCTGCCAGAGCCGCGGAA 840
 QY 281 GluAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAAGCCACTCTTTGGAGGGTGGGCTCTGGGAGCGCGCACTCCACCCATCCGTGGGCG 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProArgProArgProThrPro 320
 Db 901 CGCCAGCACACAGCGGGGCCCCCATCCACATCGCGGCCACAGTCCCTGGAGACAGCCT 960
 QY 321 CysProProValThrAlaGluThrLysHisPheLeuThrSerSerGlyAspLysGlnGlu 340
 Db 961 TGTCCCCCGGTGAGCGCCAGACCAAGCACTTCCTTACTCTCCAGGCGCAAGAGAGCAG 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1021 CTGGCGGCTCTCTTCTTCTACTAGCTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTC 1080
 QY 361 ValGluThrTrlPheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
 Db 1081 GTGGAGACCATCTTCTCTGGGTTCCAGGCCCTGGATGCCAGGACCTCCCGCAGGTTGGCCC 1140
 QY 381 ArgLeuProGluArgGlyTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 Db 1141 CGCCCTGCCCCAGCGCTACTGGCAATGCGACCCCTGTCTTCTGGAGCTGTGGGAACCAAC 1200
 QY 401 AlaGlnCysProGlyGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
 Db 1201 GCGCAGTGCCTCTACGGGGTCTCTCTCAAGACGCACTGCCCTGGAGACTGGCGTCAAC 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
 Db 1261 CCAGCAGCGCGTGTCTGTGCCCCGGAGAAAGCCCAAGGCTGTGTGGCGGCCCGCAGAGAG 1320
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
 Db 1321 GAGGACACAGACCCCCGCTGCTGTGCGAGCTGCTCCGCGACAGCAGCAGCCCTGGCAG 1380
 QY 461 ValTrpGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrProGlySer 480
 Db 1381 GTGTACGGCTGTGTGGGGCTGTGCTGCGCGGCTGTGCTGCCAGGCGCTCTGGGGCTCC 1440
 QY 481 ArgHisAsnGlnLysArgPheLeuArgAsnThrLysPhePheLeuSerLeuGlyLysHis 500
 Db 1441 AGGCAACAAAGAACCGCGCTTCTCCAGAAACCAAGAGTTCTCCCTGGGGAAGCAAT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
 Db 1501 GCCAAGCTCTGCTGAGAGCTGAGCTGGAAGATAGCGTGGGAGCACTGGCTTGGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlu 540
 Db 1561 CGCAGAGCCCAAGGGGTTGGCTGTGTTCGGCGCGCAGAGCAGCGTCTGGCTGAGGAGATC 1620
 QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTrpValValGlnLeuLeuArgSerPhe 560
 Db 1621 CTGGCCAAAGTCTCTGCACTGGCTGATGAGTGTATGCTGTGAGAGTGGCTCAGGCTTTTC 1680

QY 561 PheTrpValTrpGluThrThrPheGlnLysAsnArgLeuPheTrpArgLysSerVal 580
 Db 1681 TTTTATGTACGGAGACCAACGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGC 1740
 QY 581 TrpSerLysLeuGlnSerTrlGlyLysArgGlnHisLeuLysPheArgValGlnLeuArgGlu 600
 Db 1741 TGGACCAAGTTGCAAAAGATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGAG 1800
 QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGTGGAAGCAGAGCTCAGGCGATCGGAGAGCCAGGCCCTGCTGACCTCAGCA 1860
 QY 621 LeuArgPheLeuProLysProAspGlyLeuArgProLysValAsnMetAspTrpValVal 640
 Db 1861 CTCCGCTTCAATCCCAACCTGAGCGGGCTGGCGGCGGATTGTGAATGAGCACTACGTCGTG 1920
 QY 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGluArgLeuThrSerArgValLysAla 660
 Db 1921 GGAGCCAGAACGTTCCGCAAGAAAGAGGCGCGAGCGCTCACCTCGAGGGGTGAAGGCA 1980
 QY 661 LeuPheSerValLeuAsnThrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
 Db 1981 CTGTTCAAGGTGCTCACTACGAGCGGGCGCGGCCCTCGGCTCTGGGGCTCTGTG 2040
 QY 681 LeuGlyLeuAspAspLysHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGGCTCTGAGCAATATCAGAGGCGCTGGCGCACCTTGCTGCTGCTGGGGCCAG 2100
 QY 701 AspProProProGluLeuThrPheValLysValAspValThrGlyAlaTrpAspThrLys 720
 Db 2101 GACCCGCGCTGAGCTGACTTGTCAAGGTGATGTGACCGGGGCGGTGACCAACATATC 2160
 QY 721 ProGlnAspArgLeuThrGluValTrlPheSerTrlLysProGlnAsnThrLysCys 740
 Db 2161 CCCAGAGACGGCTACGAGAGGTATCGCAGACATATCAAAACCCCAAGAACGTATCTC 2220
 QY 741 ValArgArgTrpAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
 Db 2221 GTGGCTCGGTATGCCGTGTCCAGAAAGCCGCCATGGGCACTGCCAAGGCTTTCAAG 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTrpMetArgGlnPheValAlaHisLeu 780
 Db 2281 AGCCAGCTCTTCACTTACAGACCTCCAGCGGTATCATCGACAGTTCGTGCTCACTG 2340
 QY 781 GlnGluThrSerProLeuArgAspAlaValValLysGlnGlnSerSerSerLeuGlnGlu 800
 Db 2341 CAGGAGACCAAGCCGCTGAGGATGCCGTGATCGATCGAGCAGAGCTCTCCCTGAATGAG 2400
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLys 820
 Db 2401 GCCACAGAGGCTCTTTCACATCTTCTACGCTTCAATGTGACACCAACCGGGGCAATC 2460
 QY 821 ArgGlyLysSerTrpValGlnCysGlnGlyLysProGlnGlySerTrlLeuSerThrLeu 840
 Db 2461 AGGGCAAGTCTTACGTCCAGTCCAGGCGGAGATCCCGCAGGGGTCTCATCTCTCCAGCTG 2520
 QY 841 LeuCysSerLeuCysTrpGlyAspMetGluAsnLysLeuPheAlaGlyLysArgArgPhe 860
 Db 2521 CTCTGAGGCTGTGTACCGGACATGAGAAACAAGCTGTGTGGCGGAGTTTGGCGGGGAC 2580
 QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 Db 2581 GGGCTGCTCTCGTGTGTGTGATGATTTCTGTGTGTGATGACCTCACTCAACCAACGCG 2640
 QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTrpGlyCysValValAsnLeu 900
 Db 2641 AAAACCTTCTCAGGACCTGTGTCGAGAGTGTCCGTAGTATGGCTGGCTGTGAACCTTG 2700
 QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
 Db 2701 CGAAGACAGTGTGTAATCTCTGTAGAAAGCAGAGCCCTGGTGGCGACGCGCTTTTGT 2760

QY 921 GIMetProAlaHisGlyLeuPheProTyrCyGlyLeuLeuLeuAspThrArgThrLeu 940
DB 2761 CAGATCCGGCCACCGCCCTAATCCCTGGTGGCGCTGTCTGTGAATCCCGACCTTC 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
DB 2821 GAGGTGAGGACACTCTCAGCTATGCCGAGCTCCATCAGACCGAGTCTCACCTTC 2880
QY 961 AsnArgGlyPheIleValAlaGlyAsnMetArgArgGlyLeuPheGlyValLeuArgLeu 980
DB 2881 AACCGGGCTTCAAGGTGGAGGAACATCCGTGCAAACTCTTGGGGCTTGGCGCTG 2940
QY 981 LysCyHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
DB 2941 AAGTGTACAGCCCTGTTTCTGGATTGGAGGTAAACGCTCCACAGCGGTGTCACCAAC 3000
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
DB 3001 ATCTACAGATCTCTCCGTGCGAGCGATACAGGTTTCAAGCATGTGTGCTGCACTCCA 3060
QY 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
DB 3061 TTTCATCAGAACTTTGGAAAGAACCCACATTTTCTGCGCTCATCTCTGACAGGCC 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
DB 3121 TCCCTCTGCTACTCTCACTCTGAAAGCCAGAACGCGAGTGTGCTGGGGCGCAAGGCG 3180
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnThrLeuCysHisGlnAlaPheLeuLeu 1080
DB 3181 GCGCGGCGCTGCTGCTCCGAGCGGTGCACTGTGTGCGCACCAAGATTCCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
DB 3241 AACCTGACTGACACCGTGTCACTAGTGCACCTCTGGGGTCACTCAGGAGACGCCAG 3300
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
DB 3301 ACCCAGCTGAGTGGAGAGCTCCGCGGAGCAGACGCTGACCTGCGAGGCGCGAGCAAC 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
DB 3361 CCGGCACTGCTCTCAAGCTTCAAGACCATCTGAC 3396

RESULT 9
BD096291 3396 bp DNA linear PAT 27-AUG-2002
LOCUS Cells capable of differentiating into myocardial cells.
DEFINITION
ACCESSION BD096291 GI:22641879
VERSION WO 0148151-A/16.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Umezawa,A., Hata,N., Fukuda,K., Ogawa,S., Sakurada,K., Gojo,S. and
Yamada,Y.
TITLE Cells capable of differentiating into myocardial cells
JOURNAL Patent: WO 0148151-A 16 05-JUL-2001;
KYOWA HAKKO KOGYO CO LTD
OS Homo sapiens (human)
PN WO 0148151-A/16
PD 05-JUL-2001
PF 27-DEC-2000 WO 2000JP009323
PR 27-DEC-1999 JP 99P 372826,28-FEB-2000 WO PCTJP0001148 PR
02-NOV-2000 WO PCTJP0007741
PI AKIHINO UMEZAWA,JUNICHI HATA,KEIICHI FUKUDA,SATOSHI OGAWA,PI
KAZUHIRO SAKURADA,SATOSHI GOJO,YOJI YAMADA
PC
C12N5/06,C12N5/08,C12P21/08,C12Q1/02,A6IK35/28,A6IK35/44,A6IP9/PC
06, A6IP9/04//A6IK36/18,C12N15/12

CC Cells capable of differentiating into myocardial cells FH
Key Location/Qualifiers
FT CDS (1)..(3399).
FEATURES
source 1..3396
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 6,73e-151 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-044-692-2 (1-1132) x BD096291 (1-3396)
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGln 20
DB 1 ATGCCGCGGCTCTCCCGCTGCGAGCCGTCGCTCTGCGAGCCACTACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
DB 61 GTGCTGCGCTGCGCACTTCTGCGGCGCTGCGGAGCCCAAGGCTGCGCTGTGAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProThr 60
DB 121 CCGGGAGACCGGCGCTTCCGCGCTGTGCGCCAGTGTGCTGTGCTGCGCTG 180
QY 61 AsnAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
DB 181 GAGCAGCGGCG 240
QY 81 ValAlaArgValLeuGlnArgLeuGlyArgGlyValAlaLysAsnValLeuAlaPheGly 100
DB 241 GTGGCGCGAGTCTGACAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 PheAlaLeuLeuAspGlyValaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGCGGCTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValaTyrGlyLeuLeu 140
DB 361 AGCTACCTGCCCAACACGCTGACCGACGACGACGCGGGAGCGGGGCGTGTGCTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGCGCGCGGTGGGCGACGACGCTGTGCTCACTGTGTGCGACGCTGCGCGCTTTTGTG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuThrGlnLeuGlyAla 180
DB 481 CTGGGTGCTCCCAAGCTGCGCTCAAGAGTGTGCGGCGCGCGCGCTGTACACGCTGCGGT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 541 GGCATCAGCG 600
QY 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CCGGCTGTGGAACATATGCTCAGGAGGCGCGGGGTCTCCCTGTGGCTGCAACCCCGGGT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCGAGAGGCGCGGAGGAGTGTCCAGCGCAAGTGTGCTGTGCTCCCAAGAGGCGCGGT 720
QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 721 GCGGCTGCGCTGAGCGCGAGCGAGCGCGCTGTGGGAGGGGTCTTGGGCGCACCGGGG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValSerProAlaArgProAlaGln 280


```

421 ProAlaAlaGlyValCysAlaArgGlnProGlnGlySerValAlaAlaProGlnGln 440
Db 1261 CCAGACAGCGGTGTGTGTGCGGGAGAACCCCAAGGCTGTGTGTGCGGCCCGCAGAG 1320
QY 441 GGuApThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1321 GAGGACACAGACCCCGTGTGCGTGTGCGAGCTCTCCGACACAGCGCCCTGTGGCAG 1380
QY 461 ValTYrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrTrpGlySer 480
Db 1381 GTTATGCGCTTGTGTGGCGCTGTGCTGCGCGCGCTGTGTGCTGCGAGGCTCTGGGGCTTC 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrIleValPheIleSerLeuGlyIleHis 500
Db 1441 AGGCACACAGAACCGCGCTCTCCAGGAACACCAAGATTATCTCCCTGGGGAAGCAT 1500
QY 501 AlaIleLeuSerLeuGlnGlnLeuThrTrpIlePheSerValArgAspCysAlaTrpLeu 520
Db 1501 GCCAAGCTCTCCGTGAGAGCTGACGTGGAAGATGACGTGGGGACTGCGCTTGGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnIle 540
Db 1561 CGCAGAGAGCCCAAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 541 LeuAlaIlePheLeuHisIleTrpLeuMetSerValTYrValValGlnLeuLeuArgSerPhe 560
Db 1621 CTGGCCCAAGTCTCTGACCTGCGTGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 561 PheTYrValTYrGlnThrThrPheGlnIleValAsnArgLeuPhePheTYrArgIleSerVal 580
Db 1681 TTTTATGTACAGGAGCCACGTTTCAAAAGAACAGGCTCTTTTTCACCGGAAGATGTTC 1740
QY 581 TrpSerIleValLeuGlnSerIleGlyIleArgGlnHisLeuIleArgValGlnLeuArgGln 600
Db 1741 TGGACCAAGTGTCAAGCATTTGGAATCAACAGCACTTGAAGAGGTGTGAGCTGCGGAG 1800
QY 601 LeuSerGluAlaGlyValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 CTGTGCGAAGCAGAGGTCCAGGACATCCGGAAGCCAGGCCCGCTGCTGACATCCAA 1860
QY 621 LeuArgPheIleProIlePheProAspGlyLeuArgProIleValAsnMetAspTYrValVal 640
Db 1861 CTCCCTTCATCCCAAGCCTGACGCGGCTGCGGCGCATTTGTGAACATGACATCACTGCTG 1920
QY 641 GlyAlaArgThrPheArgArgGlnIleValArgGlnHisArgGlnHisArgGlnHisArg 660
Db 1921 GGAGCCAGAACGTTCCGACAGAAAGAGAGGCGCGGACGTTCTCACTCGAGGGTGAAGGCA 1980
QY 661 LeuPheSerValLeuAsnTYrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1981 CTGTTCAAGGTGCTCAACTACAGAGGGGGCGCGCGCGCTCTGGGGCGCTCTGTG 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGCTGTGACGATATCCACAGGGCTGCGGACCTTCTGTGTGTGTGTGTGTGTGTGT 2100
QY 701 AspProProProGlnLeuTYrPheValIleValAspValThrGlyAlaTYrAspThrIle 720
Db 2101 GACCCGCGCCCTGAGCTGTACTTGTTCAGAGTGTGAGTGTGACGGGCGCGTACGACACATC 2160
QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLeuProGlnAsnThrTYrCys 740
Db 2161 CCCCAAGACAGGCTCCAGAGGTATCCGACATATCAAAACCCCAAGACAGCTATCTGC 2220
QY 741 ValArgArgTYrAlaValAlaGlnIleValAlaHisGlyHisValArgIleValAspLeu 760
Db 2221 GTGGCGTGGGTATCGGTGTGCGAAGGCGCGCCATGGGACGTCGCAAGGCTTCAAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTYrMetArgGlnPheValAlaHisLeu 780
Db 2281 AGCCACAGTCTTACCTTGACAGACCTTCAGCCCTTACATGAGAGAGTTCGTGGCTCACCTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800

```

```

2341 CAGAGACAGCCCGCTGAGGATGCGCTGCATTCAGCAAGAGCTCTCCCTGATATGAG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
Db 2401 GCCACAGAGGAGCTTTCACAGCTTTCACAGCTTTCATGTGACACACACCCGCTGCATC 2460
QY 821 ArgGlyIleSerTYrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGGGCAAGTCTCTACGTCCAGTCCAGAGGAGATCCCGAGAGGCTCATCTCTCCAGCTG 2520
QY 841 LeuCysSerLeuCysTYrGlyAspMetGluAsnIleLeuPheAlaGlyIleArgArgAsp 860
Db 2521 CTCTCAGCTGTGTGTACCGGACATGAGAAACAAGCTGTTCGGGGGATTCGGCGGGAC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisIleuThrHisAla 880
Db 2581 GGGCTGTCTCTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTYrGlyCysValValAsnLeu 900
Db 2641 AAAACCTTCTCAGACCTGTGTCGAGGTGTCTCTGATGTAGCTGCGGTGTGAACTTG 2700
QY 901 ArgIleThrValValAsnPheProValGluAspGluAlaLeuGlyGlyTYrAlaPheVal 920
Db 2701 CGGAAGACAGTGTGAACTTCCCTGTGAGAAAGACAGAGCCCTGGGTGTGCAGGCTTTGTT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCCGCGCCACAGGCTATTTCCCTGTGTGCGCTGTGTGTGTGTGTGTGTGTGTGT 2820
QY 941 GluValGlnSerAspTYrSerSerTYrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2821 GAGGTGCAGAGGACTTCTCCAGCTATGCCCCGAGCTCCATACAGACCAGTCTACCTTC 2880
QY 961 AsnArgGlyPheIleAlaGlyArgAsnMetArgArgIleLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGGCTCTCAAGGCTGTGAGAAACATGCTCGAAACTTTGGGGTCTTGGCGGCTG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2941 AAGTGTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000
QY 1001 IleTYrIleIleLeuLeuGlnAlaTYrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTACAGATCTCTCTGTGAGGGGTACAGGTTTCAAGCATGTGTGTGTGTGTGTGTGT 3060
QY 1021 PheHisGlnGlnValTrpIleAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3061 TTTCAATCAGCAAGTTTGGAAAGAACCCACATTTTCTCGCGGTATCTGTGACAGGCGC 3120
QY 1041 SerLeuCysTYrSerIleLeuIleValAlaValAsnAlaGlyMetSerLeuGlyValAlaGly 1060
Db 3121 TCCCTCTGTCTACCTCATCTCTGAAGCCAGAAACGCGGATGTGTGTGGGGCGCAAGGGC 3180
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
Db 3181 GCGGCGGCGCTGTGCTCTCCAGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
QY 1081 LysLeuThrArgHisArgValThrTYrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3241 AAGCTGACTGCACACGCTGTCACTACGTGCCACTCTGGGGTCACTGAGACAGCCAG 3300
QY 1101 ThrGlnLeuSerArgIleLeuProGlyTYrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3301 ACGCAGCTGAGTGTGGAAGCTCCCGGGGACGAGAGCTGTGCGCTGTGAGGCGCAGCCAA 3360
QY 1121 ProAlaLeuProSerAspPheIleThrIleLeuAsp 1132
Db 3361 CCGGCACTGCTCTCAGACTTCAAGACATCTGTGAC 3396

```

RESULT 11
AR393441

QY 581 TPSSerIyLeuGlnSerIleGlyIleArgGlnIleuLeuArgValGlnLeuArgGln 600
 Db 1768 TGGTCCAAACCTGACGATCCATCGGTATCGGTGACACCTGAAACGTTTCAAGTCGGTGA 1827
 QY 601 LeuSerGlnAlaGlnValArgGlnIleArgGlnAlaArgProAlaLeuLeuThrSerArg 620
 Db 1828 CTGTCCGAAGCTGAAGTTCGTGACGACCTGTGAAGCTCGTCCGCTCTGTGACCTCCCT 1887
 QY 621 LeuArgPheIleProIySerProAspGlyLeuArgProIleValIleAspMetAspTyrValVal 640
 Db 1888 CTGCGTTTCATCCCGAAACCGGACGGCTGCGCTCGATGTGAACATGAGACTACGTTGTT 1947
 QY 641 GlyAlaArgThrPheArgArgGlnIySerArgAlaGlnArgLeuThrSerArgValIySala 660
 Db 1948 GGTGCTCGTACCTTCGTGTGTAAACGTTGCGAGCGTCTGACCTCCGCTGTAAAGCT 2007
 QY 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
 Db 2008 CTGTTCTCCGTTCTGAACACGACGACGCTGCTCGTCCGCGTCTGCTGCGTCTCCGTT 2067
 QY 681 LeuGlyLeuAspAspIleHisArgAlaTTPArgThrPheValLeuArgValArgAlaGln 700
 Db 2068 CTGGGCTGGAGACATCCACCGCTGCTTGGCGTACCTTGCTGCTGTGCTGTGCTCAG 2127
 QY 701 AspProProGlnLeuTyrPheValIySerValAspValThrGlyAlaTyrAspThrIle 720
 Db 2128 GACCCGCGCGGGAACGTACTTCGTTAAAGTTGACGTTACCGGCGCGTACGACACCATC 2187
 QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleIySerProGlnAsnThrTyrCys 740
 Db 2188 CCGCAGGACCGTCTGACCGAAGTTATCGCTTCATCATCAACCGCAGAACCATCACTCC 2247
 QY 741 ValArgArgTyrAlaValValGlnIySalaIleHisGlyIleValArgIySalaPheIyS 760
 Db 2248 GTTCGTCGTAGCGTGTGTTCAGAAAGTGTCTGACGCTGCTGTAAGGATTCAAA 2307
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgIlePheValAlaHisLeu 780
 Db 2308 TCCACGTTTCCACCTGACCGACCTGACCGCGTACATCGTCAAGTTCGTGTCACCTG 2367
 QY 781 GlnIyThrSerProLeuArgAspAlaValIleGlnIleSerSerLeuAsnGln 800
 Db 2368 CAGGAAACCTCCCGCTGCGTACCGCTGTGTATGAAACAGTCCCTCCCGAAGCAA 2427
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 Db 2428 GCTTCCTCCGTCGTGTTCAGACGTTTTCGCGTTTCATGTGCCACACCGCTGTGTATC 2487
 QY 821 ArgGlyIySerSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db 2488 CCGTGTAAATCTTACGTTCAAGTCCAGGGTATCCCGCAGGGTTCATCTGTCCACCTG 2547
 QY 841 LeuCysSerLeuCysTyrGlyAspMetGlnAsnIyLeuPheAlaGlyIleArgArgAsp 860
 Db 2548 CTGTGCTCCCTGTGCTACCGGTACATGAGAAACAAACCTGTCGTGTATCCGTCGTGAC 2607
 QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisIleuThrHisAla 880
 Db 2608 GGTCTGCTGCTGCTGCTGTGTAACGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2667
 QY 881 LysThrPheLeuArgThrLeuValArgGlyValArgGlyIyCysValValAsnLeu 900
 Db 2668 AAAACCTTCTCGTACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2727
 QY 901 ArgIySerThrValValAspAspProValGlnAspGlnAlaLeuGlyIyThrAlaPheVal 920
 Db 2728 CCGTAAACCGTGTAACTTCCCGGTGAAGACGAAAGCTCTGGGTGGCACCCCTTTCGTT 2787
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 Db 2788 CAGATGCCGCGCTCACGGTCTGTTCCTCGTGTGGGTCTGTGTGTGTGTGTGTGTGTGTGT 2847
 QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960

Db 2848 GAAGTTCAGTCCGACCTACCTCCCTACCTCCCTACCTCCCTACCTCCCTGACCTTC 2907
 QY 961 AsnArgGlyPheLeuAlaGlyArgAspMetArgArgIyLeuPheGlyValLeuArgLeu 980
 Db 2908 AACCGTGTTCGTAAGCTGT 2967
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValIleAsnSerLeuGlnThrValCysThrAsn 1000
 Db 2968 AATGCCACTCCCTGCTTCTGTGACCTTGACGTTAACTCCCTGACACCGTTTGACCAAC 3027
 QY 1001 IleTyrIySalaLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db 3028 ATCTACAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3087
 QY 1021 PheHisGlnGlnValTTPIySerProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db 3088 TTCACACGACGATTTGGAAAAACCGACCTTCTCTGCGGTATTCGACACACGCT 3147
 QY 1041 SerLeuCysTyrSerIleLeuIySalaIySerAspAlaGlyMetSerLeuGlyAlaIySgly 1060
 Db 3148 TCCCTGTGCTACTCCATCTGTGAACCTGTAACAAACGCTGTGTATCTCTGCTGTAAAGT 3207
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTTPLeuCysHisGlnAlaPheLeuLeu 1080
 Db 3208 GCTGCTGGTCCGCTGCGCTCCGACGACTGTCAGTGTGTGTGTGTGTGTGTGTGTGTGT 3267
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrArgIle 1100
 Db 3268 AAACGTACCGCGTACCGGTATCTTACGTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGT 3327
 QY 1101 ThrGlnLeuSerArgIyLeuProGlyThrThrLeuThrAlaLeuGlnAlaIleAsn 1120
 Db 3328 ACCGACGTCTCCCGTAACTGCGGCTACACCTGACCGCTCTGGAAGCTCTGTGTAC 3387
 QY 1121 ProAlaLeuProSerAspPheIyThrIleLeuAsp 1132
 Db 3388 CCGGCTGCTGCGTCCGACCTTCAAAACCATCTGTGAC 3423

RESULT 12
 ARI04587 4015 bp DNA linear PAT 14-FEB-2001
 LOCUS ARI04587
 DEFINITION Sequence 224 from patent US 6093809.
 ACCESSION ARI04587
 VERSION ARI04587.1 GI:12817295
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 4015)
 AUTHORS Cech,T.R. and Lingner,J.
 TITLE Telomerase
 JOURNAL Patent: US 6093809-A 224 25-JUL-2000;
 FEATURES
 source 1..4015
 /organism="Unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 7.86e-151 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-044-692-2 (1-1132) x ARI04587 (1-4015)

QY 1 MetProAlaGlnProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGln 20
 Db 56 ATGCCGCGGCTCCCGCTGCGACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 115

QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
DB 116 GTGCTGCCCCGTCAGCCAGTTCGTGCGCGCCGCGGAGCCCAAGGCGTGGGCTGGAG 175
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
DB 176 CCGGGGACCCCGGCGCTTCCGCGGCGTGTGGCCAGTGCCTGGTGTGGTGGCCCTGG 235
QY 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuGlyLeu 80
DB 236 GACGACAGCGCGCCCGCCCGCCCTCTCCGCAAGTGTCCCTGAGAGAGCTGG 295
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyArgGlyAlaAlaAsnValLeuAlaPheGly 100
DB 296 GTGGCCCGAGTGTGCAAGGCTGTGCGAGCGCGGCAAGACGTGCTGGCTTGGC 355
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 356 TTGCGGCTGTGAGCGGGGCGCGGGGGGCGCCCGAGGCGCTTCAACACAGCGTGGC 415
QY 121 SerTrpLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140
DB 416 AGCTACCTGCGCAACGCGTGAACCGACCTGCGGGAGCGGGCGTGGGGCTGTG 475
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 476 CTGCGCGCGTGGCGAGCGAGCTGTGTTCACCTGTGACAGCTGGCGCTTGTG 535
QY 161 LeuValAlaProSerCysAlaTrpGlnValCysGlyProProLeuTrpGlnLeuGlyAla 180
DB 536 CTGGGTGCTCCAGCTGCGCTACAGTGTGCGGGCGCGCTGTACACAGCTCGCGCT 595
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 596 GCCACTCAGCGCGCGCCCGCCCAACGCTAGTGAACCCGAAGGCGTGGGATCCGA 655
QY 201 ArgAlaTrpAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 656 CGGGCTGGAACCTAGCGTCAAGGAGCGCGGGTCCCTCGGGCTGGCCAGCCGGGT 715
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 716 GCGAGGAGGGCGGGGCGAGTGCACGCAAGTCTGCGCCCAAGAGGCCAGCGCT 775
QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
DB 776 GCGCCTGCGCTGAGCGGAGCGGACGCGCTGTGGAGGAGGAGTGTGGGCCACCGGGC 835
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGln 280
DB 836 AGGACGCTGAGCCGAGTGAACGTGTCTGTGTGTGTCACTGCAAGCCGCGGAA 895
QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 896 GAAGCCACACTCTTGGAGGAGTGCCTCTGGCAAGCGCACTCCACCACTCCGTGGGC 955
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
DB 956 CGCAGACCAACGCGGGCGCCCAACCAATCGGCGCAACGCTCCGTGGACACGCT 1015
QY 321 CysProProValTrpAlaGlnThrLysHisPheLeuTrpSerSerGlyAspLysGlnGln 340
DB 1016 TGTCTCCCGGTGAGCGGAGCAACAGACTTCTCTCACTCTCAAGCGACAGAGACAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1076 CTGGGCGCTCTCTCTCACTCAAGCTCTGAGGCGCAAGCTGAGGCGCTCGAGGCTC 1135
QY 361 ValGlnThrTrpLeuLeuGlySerArgProTrpMetProGlyTrpThrProArgArgLeuPro 380
DB 1136 GTGAGACATCTTCTGTGGTTCAGGCGCTGAGAGCCAGGAGACTCCCGGAGGTGCGC 1195
QY 381 ArgLeuProGlnArgTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400

DB 1196 CGCCTGCCCAAGCCCTACTGGCAATGCGGCGCTGTCTTGGAGCTGTGGGAAACAC 1255
QY 401 AlaGlnCysProTrpGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1256 GCGAGTGCCTCCCTAGGGGAGTCTCTCAAGCGACTGCGCGTGCAGCTGCGGTCAAC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGln 440
DB 1316 CCAAGCGCGGTGTGTGTGCGCGGAGAGAGCCCAAGGGCTGTGTGGCGGCCCCGAGAG 1375
QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
DB 1376 GAGGACACAGACCCCGCTGCGCTGTGACGTGTCCCGCAGACAGAGCGCTTGGCAG 1435
QY 461 ValTrpGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
DB 1436 GTGTAGGCTGTGTGCGGGCGCTGCTGCGCGGCTGTGGTCCCAAGGCTTGGGGCTCC 1495
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHis 500
DB 1496 AGCCCAACAGAACGCGCTTCTCAAGAACCAAGAACTTCACTCCCTGGGAAAGCAT 1555
QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
DB 1556 GCCAAGCTCTGCTGCAGAGCTGACGTGGAAGTGAAGCGCGGACGTGGCTTGGCTG 1615
QY 521 ArgArgSerProGlnValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnLe 540
DB 1616 CCGAGAGCGCCAGGGGTGGTGTGTTCGCGCGCAGAGACACGTCTGCGTGAAGATC 1675
QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTrpValGlnLeuLeuArgSerPhe 560
DB 1676 CTGGCAAGTTCTCTCACTGCTGATGATGTGTGTCGTCTGCAAGCTCTCAAGGCTTTC 1735
QY 561 PheTrpValThrGlnThrThrPheGlnLysAsnArgLeuPheTrpArgLysSerVal 580
DB 1736 TTTTATGTCAACGAGACACAGTTTCAAAAGAACAGGCTTTTCTTACCGAAGGTGTC 1795
QY 581 TrpSerLysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGln 600
DB 1796 TGGAGCACTTCAGAACATTTGGATTCAGACAGCATTTGAGAGGGTGTGAGTGGGAG 1855
QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
DB 1856 CTGTGGAAAGAGAGGTCAAGCATCGGAAGCCAGGCGCCCTCTGACTGATCCAGAG 1915
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTrpValVal 640
DB 1916 CTCCGCTTCATCCCAAGCCTGACGCGCTGCGCGGATTTGTGAACATGACTACGTG 1975
QY 641 GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
DB 1976 GAGACAGAACCTTCCGAGAGAAAGAGGCGAGGCGTCACTCACTCGAGGGTGAAGCA 2035
QY 661 LeuPheSerValLeuAsnTrpGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
DB 2036 CTGTTCAGGTGTCAACTACAGCGGCGCGCGCCCGCTCTGTGGCGCTCTGTG 2095
QY 681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
DB 2096 CTGGGCTGTGACATTTCCAGAGGCTGCGCACCTTGTGTGTGTGTGTGGGCGCCAG 2155
QY 701 AspProProGlnLeuLeuTrpPheValLysValAspValThrGlyAlaTrpAspThrIle 720
DB 2156 GACCCGCGCTGAGCTGTGACTTTGTCAAGGTGAGTGAACGGGGCGCTGACACCATC 2215
QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleLysArgProGlnAsnThrTrpCys 740
DB 2216 CCCAGAGACGCTCAAGAGGTCAATCGCAGCATCATCAAAACCCAGAACAGTACTGC 2275
QY 741 ValArgArgTrpAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLys 760

Db 2276 GTGCGTCGATATGCGGTGTCAGAAAGCGCCCATGGGACGTCGCAAGCCTTTCAG 2335
 Qy SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
 Db 2336 AGCCACGTCCTACCTTGAACACCTCCAGCCGTCATGACGACGTCGTCGTCACCTG 2395
 Qy GlnGlnThrSerProLeuArgAspAlaValAlaIleGlnGlnSerSerSerLeuAsnGln 800
 Db 2396 CAGAGACACAGCCGCTGAGGAGATGCCGTCATCGACAGCAAGCTCCCTCGTGAATAG 2455
 Qy AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisIleAlaValArgIle 820
 Db 2456 GCCACAGATGGCTCTTCGACGCTTCCATCCGCTTCAATGTGCACACACCGCCGTGGCATC 2515
 Qy ArgGlyIlySerSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db 2516 AGGGGCAAGTCTTACGTCACAGTCCAGGGGATCCGCAAGGCTCCATCTCTCCACGCTG 2575
 Qy LeuCysSerLeuCysTyrGlyAspMetGluAsnIlyLeuPheAlaGlyIlyIleArgArgAsp 860
 Db 2576 CTCCTCAACCTCTGCTACGCGACATGAGAAACAGCTTTGCGGGATTCGCGCGGAC 2635
 Qy GlysLeuLeuLeuValArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 Db 2636 GGGCTGCTCTGCTGGTGGATGATTTCTGTGGTGAACACTCACCTCACCCACGCG 2695
 Qy LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrGlyCysValValAsnLeu 900
 Db 2696 AAAACCTTCTCAGAGACCTGTGTCGAGGTGTCCCTGATAGTGGCTGTGTGAACCTTG 2755
 Qy ArgIlySerThrValAlaAspPheProValGluAspGlnAlaLeuGlyGlyTyrHisAlaPheVal 920
 Db 2756 CGGAAGACAGTGTGTAACCTCCCTGTAAAGACAGGCCCTGGGTGCAACGCTTTTGT 2815
 Qy GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 Db 2816 CAGATGCGGCGCCACGCTATATCCCTGTGTCGCGCTGCTGTGATACCCGACCCCTG 2875
 Qy GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db 2876 GAGGTGACAGAGGACTACCTCCAGTATGCGGACCTCCATCAGACGCTCTCACCTTC 2935
 Qy AsnArgGlyPheLeuAlaGlyArgAspMetArgArgIlyLeuPheGlyValAlaLeuArgLeu 980
 Db 2936 AACCCGCTTCAAGGCTGGAGAAACATGCTCCGAACTCTTTGGGGTCTTGGCGCTG 2995
 Qy LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 Db 2996 AAGTGTACAGGCTGTCTGTGATTTGACAGTGAACAGCCTCCAGACGCTGTGCACCAAC 3055
 Qy IleTyrIlyHisIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db 3056 ATCTCAAGATCTCTCTGTGAGGGGTACAGGTTTCAGCAGCATGTGTGTGACGCTCCA 3115
 Qy PheHisGlnGlnValTyrIlyAspProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db 3116 TTTCTATCAGCAGTTTGAAGAACCCCACTTTTCTCGGCTCATCTCTGACAGGCTC 3175
 Qy SerLeuCysTyrSerIleLeuIlyAsnAlaIlyAsnAlaGlyMetSerLeuGlyValIlyGly 1060
 Db 3176 TCCCTCTGCTACTCATCTGAAGCAAGCAAGGAGATGCGCTGGGGGCAAGGAGC 3235
 Qy AlaAlaIlyProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
 Db 3236 GCGGCGGCTCTGCTCCCTCCAGAGCGGTGAGTGTGTGCACCAACCATTTCTGCTC 3295
 Qy LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3296 AAGCTGACCTCGACCGCTGTACACGTCGCACTCTGGGCTCACTGAGACAGCCGAC 3355
 Qy ThrGlnLeuSerArgIlyLeuProGlyTyrThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 Db 3356 ACGCAGCTGATGTGGAAGCTCCCGGGGAGAGACGCTGACTGCTGGAGGCGCCAGCAAC 3415

Qy 1121 ProAlaLeuProSerAspPheIlySerThrIleLeuAsp 1132
 Db 3416 CCGGCACTGCTCCTCAGACTTCAAGACATCTCTGAC 3451
 RESULT 13
 AR175848 4015 bp DNA linear PAT 17-DEC-2001
 LOCUS AR175848
 DEFINITION Sequence 224 from patent US 6309867.
 ACCESSION AR175848
 VERSION AR175848.1 GI:17917147
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 4015)
 AUTHORS Cech, T.R. and Nakamura, T.
 TITLE Telomerase
 JOURNAL Patent: US 6309867-A 224 30-OCT-2001;
 FEATURES
 source location/Qualifiers
 1..4015
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,866-151 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Gaps: 0
 Db: 6
 US-10-044-692-2 (1-1132) x AR175848 (1-4015)
 Qy 1 MetProArgAlaProArgCysArgAlaValAlaArgSerLeuLeuArgSerHisIlyArgGln 20
 Db 56 ATGCCGCGGCTCCCGGCTGCGGACCGGTGGCTCCGTCGTCGACGACCACTACCGCGAG 115
 Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
 Db 116 GTGCTGCGCTGGCCACGCTTCGTGCGGCGCTGGGGGCCCCAGGGCTGGCGCTGTGTGACG 175
 Qy 41 ArgGlyAspProProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProThr 60
 Db 176 GCGGGGAGACCGGCGGCTTTCGCGGCTGGTGGCTGAGTCTGTGTGCTGTGCTGCTG 235
 Qy 61 AspAlaArgProProProAlaAlaPheArgPheArgGlnValSerCysLeuIlyGlnLeu 80
 Db 226 GACGCAAGCGCGCCCGCGCGCCCTCTCCGCAAGGTGTCTGCTGTAAGAGAGCTG 295
 Qy 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaIlyAsnValAlaPheGly 100
 Db 296 GTGGCCCAAGTGTCTCAGAGGCTGTGCAAGCGCGCGGAGAAAGTGTGCTGCTGCGCT 355
 Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyIlyProProGlnAlaPheThrThrSerValArg 120
 Db 356 TTGCGGCTGTGAGAGGGGCGCGCGGGGCGCCCGGAGGCTTTCACACAGCGTGGC 415
 Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgIlySerGlyAlaIlyProIlyLeuLeu 140
 Db 416 AGCTACCTGCCCAACACGCTGACCGACCTGCGGGGAGGCGGGGCTGGGGGCTGCTG 475
 Qy 141 LeuArgArgValGlyIlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 476 CTGGCGCGGTGGGGGAGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 535
 Qy 161 LeuValAlaProSerCysAlaIlyArgIlyValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 536 CTGGTGGCTCCCAAGCTGGGCTTACCAAGGTGTGCGGGGCGCGCTTACCAAGCTTCCGCGCT 595
 Qy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200

Db	596	GCCACATCAGGCGCCGCCGCCACACAGCTAGTGGACCCCAAGGCGCTGTGGATGCGAA	655
QY	201	ATGATATPrpnhisservalArgIuaIagIyValProIeuGIyLeuProIaIProGIy	220
Db	656	CGGCGCTGGAAACCATATAGCTCAAGGAGGCGGGGGTCCCTCTGGGCTCCAGGCCCGGGGT	715
QY	221	AlaArgnArgnArgGIyGIySerIaIaSerATGSerLeuProLeuProLyAsrProhArg	240
Db	716	GCGAGAGAGGCGGGGGCACTGCCAGCCCAAGCTCCCGTTCCCAAGAGGCGCAGGCGT	775
QY	241	GIyAlaIaIaProGIuProGIuArgThrProValGIyGIuGIySerTrpAlaHisProGIy	260
Db	776	GGCGCTGCGCCCTGAGCGCGAGCGGAGCGCGCTGGCGAGGGGTCTGGGCCACCGCGGAC	835
QY	261	ArgThrArgGIyProSerAspArgGIyPheCysValValSerProIaIaArgProIaGIu	280
Db	836	AGGAGCGCTGGACCGAGTGAACGGGTTTCTGTGTGTGTCTCACTCCAGACCCCGCA	895
QY	281	GIuAlaThrSerLeuGIuGIyAlaLeuSerGIyThrArgHisSerHisProSerValGIy	300
Db	896	GAAAGCACTCTTTGAGGGGTGGCTCTTGACACCGCCACTCCACCCATCCGTGGGC	955
QY	301	ArgGIuHisHISalagIyProProSerSerThrArgProProhArgProTrpAspThrPro	320
Db	956	CGCCGAGCACCGGCGGGCCCCCATCCACATCGGGGACACCACTCTCTGGAGACGCTT	1015
QY	321	CysProProValIYyAlaGIuThrLysHisPheLeuThySerSerGIyAspLyGIuGIu	340
Db	1016	TCTCCCCCGGTGTATGCCGAGACCAACACTTCTCTACTCTCAAGGCGACAAGAGCAG	1075
QY	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGIyAlaArgAgleu	360
Db	1076	CTGCGCGCCCTCTTCTCACTGACTCTTGAGGCCAGCTGACTGGCGCTCGGAAGCTC	1135
QY	361	ValGIuThrIlePheLeuGIySerArgProTrpMetProGIyThrProArgAgleuPro	380
Db	1136	GTGGAGACCATCTTTCTGGGTTCCAGGCGCTGAGATGCCAGGAGACTCCCGCAGATTGCC	1195
QY	381	ArgLeuProGIuArgTyTTrpGImeCArgProLeuPheLeuGIuLeuLeuGIyAsnHis	400
Db	1196	GCGCTGCCCCACGCGTACTGGCAATGGGCGCCCTGTCTTGAGGCTGCTTGGAAACAC	1255
QY	401	AlaGIuCysProTyGIyValLeuLeuLysThrHisCysProLeuArgAlaIaValThr	420
Db	1256	GCGCAATGCCCTTACGGGGTGTCTCTCAAGACGACTGCCGCTGGAGCTGGCGTACC	1315
QY	421	ProIaIaGIyValCysAlaArgGIuLyProGIuLysSerValAlaIaProGIuGIu	440
Db	1316	CCAGCAGCGGGGTGTGTGCTCCGGGAGAAAGGCCCCGAGGCTCTGTGGGGCGCCCGAAGAG	1375
QY	441	GIuAspThrAspProhArgArgLeuValGIuLeuLeuArgGIuHisSerSerProTrpGIu	460
Db	1376	GAGGAAACAGACCCCCGCTGCGCTGGTGAAGCTGCTCCGACACACAGAGGCCCTGGCAG	1435
QY	461	ValTyGIyPheValArgIaCysLeuArgAgleuValProProGIyLeuTrpGIySer	480
Db	1436	GCTHAGCGCTGTGGGGGCTGGCGTGGCGCGGCTGTGGGCCCCGAGGCTCTGGGAGCTCC	1495
QY	481	ArgHisAsnGIuArgArgPheLeuArgAsnTrpLysPheIleSerLeuGIyLysHis	500
Db	1496	AGGCACAAACMAAGCGGCTTCTCCAGAAACACMAAGATTATCTCTCTGGGAACAT	1555
QY	501	AlaIleuSerLeuGIuGIuLeuThrTrpLysMetSerValArgAspCysAlaIaTrpLeu	520
Db	1556	GCCAGCTTCTCGTCAGAGAGCTGAGCTGAAAGATAGAGCTGCGGAGCTGCGGCTTGCTG	1615
QY	521	ArgArgSerProGIyValGIyCysValProAlaIaGIuHisArgLeuArgGIuGIuIle	540
Db	1616	CGCAGAGCCCAAGGGGTGTGCTGTGTTCCGGCGCGAGACACCGTCTGCTGGAGGATC	1675
QY	541	LeuAlaIysPheLeuHisTrpLeuMetSerValIYyValValGIuLeuLeuArgSerPhe	560
Db	1676	CTGGCCAAAGTTCGACATGGCTGATGAGTGTACGTGTGAGAGTGTGTGACGCTTTC	1735

QY	561	PheTYrValThrGIuThrThrPheGlnIlybAnArgLeuPhePheTYrArgIlybSerVal	580
Db	1736	TTTTATGTCAAGGAGACCAAGTTTCAAAAGAACAGAGCTCTTTTCTACCGGAAGAGTCTC	1795
QY	581	TrpSerIlybLeuGlnSerIleGlyIleArgGlnHisLeuIlybArgValGlnLeuArgIu	600
Db	1796	TGGAGCAAGTTGCAAAAGCAATTGGATTCAGACGACTTGAAGAGGTGCACACTCGGGAG	1855
QY	601	LeuSerGIuAlaGIuValArgGlnHisArgGIuAlaArgProAlaLeuLeuThrSerArg	620
Db	1856	CTGTCCGAGAACCAAGAGTCAAGCGACATCCGGAAGCCAGAGCCCGCTGTCTACGTCACGA	1915
QY	621	LeuArgPheIleProIlybProAspGIyLeuArgProIleValAsnMetAspTYrValVal	640
Db	1916	CTCGCTTCATCCCAAGCTCAGAGGGGCTCGGCGCATTTGTGATCATAGACTACGTCGTG	1975
QY	641	GIyAlaArgThrPheArgArgGIuIlybArgAlaGIuArgLeuThrSerArgValIlybAla	660
Db	1976	GGAGCCAGAACGTTCCGACAGAAAAGAGGGCGAGCGTCTCACTCCAGAGGTGAAGGCA	2035
QY	661	LeuPheSerValLeuAsnTYrGIuArgAlaArgArgArgProGIyLeuLeuGIyAlaSerVal	680
Db	2036	CTGTTCAGCCGTGCATCACTAGAGGGGGGGGGCGCCGCGCTCTCGGGCGCCCTCTGTG	2095
QY	681	LeuGIyLeuAspAspIleHisArgAlaAlaTYrArgThrPheValLeuArgValArgAlaGln	700
Db	2096	CTGGGCTCGAGCAGATTCACAGAGGCTGGAGCACTTGCTGTGTGTGTGGGGCCAG	2155
QY	701	AspProPheProGIuLeuTYrPheValIlybValAspValThrGIyAlaTYrAspThrIle	720
Db	2156	GACCCGCGCGCTGAGCTGTACTTGTCTCAAGTGAAGTACAGGGCGCGTACACACACATC	2215
QY	721	ProGlnAspArgLeuThrGlnValIleAlaSerIleIleIlybProGlnAsnThrTYrCys	740
Db	2216	CCCCAGACAGAGCTCAAGAGGTATCGCCAGCATCATCAACCCAGAACACGTACTGC	2275
QY	741	ValArgArgTYrAlaValAlaGlnIlybAlaHisGIyHisValArgIlybAlaPheIlyb	760
Db	2276	GTGGCTCGGTATGCGGTGTCCAAAGAGCGCCCATGGAGCATCCGCAAGGCTTCAAG	2335
QY	761	SerHisValSerThrLeuThrAspLeuGlnProTYrMetArgGlnPheValAlaHisLeu	780
Db	2336	AGCCAGCTCTCACTTCTACACGACTCCAGCCGATATCGGACAGTTGGGCTCACTGC	2395
QY	781	GlnIuThrSerProLeuArgAspAlaValIleGlnIuThrSerSerIleuAsnGln	800
Db	2396	CAGAGAACCAAGCCCCCTGAGGAGATGCCGTCTCTACAGAGAGACTCTCTCCGAATGAG	2455
QY	801	AlaSerSerGIyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
Db	2456	GCCAGCAGTGGGCTCTTGACGTCTTCTACGCTTCAATGATGACACGCGCGGCGATC	2515
QY	821	ArgGIyIlybSerTYrValGlnCysGlnGIyIleProGlnIlybSerIleuSerThrIleu	840
Db	2516	AGGGGCAAGCTCAAGTCACAGTCCAGGGAGATCCCGCAGGGCTCCATCTCTCCAGCGTG	2575
QY	841	LeuCysSerIleuCysTYrGIyAspMetGIuAsnIlybLeuPheAlaGIyIleArgArgAsp	860
Db	2576	CTCTGACGCTGTGCTACGGCGCAATGGAGAACAGACTGTTTGGCGGGATTCGGCGGGAC	2635
QY	861	GIyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
Db	2636	GGGCTGCTCTCGTGTTGTGTGATGATTTCTGTGTGTGAGACACTCACTCCACCAAGCG	2695
QY	881	LysThrPheLeuArgThrIleuValArgGIyAlaProGIuTYrGIyCysValValAsnLeu	900
Db	2696	AAACACTTCTCCAGGACCTGTATCCGAGGTGTCTCTGAGTATGGCTGTGTGTGATCTTG	2755
QY	901	ArgIlybThrValValAsnPheProValGlnAspGIuAlaLeuGIyGIyThrAlaPheVal	920
Db	2756	CGGAGACAGTGTGATCTTCTCTGTGAAGAGCGAGGCCGTGGGGGACGCGCTTTTGTT	2815

QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 DB 2816 CAGATGCCGGCCACGAGCTATTCCCTGCTGCGGCTCTCTGTGATACCCGGACCTG 2875
 QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 DB 2876 GAGGTGCAGAGGACACTCCAGCTATGCCGAGCTCCATCAGAGCCAGTCTCACTTC 2935
 QY 961 AsnArgGlyPheLeuAlaGlyArgAsnMetArgValGlyLeuPheGlyValLeuArgLeu 980
 DB 2936 AACCGGGCTTAAGGCTGGAGAAACAGCCGCGAACTCTTGGGGCTTGGCGGCTG 2995
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 DB 2996 AAGTGTCAAGGCTGTTCTGGATTGGACGGTGAACAGCTCCAGCGGTGGACCAAC 3055
 QY 1001 IleTyrLeuGlyLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 DB 3056 ATCTACAAAGATCTCTCTGTCAGGCGTACAGGTTTCAAGCATGTGTGTCGACGCTCCA 3115
 QY 1021 PheHisGlnGlnValTyrPheAsnProThrPheLeuArgValIleSerAspThrAla 1040
 DB 3116 TTTCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGGTCACTTCTGACAGAGCC 3175
 QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGly 1060
 DB 3176 TCCCTCTGCTACTCTCATCTCTGAAGCAAGCAAGCGAGATGTCTGGGGGCCCAAGGCG 3235
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrLeuCysHisGlnAlaPheLeuLeu 1080
 DB 3236 GCGCGGGGCTCTGCGCTCCGAGGCGTGCAGTGTCTGCGACCAACATCTCTGCTC 3295
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 DB 3296 AAGCTGACTCGACCGTGTCACTACGTGCCATCTCTGGGTCACTCGAGCAGCCAG 3355
 QY 1101 ThrGlnLeuSerArgLysLeuProGlyTyrThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 DB 3356 AGCGAGCTGAGTCGAAAGCTCCCGGGAGAGACCGCTGACCTGAGAGGCCCGCAGCAAC 3415
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 DB 3416 CCGGCACTGCCTCAGACTTCAAGACATCTGAGC 3451
 RESULT 14
 LOCUS BD218834 4015 bp DNA linear PAT 17-JUL-2003
 DEFINITION Method and composition for inducing immune response to telomerase
 antigen.
 accession BD218834
 version BD218834.1 GI:33028604
 keywords JP 2002509716-A/1.
 source Homo sapiens (human)
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 4015)
 Gaeta,F.C.A.
 Method and composition for inducing immune response to telomerase
 antigen
 Patent: JP 2002509716-A 1 02-APR-2002;
 JOURNAL UNIVERSITY TECHNOLOGY CORP
 OS Homo sapiens (human)
 PN JP 2002509716-A/1
 PD 02-APR-2002
 PF 30-MAR-1999 JP 2000541280
 PR 31-MAR-1998 US 60/112006
 PI FEDERICO C A GAETA
 PC C12N5/06,A61K35/14,A61K38/43,A61K39/00,A61P35/00,A61P37/00, PC
 C12N5/10,
 PC C12N5/09,C12N5/00,A61K37/48,C12N5/00,C12N5/00 CC human
 telomerase reverse transcriptase (HTRT) FH Key
 Location/Qualifiers

FEATURES FT CDS (56)..(3454).
 source location/Qualifiers
 1..4015
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,866-151 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-044-692-2 (1-1132) x BD218834 (1-4015)
 QY 1 MetProAlaGlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 DB 56 ATGCCGCGGCTCCCGCTGCGAGCCGTGCGCTCTCTGCGAGCCACTACGCGAG 115
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
 DB 116 GTGCTGCGCTGGCCACGCTTGTGCGCGCTGGGGCCCAAGGCTGGCGCTGTGAC 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 DB 176 CGCGGGAGACCGGCGGCTTTCGCGCGCTGTGGCCAGTGTCTGTGTGCTGCGCTGG 235
 QY 61 AsnAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
 DB 236 GACGACG 295
 QY 81 ValAlaArgValLeuGlnArgLeuGlyCysGlyArgGlyAlaLysAsnValLeuAlaPheGly 100
 DB 296 GTGGCGCGAGTCTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 355
 QY 101 PheAlaLeuLeuAspGlyValAlaArgGlyLysProProGlnAlaPheThrSerValArg 120
 DB 356 TTGCGGCTGTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeuLeu 140
 DB 416 AGCTACCTGCCCAACACGCTGACGACGACGACGACGACGACGACGACGACGACGACG 475
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 DB 476 CTGCGCGCGGTGGGCGAGCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 DB 536 CTGGGTGCTCCCAAGCTGCGCTTACAGAGTGTGCGGCGCGCGCGCGCGCTGACAGCT 595
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
 DB 596 GCCACTCAGAGCG 655
 QY 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB 656 CGGCGCTGGAACATAGCTCAGGAGGCGGGGTCTCCCTGGGCTGCGACCGCGGAGT 715
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB 716 GCGAGAGCGCGGGGGCGAGTCCAGCGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 775
 QY 241 GlyAlaAlaProGlyProGlyLysArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
 DB 776 GCGCGCTGCGCTGAGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 835
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 DB 836 AGGAGCGGTGAGCCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895

QY	281	GlulAaThSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
Db	896	GAACCACACCTTTTGGAGGGGTGGCGCTCTCGGCACCGGCACCTCCACCACTCCGGGAC	955
QY	301	ArgGlnHisLeuHisAlaGlyProProSerSerHisArgProProArgProTyrAspThrPro	320
Db	956	CGCAGACACACCGGGGGCCCCCATTCACATCCGGGCCACACAGTCCCTGGGACACGGCT	1015
QY	321	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
Db	1016	TGTCCCCCGGTGTACGCCGAGACCAACACACTTCTCTACTCTCCAGGCACAAAGAGCAG	1075
QY	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
Db	1076	CTGGGGCCCTCTCTCTACTACAGCTCTCTAGAGGCCACAGCTTACCTGACCGCTCGAGAGCTC	1135
QY	361	ValGluThrLysPheLeuGlySerArgProTyrPheProGlyThrProArgArgLeuPro	380
Db	1136	GTGAGAGACCATCTTCTTGCGGTTCAGAGCCCGTGGATGCCAGGAGCTCCCGCAGATTGGCC	1195
QY	381	ArgLeuProGlnArgTyrTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
Db	1196	CGCCGCCCCACGCGGTACTGGCAATGGGCGCCCTGTGTTCTGAGCTGCTTGGGAACACAC	1255
QY	401	AlaGlnCysProTyrGlyValAlaLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
Db	1256	GCGCAGTCCCTCTACGGGGGTGCTCTCTACAGACGACACTGCCGCGTGGAGCTGGGATCAC	1315
QY	421	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGln	440
Db	1316	CCAGACGCGGGGTGTGTGTGCCGGGAGAGGCCACAGAGGCTGTGTGGGGGCCCCCGAGAG	1375
QY	441	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln	460
Db	1376	GAGACACACAGACCCCCGTCGCTGGTGTGACGTGCTCCGACAGCACACAGCCCCCTGGCAG	1435
QY	461	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrTrpGlySer	480
Db	1436	GTGTACGGCTTGTGTGCGGGCCCTGCTCGCGCGCGGGGTGGGCCCCAGAGCTCTGGAGCTCC	1495
QY	481	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHis	500
Db	1496	AGGCACAAAGAACGCGCTTCTCTCAGAACACACAGAACTTCACTCCCTGGGAAACAT	1555
QY	501	AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaThrLeu	520
Db	1556	GCCAACTCTCGGTGCAGAGCTGACGTGAGAGTGAAGACGTCGGCGGACTGCGCTTGGCTG	1615
QY	521	ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlnLe	540
Db	1616	CGCAGAGGCCCAAGGGGTGTGCTGTGTCCGGCGCGAGACACAGTCTCCGTGAGAGATC	1675
QY	541	LeuAlaLysPheLeuHisThrLeuMetSerValTyrValAlaGluLeuLeuArgSerPhe	560
Db	1676	CTGGCCAACTCTCGACTGGCTGAGTGAAGTGTGTACGTGTGACACTCTCAGAGCTTTTC	1735
QY	561	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
Db	1736	TTTTATGTCCGAGAGCACAGTTCCTAAAGAACAGGCTTTTCTTACCGGAGAGATCTC	1795
QY	581	TyrSerLysLeuGlnSerLysGlyLysLeuArgGlnHisLeuLysArgValGlnLeuArgGlu	600
Db	1796	TGGAGCAAGTTGCMAAGCATTTGGAAATCACAACACACTTGAAGAGGTGAGCTGGCGAG	1855
QY	601	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
Db	1856	CTGTCCGAAACAGAGGTCAAGACAGCATCCGGAAGCCAGAGCCCGCTGTGTACGTCACAGA	1915
QY	621	LeuArgPheLysProLysProArgPylLeuArgProLysValAsnMetAspTyrValVal	640
Db	1916	CTCCGTTTATCCCAAGCCTGACAGGGCTCGCGCCCATTTGTGAACATGACATGACATGCTGTG	1975

QY	641	GIYVAIaargThrPheargArgGluIuysargAlaGIuwaIrgLeuThrSerArgValIysAla	660
Db	1976	GGAGCCGAACGTGTTCCGACAGAGAAAGAGGGCCGAGCGCTTCACCTCGAGGGGTGAAGCA	2035
QY	661	LeuPheSerValIleuAsnArgGluwArgAlaAcGArgProGlyLeuLeuGlyAlaSerVal	680
Db	2036	CTGTTCAAGCTGCTCAACTACAGACGGCGGCGCGGCCGCCGCTCTCGAGCGCCCTGTG	2095
QY	681	LeuGlyLeuAspAspIleHisargAlaATPArgThrPheValIleuArgValArgAlaGln	700
Db	2096	CTGGGCGCTGGACCAATATCCACAGGGCGCTGGCGGACCTTCGTGCTCGTGTGGGGCCAG	2155
QY	701	AspProProProGluLeuArgPheValIysValAspValThrGlyAlaArgAspThrIle	720
Db	2156	GACCGCGCGCTTGAGCTGACTGTCTTGTCCAGAGTGAGTGAACGGGGCGGTAGACACCATC	2215
QY	721	ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	740
Db	2216	CCCCAGGACAGGCTCACGAGAGTCATCGCCACGATCATCAAAACCCAGAAACGTAATGTC	2275
QY	741	ValArgArgTyrAlaValIleGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760
Db	2276	GTCGCTCGGTATGGCCGTGTCTCAGAAAGCCGCCATGGGCACTCCGCAAGCCCTTCAAG	2335
QY	761	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu	780
Db	2336	AGCCACGCTCTACTTACCTTGACAGACCTTCACGCGTAATGAGACAGTCTGTGCTCACTG	2395
QY	781	GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerLeuAsnGlu	800
Db	2396	CAGGAGACACACCCGCTGAGGAGAGCGGTGTCAATCAGACAGAGCTCTCTCCGTAATG	2455
QY	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle	820
Db	2456	GCCACAGATGGCTCTTGACAGCTTCTTCTTAAGCTTCAATGACACACGCGCGCCATC	2515
QY	821	ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleuSerThrLeu	840
Db	2516	ACGGGCAAGTCTCTACGTCACTGTCCAGGGATCCCGAGGAGCTTCATCTCTCCAGCTG	2575
QY	841	LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	860
Db	2576	CTCTGACGCTGTGCTTACGCGACATCGAGAAACAAGCTTTGCGGGGATTCGCGCGGAC	2635
QY	861	GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
Db	2636	GGGCTGCTCTGCGTGTGGTGAATTTCTGTGTGTGACACTCACTCCACCCACGCG	2695
QY	881	LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
Db	2696	AAACCTCTCTAGAACCTCTGTCCGAGGTGTCCCTAGATATGGCTCGAGGTGAATCTTG	2755
QY	901	ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrHisPheVal	920
Db	2756	CGGAACACAGTGTGAATCTTCCCTGTAAACACAGAGGCCGTGGGTGGCACGGCTTTGTT	2815
QY	921	GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu	940
Db	2816	CAATCCCGACCGACCGACTTATTCCTCGGTGCGGCTCGTGGCTGTGATACCCGGAACCTG	2875
QY	941	GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
Db	2876	GAGGTCCAGAGCGACTACTCCAGCTATGCCGACCTCATCAAGAGCCAGTCTCACTTC	2935
QY	961	AsnArgGlyPheLysValAlaLysArgAsnMetArgArgLysIleAspPheGlyValLeuArgLeu	980
Db	2936	AACCGCGGCTTCAAGGCTGGAGAAACATGCGTCCGAAATCTTTGGGGTCTTTCGGCTG	2995
QY	981	LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
Db	2996	AAGTGTCAACGCTGTGTTCTTGATTTGACAGGTGAACAGCTCTCAGAACGSGTGTGACCAAC	3055
QY	1001	IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020

Db 3056 ATCTACAGATCTCTGCTGAGGCTACAGATTTTCAGCATGTCGTGACGCTCCCA 3115
Qy 1021 PheHISgInGlnValTrpLysAsnProThrPhePheLeuArgValIleSerThrAla 1040
Db 3116 TTTTCATCAGCAGATTGGAGAACCCACATTTTCTCCGCGGTCACTCTCAACAGCGCC 3175
Qy 1041 SerLeuCyTYSerIleLeuValAlaValAsnAlaGlyMetSerLeuGlyAlaValGly 1060
Db 3176 TCCCTCTGCTACTCATCTCTGAAGCCAGAACCGGAGATGTCCTGGGGGCCAAGGCC 3235
Qy 1061 AlaAlaGlyProLeuProSerGlyAlaValGlnTrpLeuCyHISgInAlaPheLeu 1080
Db 3236 GCGCGCGGCTCTGCTGCTCCAGGCGCTGAGTGGCTGCAACCAAGCATTCCTGCTC 3295
Qy 1081 LysLeuThrArgHISArgValThrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACCGTGTACCTACGTCACCTCTGGGTCACTCAAGACAGCCAG 3355
Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTGGAGAGCTCCCGGGAGACAGCTGACTGCTCTGGAGGCCGACGCAAC 3415
Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGCACTGCTCTCAAGACTTCAAGACCATCTGAGAC 3451

RESULT 15

LOCUS E36793 4015 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36793
VERSION E36793.1 GI:13022756
KEYWORDS JP 1999253177-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M.,
Calvin, B.H., and William, H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 1 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 1999253177-A/1
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643, 18-APR-1997 US 08/444,419, PR
25-APR-1997 US 08/846,017, 06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050, 14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951, 14-AUG-1997 US 08/915,503, PI THOMAS
R SECHI, JOCHIMU RINGER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HAREI, WILLIAM H ANDREWS
PC C12N15/09, A61K31/70, A61K38/55, A61K39/395, A61K39/395, A61K48/00,
PC C12O1/02,
PC C12O1/48, C12O1/68, G01N33/15, G01N33/48, G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/12, C12P21/08, C12N1/19, PC
C12R1/84,
PC (C12N1/21, C12R1 19), (C12N9/12, C12R1 19), (C12N9/12, C12R1 84),
PC (C12N9/12, C12R1 91), C12N15/00, A61K37/64, C12N5/00 CC
Strandedness Single,
CC Topology Linear,
FH Key Location/Qualifiers
FT CDS 56 3454

FEATURES

source

1 4015
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon 32644"

ORIGIN

Alignment Scores:

Pred. No.: 7,866-151
Score: 5961.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
Gaps: 0

US-10-044-692-2 (1-1132) x E36793 (1-4015)

Qy 1 MetProAlaAlaProArgCyArgAlaValArgSerLeuLeuArgSerHisTrpArgIu 20
Db 56 ATGCCGCGGCTCTCCCGCTGCGAGCCGCTGCTCTGCTGCGAGCCATCAACCGCGAG 115
Qy 21 ValLeuProLeuValThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
Db 116 GTGTGCGGCTGCGAGCTGCTGCGGCGCTGCGGCGCCAGAGGCTGCGGCTGCTGCG 175
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCyArgLeuValCyValProTrp 60
Db 176 CCGGGGACCCCGGCGCTTCCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 235
Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCyLeuLysGlyLeu 80
Db 236 GACGACGCGCGCCCGCGCCCGCTCTCTCCGCGAGTGTCTGCTGCAAGAGGCTG 295
Qy 81 ValAlaArgValLeuGlnArgLeuCyGlnArgGlyValAlaValAsnValLeuAlaPheGly 100

Page 28

uuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
ACGATATCCACAGGGCTTGGCGCACCTTCGTGCTGCGTGTGTCGGGCCCCAG 2155
uLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
GTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC 2215
ValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
ATTCGCCAGCATCATCAACCCCGAGAACACGTACTGC 2275
AlaAlaHisGlyHisValArgLysAlaPheLys 760
TCCCATGGGCACGTCCGCAAGGCCTTCAAG 2335
TyrMetArgGlnPheValAlaHisLeu 780
TGGCAGAGTTCGTGGCTCACCTG 2395
LysSerSerSerLeuAsnGlu 800
CTCTCTCTCTGTAATGAG 2455
AlaValArgIle 820
GTGCGCATC 2515
ThrLeu 840
GTG 2575
860

QY 321 CysProProValTyrAlaGluThrIysHisPheLeuTyrSerSerGlyAspIysGluGln 340
DB 1016 TGTCCCCCGGTGTACCCCAAGACCAAGCACTTCTCTACTCTCAGGCGACAGAGAGCAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgLeu 360
DB 1076 CTGGCGCCCTCTCTACTCAGCTCTGAGGCCAGCCTGACTGGCCCTCGAGGCTC 1135
QY 361 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
DB 1136 GTGGAGACCACTTTCTGGGTTCCAGAGCCCTGGATCCAGAGACTCCCGCAGTTGCCC 1195
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGluLeuLeuGlnIysHis 400
DB 1196 CGCTGCCCCAGGCTACTGCAAAATGGGCCCTCTTTCTGGAGCTGTGGGAACCAAC 1255
QY 401 AlaGlnCysProTyrGlyValLeuLeuIysThrHisCysProLeuArgAlaAlaValThr 420
DB 1256 GCGCAGTGCCTACGGGGTGTCTCTCAAGACGCACTGGCCCTGCGAGCTGGGTCAACC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGluIysProGlnGlySerValAlaAlaProGlnGlu 440
DB 1316 CCAAGACCCGCTGTGTGCCCCGAGAAAGCCCCAGAGCTGTGGCGGCCCGAGAG 1375
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1376 GAGGACACAAACCCCGCTCCCTGCTGCACTCTCCGCGACACAGAGCCCTGGCAG 1435
QY 461 ValTyrGlyPheValAlaArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB 1436 GTGTACGGCTTCTGCGCGGCTGCTGCGCGGCTGTGCTGCCAGGCTCTGTGGGCTCC 1495
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrIysIysPheIleSerLeuGlyIysHis 500
DB 1496 AGGCACACAAACCCCGCTCTCTGAGAACACCAAGAACTTCTCTCTGGGAAAGCAT 1555
QY 501 AlaIysLeuSerLeuGlnGluLeuThrTyrIysMetSerValArgAspCysAlaTyrLeu 520
DB 1556 GCCAAGCTCTGCGCAGAGAGCTGACGTGAAGATGACGCGGAGCTCGCTGGCTG 1615
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlnIle 540
DB 1616 CGCAGAGCCCAAGGGTGTGCTGTGTTCCGCGCCCAAGACACCCCTGCTGAGAGATC 1675
QY 541 LeuAlaIysPheLeuHisTyrPheLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
DB 1676 CTGGCCAGTTCCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATG 1735
QY 561 PheTyrValThrGluThrThrPheGlnIysAsnArgLeuPhePheTyrArgIysSerVal 580
DB 1736 TTTTATGTCAAGGACCAAGCTTTCAAAAGAACAGGCTTTTCTACCGGAGAGTGTG 1795
QY 581 TrpSerIysLeuGlnSerIleGlyTyrLeuArgHisIleLeuArgValGlnLeuArgGlu 600
DB 1796 TGGAGCAAGTTGCAAGCATTTGGATTCAGACGACCTTGAAGAGAGTGCAGCTCGGAG 1855
QY 601 LeuSerGluIaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
DB 1856 CTGTGGAGACAGAGGTCAGGACGATCGGAGAGCCAGGCCCGCTCTGCACTTCACA 1915
QY 621 LeuArgPheIleProIysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
DB 1916 CTCGCCCTTCAATCCCAAGCTGACGGGCTGCGCGCATTTGAAACATGACTACGCTG 1975
QY 641 GlyAlaArgThrPheArgArgGlyIysArgValaGlnArgLeuThrSerArgValIysAla 660
DB 1976 GGAAGCAGAACTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCA 2035
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
DB 2036 CTGTTCAGGTCTCACTACAGAGCGGCGCGGCCCTCGGCTCTGTGGGCGCTCTGTG 2095

QY 681 LeuGlyIle 680
DB 2096 CTGGGCGCTGAG 680
QY 701 AspProProProG 680
DB 2156 GACCCGCGCTGAGC 680
QY 721 ProGlnAspArgLeuThrGln 680
DB 2216 CCCCAGGACAGGCTCACGAGGTG 680
QY 741 ValArgArgTyrAlaValIaGlnIys 680
DB 2276 GTGGCTGGTATGCGGTGTCCAGAGAGC 680
QY 761 SerHisValSerThrLeuThrAspLeuGlnPro 680
DB 2336 AGCCACGCTCTACTTACAGACCTCCAGCCGTAC 680
QY 781 GlnGluThrSerProLeuArgAspAlaValValIleGlu 680
DB 2396 CAGAGACCAACCCGCTGAGGATGCGCTCGTCAATCGACAGAC 680
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis 680
DB 2456 GCCACAGTGGCTCTTGTGACGCTCTTCTTACGCTTCAATGTCACACAGC 680
QY 821 ArgGlyIysSerTyrValGlnCysGlnGlyIleProGlnIysSerIleLeuSer 680
DB 2516 AGGGCAAGTCTTACGCTCAGTGCAGAGGATCCGCGAGGCTCCATCTCTCCAGC 680
QY 841 LeuCysSerLeuCysTyrGlyIysPheMetGluAsnIysLeuPheAlaGlyIleArgArgAsp 680
DB 2576 CTCTCAGGCTGTGTCTAGCGGACATGAGAACAAAGCTGTTGGGGATTTGGCGGAGC 26.
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
DB 2636 GGGCTGCTCTCTGCGTTGGTGGATGATTTCTTTGGTGGACACCTCACTCACCCAGCG 2695
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
DB 2696 AAAACCTTCTCAGGACCTTGTCCAGAGTGTCCCTGAGTATGCTGTGTGTGAACCTTG 2755
QY 901 ArgGlyThrValValAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheVal 920
DB 2756 CGAAGACAGTGTGAATCTTCCGTGAAGAGAGAGGCTGGGTGGACCGGCTTTGTG 2815
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
DB 2816 CAGATCCGCGCCACAGGCTTATTTCCCTGTGTGGCTGTGCTGATACCGGACCTTG 2875
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
DB 2876 GAGGTCCAGAGCACTACCTCAGCTATGCGGACCTTCATCAGAGCCAGTCTCACCTTG 2935
QY 961 AsnArgGlyPheLeuValaGlyArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu 980
DB 2936 AACCGGCGCTTCAAGGCTGAGAGAACATGCGTGGCAACTTTTGGGGCTCTTGGGGCTG 2995
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
DB 2996 AAGTGTCAAGCTTGTCTGTGATTTGGAGTGAACAGCTCCOAGACGAGTGGCAACAA 3055
QY 1001 IleTyrIysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
DB 3056 ATCTACAAGATCTCTGCTGACGAGGTACAGGTTTCAAGCATGTGTGTGACGCTCCA 3115
QY 1021 PheHisGlnGlnValIleTyrIysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
DB 3116 TTTCATCAGAACTTTGAGAGAACCCCACTTTTCTGCGGTCAATCTCTGACAGGCGC 3175
QY 1041 SerLeuCysTyrSerIleLeuIysAlaIysAsnAlaGlyMetSerLeuGlyAlaIysGly 1060

```
Db      3176  TCCCTCTGCTACTCCATCCGTAAGCAAGAAAGCAGGATGTCGCTGGGGGCAAGGAC 3235
Qy      1061  ALAAlAGIYProLeuProSerGIuAlaValGlnTrpLeuCySHIGlnAlaPheLeu 1080
Db      3236  GCCGCCGGCCCTCTGCTGCCAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC 3295
Qy      1081  LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db      3296  AAGCTGACTCGACACCGTGTCACTACGTGCCACTCTCTGGGTCACTCAGGACAGCCCA 3355
Qy      1101  ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db      3356  ACGCAGCTGAGTCGGAGAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACAGCCA 3415
Qy      1121  ProAlaLeuProSerAspPheLeuThrIleLeuAsp 1132
Db      3416  CCGGCACTGGCCCTCAGACTTCAAGACCAATCTGGAC 3451
```

Search completed: October 28, 2004, 12:50:01
Job time : 11572 secs

This Page Blank (uspto)

Db 241 ACGCCGCCCCCGCCGCCCCCTCTCCGCGCAGGTGTCTGCTGAGGAGCTGTGCG 300
QY 301 CCGAAGTCTGCAGAAAGCTGTGCGAGAGCGCGCGGAGAAAGTGTCTGCTTCCGCTTCCG 360
Db 301 CCGAAGTCTGCAGAAAGCTGTGCGAGAGCGCGCGGAGAAAGTGTCTGCTTCCGCTTCCG 360
QY 361 GCTGCTGGAAGCGGGGCGCGGGGGCCCCCGGAGGCTTTCACACCAAGCGTGGCAGCTA 420
Db 361 GCTGCTGGAAGCGGGGCGCGGGGGCCCCCGGAGGCTTTCACACCAAGCGTGGCAGCTA 420
QY 421 CCGTCCCAACAGCTGACCGAGCTGCGGGGAGAGCGGGCGTGGGGGCTGTGCTGCG 480
Db 421 CCGTCCCAACAGCTGACCGAGCTGCGGGGAGAGCGGGCGTGGGGGCTGTGCTGCG 480
QY 481 CCGCGTGGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 CCGCGTGGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 GCGTCCAGCTGAGCTTACAGAGTGTGCGGGCGCGCTGTACAGCTCGGCGCTGCGAC 600
Db 541 GCGTCCAGCTGAGCTTACAGAGTGTGCGGGCGCGCTGTACAGCTCGGCGCTGCGAC 600
QY 601 TCAAGCCCGGCCCCCGCCACACGCTAGTGAAGCTCCGAAAGCGTGTGGATGCAACGGGC 660
Db 601 TCAAGCCCGGCCCCCGCCACACGCTAGTGAAGCTCCGAAAGCGTGTGGATGCAACGGGC 660
QY 661 CTGGAACCAATAGGCTGAGGGAGCGGGGCTCCCTGGGCGCTGCGCAGCCCGGGGTGAG 720
Db 661 CTGGAACCAATAGGCTGAGGGAGCGGGGCTCCCTGGGCGCTGCGCAGCCCGGGGTGAG 720
QY 721 GAGGCGCGGGGAGTGCAGCGGAGTGTGCGGTTGCGGAGGCGGCGGCGGCGGCGGCGG 780
Db 721 GAGGCGCGGGGAGTGCAGCGGAGTGTGCGGTTGCGGAGGCGGCGGCGGCGGCGGCGG 780
QY 781 TGCCTCTGAGCGCGGAGCGAGCGCCCGTTGGGCGAGGGTCTGTGGCCCACTCGGGCAGAC 840
Db 781 TGCCTCTGAGCGCGGAGCGAGCGCCCGTTGGGCGAGGGTCTGTGGCCCACTCGGGCAGAC 840
QY 841 GCGTGAACGAGTGAACGCTGT 900
Db 841 GCGTGAACGAGTGAACGCTGT 900
QY 901 CACCTCTTGAAGGAGT 960
Db 901 CACCTCTTGAAGGAGT 960
QY 961 GCAACAGCGGGGCCCCCGCATTCACATGCGGGCCACACGTCCTGGGACACGCGCTGTGCC 1020
Db 961 GCAACAGCGGGGCCCCCGCATTCACATGCGGGCCACACGTCCTGGGACACGCGCTGTGCC 1020
QY 1021 CCGGCTGTAGCGCGAGACCAAGACCTTCTCTACTCTCTGAGGAGCAAGGAGGAGCTGCG 1080
Db 1021 CCGGCTGTAGCGCGAGACCAAGACCTTCTCTACTCTCTGAGGAGCAAGGAGGAGCTGCG 1080
QY 1081 GCGCTCTTCTCTACTGAGCTCTGTAGGCGCCAGCTGTGAGCGCTCTGAGGAGCTGTGGA 1140
Db 1081 GCGCTCTTCTCTACTGAGCTCTGTAGGCGCCAGCTGTGAGCGCTCTGAGGAGCTGTGGA 1140
QY 1141 GACCACTTCTGTGGTTCAGAGGCTGTGATGCGAGGAGCTCCCGAGAGTGTGCGCGCT 1200
Db 1141 GACCACTTCTGTGGTTCAGAGGCTGTGATGCGAGGAGCTCCCGAGAGTGTGCGCGCT 1200
QY 1201 GCGCCAGCGCTACGAGCAATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
Db 1201 GCGCCAGCGCTACGAGCAATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261 GTCGCTTACGAGGAGTGTCTCTCAAGAGCACTGCGCGCTGAGAGCTGCGGCTGACCCGAGC 1320
Db 1261 GTCGCTTACGAGGAGTGTCTCTCAAGAGCACTGCGCGCTGAGAGCTGCGGCTGACCCGAGC 1320
QY 1321 AGCGGCTGTGTGCTGCGCGGAGAGAGCCGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
Db 1321 AGCGGCTGTGTGCTGCGCGGAGAGAGCCGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380

QY 1381 CACAGACCCCGTGTGCTGTGAGCTGTCCGCGACAGACAGGCGCTGTGAGGAGTGA 1440
Db 1381 CACAGACCCCGTGTGCTGTGAGCTGTCCGCGACAGACAGGCGCTGTGAGGAGTGA 1440
QY 1441 CCGCTTGTGCGGGCGCTGCGCGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1500
Db 1441 CCGCTTGTGCGGGCGCTGCGCGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1500
QY 1501 CAACGAAAGCGCTTCTCTAGGAAACCAAGAAATCTCTCTGTGGGAGAGTCCCA 1560
Db 1501 CAACGAAAGCGCTTCTCTAGGAAACCAAGAAATCTCTCTGTGGGAGAGTCCCA 1560
QY 1561 GCTCTGCTGCAAGAGCTGAGGAGTGAAGTGAAGCGGAGCTGCGCTGTGCTGCGCAG 1620
Db 1561 GCTCTGCTGCAAGAGCTGAGGAGTGAAGTGAAGCGGAGCTGCGCTGTGCTGCGCAG 1620
QY 1621 GAGCCAGGGGTTGT 1680
Db 1621 GAGCCAGGGGTTGT 1680
QY 1681 CAACTTCTGCACTGCTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
Db 1681 CAACTTCTGCACTGCTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
QY 1741 TGTCAAGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTGTGAG 1800
Db 1741 TGTCAAGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTGTGAG 1800
QY 1801 CAACTTCAAAAGATTTGATGACAGCACTTGAAGAGGTTGACGCTGCGGAGCTGTG 1860
Db 1801 CAACTTCAAAAGATTTGATGACAGCACTTGAAGAGGTTGACGCTGCGGAGCTGTG 1860
QY 1861 GGAAGAGAGGTTGAGGAGCAATCGGGAAGCGCGCGCGCTGTGAGCTGTGCAAGTCCG 1920
Db 1861 GGAAGAGAGGTTGAGGAGCAATCGGGAAGCGCGCGCGCTGTGAGCTGTGCAAGTCCG 1920
QY 1921 CTTTCATCCCAAGGCTGAGCGGCTGTGCGGCTGTGAGTGTGAACTAAGTGTGGAAGC 1980
Db 1921 CTTTCATCCCAAGGCTGAGCGGCTGTGCGGCTGTGAGTGTGAACTAAGTGTGGAAGC 1980
QY 1981 CAGAACGTTCCGAGAGAAAGAGGCGCGAGCGTCTCACCTGTAGGAGTGAAGCACTGTT 2040
Db 1981 CAGAACGTTCCGAGAGAAAGAGGCGCGAGCGTCTCACCTGTAGGAGTGAAGCACTGTT 2040
QY 2041 CAGCGTGTCAACTAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
Db 2041 CAGCGTGTCAACTAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
QY 2101 CTTGAGAGTATTCACAGGCGCTGTGCGCACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Db 2101 CTTGAGAGTATTCACAGGCGCTGTGCGCACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
QY 2161 GCGGCTGTAGCTGTATTTGTCAAGGTGTGTGAGGCGCGGTATGAGACCACTCCCGCA 2220
Db 2161 GCGGCTGTAGCTGTATTTGTCAAGGTGTGTGAGGCGCGGTATGAGACCACTCCCGCA 2220
QY 2221 GGAAGGCTTCAAGGAGTATGCGCGAGCATCAACCCAGAAACGATCATGCGGTGCG 2280
Db 2221 GGAAGGCTTCAAGGAGTATGCGCGAGCATCAACCCAGAAACGATCATGCGGTGCG 2280
QY 2281 TCGGTATGCGGTGTGCAAGAGCGCGCGAGTGTGCGACGTCGCAAGGCTTCAAGAGCA 2340
Db 2281 TCGGTATGCGGTGTGCAAGAGCGCGCGAGTGTGCGACGTCGCAAGGCTTCAAGAGCA 2340
QY 2341 CGTCTTACCTTGAACAGACTTCAAGCGGTATGAGCAAGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 CGTCTTACCTTGAACAGACTTCAAGCGGTATGAGCAAGTGTGTGTGTGTGTGTGTGTGTGT 2400
QY 2401 GACCAAGCGCGTGAAGGAGT 2460
Db 2401 GACCAAGCGCGTGAAGGAGT 2460

OY	2461	CAGTGGCTCTTCCAGCGCTTCCATACGCTTATATGGCCACACGCGCGGACATCAGGGG	2550
Db	2461	CAGTGGCTCTTCCAGCGCTTCTCTACGCTTCAATGTGCCACACGCGCGGACATCAGGGG	2520
OY	2521	CAAGTCTCACTCCAGTCCAGTCCAGGGGATCCCCCAGGGGCTCAATCCCTTCCAGCGTCTCTG	2580
Db	2521	CAAGTCTCACTCCAGTCCAGTCCAGGGGATCCCCCAGGGGCTCAATCCCTTCTCCAGCGTCTCTG	2580
OY	2581	CAGCCTGTGCTACCGCGCATATGAGAAACAACCTGTTTCGGGGGAAATCGCGCGGACGCGCT	2640
Db	2581	CAGCCTGTGCTACCGCGCATATGAGAAACAACCTGTTTCGGGGGAAATCGCGCGGACGCGCT	2640
OY	2641	GCTCCTGGGCTTGGTGGATGGAATTTCTGTGTGTGACAATCACTCAACCCACGGGAAAC	2700
Db	2641	GCTCCTGGGCTTGGTGGATGGAATTTCTGTGTGTGACAATCACTCAACCCACGGGAAAC	2700
OY	2701	CTTCCCTCAGAACCCCTGATCCAGAGTGTCCCTGAGATATGGCTGCGTGTGAATTCGGAA	2760
Db	2701	CTTCCCTCAGAACCCCTGATCCAGAGTGTCCCTGAGATATGGCTGCGTGTGAATTCGGAA	2760
OY	2761	GACAGTGTGAATCTTCCCTGTAGAAAGCAGAGCCCTGGGTGACAGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGAATCTTCCCTGTAGAAAGCAGAGCCCTGGGTGACAGGCTTTTGTTCAGAT	2820
OY	2821	GCCGCCCCACGGCCCTATTCCTCCGTGTGGGCTGTGTGTGATATCCCGGACCTCGAGGT	2880
Db	2821	GCCGCCCCACGGCCCTATTCCTCCGTGTGGGCTGTGTGTGATATCCCGGACCTCGAGGT	2880
OY	2881	GCAGAGCAGTACTCTCAGCTATATGCCCGGACCTCATCAGAGCCAGTCTCACCTTCAACG	2940
Db	2881	GCAGAGCAGTACTCTCAGCTATATGCCCGGACCTCATCAGAGCCAGTCTCACCTTCAACG	2940
OY	2941	CGGCTTCAAGGCTGGAGAGAAATGCGTTCGCAAACTCTTGGGGGTCTTGGGCTGGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGAGAGAAATGCGTTCGCAAACTCTTGGGGGTCTTGGGCTGGAAGTG	3000
OY	3001	TCACAGCCTGTCTTCTGGAATTTGCAAGTGAACAGCTCCAGACGGTGTGCACCAATCTA	3060
Db	3001	TCACAGCCTGTCTTCTGGAATTTGCAAGTGAACAGCTCCAGACGGTGTGCACCAATCTA	3060
OY	3061	CAAGATTCCTCCGTGCGAGGCGTACAGGTTTCAGGCATGTGTGCTGCAGCTCCCATTTCA	3120
Db	3061	CAAGATTCCTCCGTGCGAGGCGTACAGGTTTCAGGCATGTGTGCTGCAGCTCCCATTTCA	3120
OY	3121	TCAGCAATTTGGAGAAACCCACATTTTCTGCGCGTCAATCTCTGACAGCGCTCCCT	3180
Db	3121	TCAGCAATTTGGAGAAACCCACATTTTCTGCGCGTCAATCTCTGACAGCGCTCCCT	3180
OY	3181	CTGCTACTTCATCTCTGAAGCCAGAAACCGAGGATGTGCTGGGGGCGAAGGGGCGCGC	3240
Db	3181	CTGCTACTTCATCTCTGAAGCCAGAAACCGAGGATGTGCTGGGGGCGAAGGGGCGCGC	3240
OY	3241	CGGGCCCTGTGCCCTCGAGGGCGGTGCAAGTGGTGGACCAAGATTCCTGCTCAACT	3300
Db	3241	CGGGCCCTGTGCCCTCGAGGGCGGTGCAAGTGGTGGTGGACCAAGATTCCTGCTCAACT	3300
OY	3301	GACTCTGACACCGTGTCACTTACGTGCACTCCTGTGGGTCACTCAGGACAGCCACAGCGCA	3360
Db	3301	GACTCTGACACCGTGTCACTTACGTGCACTCCTGTGGGTCACTCAGGACAGCCACAGCGCA	3360
OY	3361	GCTGAGTGGAGAGCTTCCGGGGACAGCCTGACTCCTCGAGGGCGGACAGCCACCCCGC	3420
Db	3361	GCTGAGTGGAGAGCTTCCGGGGACAGCCTGACTCCTCGAGGGCGGACAGCCACCCCGC	3420
OY	3421	ACTGCCCTCAGACTTCAAGAACCATCTGTGATGAGGACACCGCGCCACAGCGAGCGCA	3480
Db	3421	ACTGCCCTCAGACTTCAAGAACCATCTGTGATGAGGACACCGCGCCACAGCGAGCGCA	3480
OY	3481	GAGCAGACACACGACGCGCTGTCAAGCGGGGCTTACGTCCACAGGAGAGGAGGGCGGC	3540
Db	3481	GAGCAGACACACGACGCGCGCTGTCAAGCGGGGCTTACGTCCACAGGAGAGGAGGGCGGC	3540
OY	3541	CACACCCACGCGCGCATCGGCTTGGAGTCTGAGGCTGATGATGTTTGGCCGAGGCTTG	3600

Db	3541	CACACCAGGCCGCCACCGCTGGGAGCTGAGGCGCTGAGTGAAGTGTTCGGCCAGGCGCTG	3600
Qy	3601	CATGTCCGGCTGAAGGCTGAAGTGTCCGGCTGAGGCGCTGAGCGAGTGTTCACGCCAAGGCT	3660
Db	3601	CATGTCCGGCTGAAGGCTGAAGTGTCCGGCTGAGGCGCTGAGCGAGTGTTCAGGCCAAGGCGCT	3660
Qy	3661	GAGTGTCCAGACACACTGCGGCTTTTCACCTTCCCAKAGGCTGGGGGCTCGGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGACACACTGCGGCTTTTCACCTTCCCAKAGGCTGGGGGCTCGGCTCCACCCCA	3720
Qy	3721	GGGCGAGTGTTCCTCCACAGGAGCCGGGCTTCACATCCCACTAGAGAAATGTCACATCC	3780
Db	3721	GGGCGAGTGTTCCTCCACAGGAGCCGGGCTTCACATCCCACTAGAGAAATGTCACATCC	3780
Qy	3781	CCAGATTCGSCATTGTTTCACCCCTCGGCGCTGCTCCTTTGCTCTTCCACCCCAACCAATCC	3840
Db	3781	CCAATTCGSCATTGTTTCACCCCTCGGCGCTGCTCCTTTGCTCTTCCACCCCAACCAATCC	3840
Qy	3841	AGGTGAGAGCCCTGAGAGGACCCCTGAGAGCTCTGGAAATTTGGAGTGAACCAAAAGTGTG	3900
Db	3841	AGGTGAGAGCCCTGAGAGGACCCCTGAGAGCTCTGGAAATTTGGAGTGAACCAAAAGTGTG	3900
Qy	3901	CCCTGTACACAGGCGAGAGACCTCTGACCTGGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
Db	3901	CCCTGTACACAGGCGAGAGACCTCTGACCTGGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
Qy	3961	GAGGTGCTGTGGAGTAAATTAAGTAATATATGAGTTTTCAGTTTGGAAAAAAA	4015
Db	3961	GAGGTGCTGTGGAGTAAATTAAGTAATATATGAGTTTTCAGTTTGGAAAAAAA	4015

[illegible]

Db	241	AGGCGCGCCCCCGCGCCCCCTCTTTCGACAGGTGTCTGTCTGAAGAGCTGTGTGC	300
QY	301	CCGAGTGTCTGAGAGGCTGTGCAGCGCGAGCAAGAACGTGTGTGCCTTCGAGCTTCGC	360
Db	301	CCGAGTGTCTGAGAGGCTGTGCAGCGCGAGCAAGAACGTGTGTGCCTTCGAGCTTCGC	360
QY	361	GCTGTGTGACGGGGGCCCGCGGGGGGCCCGCCGAGAGCTTTCACCAACAGCTGTGCAGCTA	420
Db	361	GCTGTGTGACGGGGGCCCGCGGGGGGCCCGCCGAGAGCTTTCACCAACAGCTGTGCAGCTA	420
QY	421	CCTGCGCCAAACGAGTGAACGACACTTCGCGGGAGCGGGGCGTGTGGGGCTGTCTGTGC	480
Db	421	CCTGCGCCAAACGAGTGAACGACACTTCGCGGGAGCGGGGCGTGTGGGGCTGTCTGTGC	480
QY	481	CCGCGTGGGCGACGACGTGTGTGTCACTGTGTGACAGCTGTGCAGCTCTTTGTGTGTGT	540
Db	481	CCGCGTGGGCGACGACGTGTGTGTCACTGTGTGACAGCTGTGCAGCTCTTTGTGTGTGT	540
QY	541	GGCTCCCAAGCTGCGGCTACAGAGGTGTGGGGCGCGCGGTGACAGCTCGAGCGTGCAC	600
Db	541	GGCTCCCAAGCTGCGGCTACAGAGGTGTGGGGCGCGCGGTGACAGCTCGAGCGTGCAC	600
QY	601	TCAGGCGCGGCCCCCGCCACAAGCTAATGGAACCCGGAAGGCGCTGTGGATGCAACGGGC	660
Db	601	TCAGGCGCGGCCCCCGCCACAAGCTAATGGAACCCGGAAGGCGCTGTGGATGCAACGGGC	660
QY	661	CTGGAACCATATAGCGTCAAGGAGGCGGGGGTCCCTGTGGGCGTGCAGCGCCGGGTGAG	720
Db	661	CTGGAACCATATAGCGTCAAGGAGGCGGGGGTCCCTGTGGGCGTGCAGCGCCGGGTGAG	720
QY	721	GAGGCGCGGGGAGCAGTGTGCAGCGCAAGTCTGCGTGTGCCAAGAGGCCCAAGCGTGTGCGC	780
Db	721	GAGGCGCGGGGAGCAGTGTGCAGCGCAAGTCTGCGTGTGCCAAGAGGCCCAAGCGTGTGCGC	780
QY	781	TGCCCCCTAAGCCCGAGCGGACGCCCCGTGTGGGCAAGGAGTCTGTGGGCCACCGGGCAAGAC	840
Db	781	TGCCCCCTAAGCCCGAGCGGACGCCCCGTGTGGGCAAGGAGTCTGTGGGCCACCGGGCAAGAC	840
QY	841	GCGTGAACGAGTGAACCGTGTGTCTGTGTGTGTGACCTTCAGACCCGCGCAAGAAC	900
Db	841	GCGTGAACGAGTGAACCGTGTGTCTGTGTGTGTGACCTTCAGACCCGCGCAAGAAC	900
QY	901	CACCTCTTTGAGAGGCTGCTCTCTGTGCAACGCGCCACTTCCACCCATCTGTGGCGGCCA	960
Db	901	CACCTCTTTGAGAGGCTGCTCTCTGTGCAACGCGCCACTTCCACCCATCTGTGGCGGCCA	960
QY	961	GCAACAGGCGGGGGCCCCCATCCACATGCGGGGCAACAGTGCCTGTGGGACAAGCCTGTGCC	1020
Db	961	GCAACAGGCGGGGGCCCCCATCCACATGCGGGGCAACAGTGCCTGTGGGACAAGCCTGTGCC	1020
QY	1021	CCCGGTGTAGCGCGAGACCAAGCACTTCTCTAATCTCAGGCGCAAGAGAGCACTGTGC	1080
Db	1021	CCCGGTGTAGCGCGAGACCAAGCACTTCTCTAATCTCAGGCGCAAGAGAGCACTGTGC	1080
QY	1081	GCCCTCTCTTCTAATCACTCACTCTCTGAGGCGCAGACTGACTGAGCGTGTGGAAGCTGTGGA	1140
Db	1081	GCCCTCTCTTCTAATCACTCACTCTCTGAGGCGCAGACTGACTGAGCGTGTGGAAGCTGTGGA	1140
QY	1141	GACCATCTTTCTGGGTTTCAAGGCGCTGTGATGCAAGAGACTCCCGCAAGTTTGC	1200
Db	1141	GACCATCTTTCTGGGTTTCAAGGCGCTGTGATGCAAGAGACTCCCGCAAGTTTGC	1200
QY	1201	GCCCCAGCGCTACTGTGCAAAATGCGGCCCTGTTTCTGGAAGCTGTGTGGAAACACGCGCA	1260
Db	1201	GCCCCAGCGCTACTGTGCAAAATGCGGCCCTGTTTCTGGAAGCTGTGTGGAAACACGCGCA	1260
QY	1261	GTCGCCCTTAAGGAGGTCTCTCAAGAGGCACTGTGCGGCTGTGAGCTGTGGTCAACCAAGC	1320
Db	1261	GTCGCCCTTAAGGAGGTCTCTCAAGAGGCACTGTGCGGCTGTGAGCTGTGGTCAACCAAGC	1320
QY	1321	AGCGCGGTGTGTGTGCGCGGAGAAAGCCCAAGGACTCTGTGTGCGGCGCCCAAGAGAAAGA	1380

Db	1321	AGCCGCTGTCTGTGTCCCGGAGAGAACCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGAGA	1380
Qy	1381	CACAGATCCCGCTGTGCTGTGTGACGTTGTCCTCCGACGACAAGACCCCTGGACGGTGTGA	1440
Db	1381	CACAGATCCCGCTGTGCTGTGTGACGTTGTCCTCCGACAGCAGACGCCCTGGACGGTGTGA	1440
Qy	1441	CGGCTGTGTGGGGGCTGGCTGGCGCGGGCTGTGTGTCCCGACGACCTCTGTGGGGCTCCAGCA	1500
Db	1441	CGGCTTGTGTGGGGCTGTGTGGCGCGGGCTGTGTGTCCCGACGACCTCTGTGGGGCTCCAGCA	1500
Qy	1501	CAACGAACGCCGCTTCTCCAGGAACACCAAGAAATTATCTCCCTGGGGAAAGCATGCGAA	1560
Db	1501	CAACGAACGCCGCTTCTCCAGGAACACCAAGAAATTATCTCCCTGGGGAAAGCATGCGAA	1560
Qy	1561	GCTCTCCGTGAGAGACGTGACGTGTGAAGATGAGGGGTCCGGACCTGGCGCTTGGCGCGCAG	1620
Db	1561	GCTCTCCGTGAGAGACGTGACGTGTGAAGATGAGGGGTCCGGACCTGGCGCTTGGCGCGCAG	1620
Qy	1621	GAGCCCAAGGGGTTGGCTGTGTTCGGGCGCGACAGCACCGTCTCGGTGAGAGAGATCTGGGC	1680
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCGGGCGCGACAGCACCGTCTCGGTGAGAGAGATCTGGGC	1680
Qy	1681	CAAGTTCCTGCATCTGGCTGATGAGTGTGTACGTGTGTGAGCTGCTCAAGTCTTTCTTTTA	1740
Db	1681	CAAGTTCCTGCATCTGGCTGATGAGTGTGTACGTGTGTGAGCTGCTCAAGTCTTTCTTTTA	1740
Qy	1741	TGTCAACGAGACCAAGTTTCAAAAGAAACAGGCTCTTTTTCACACGGAAAGATGTCTGAG	1800
Db	1741	TGTCAACGAGACCAAGTTTCAAAAGAAACAGGCTCTTTTTCACACGGAAAGATGTCTGAG	1800
Qy	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCATTTGAAGAGGGTGACGTGCGGAGCTGTCTC	1860
Db	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCATTTGAAGAGGGTGACGTGCGGAGCTGTCTC	1860
Qy	1861	GGAAGCAGAGGTCACGACGATCGGGAAAGCCAGGCGCGGCTGTGTACGTGTCAACATCCG	1920
Db	1861	GGAAGCAGAGGTCACGACGATCGGGAAAGCCAGGCGCGGCTGTGTACGTGTCAACATCCG	1920
Qy	1921	CTTCATCCCAAGGCTGACGGGCTGTGGCGCGCATTTGTGAACATGGAACCTACGTGTGGAGC	1980
Db	1921	CTTCATCCCAAGGCTGACGGGCTGTGGCGCGCATTTGTGAACATGGAACCTACGTGTGGAGC	1980
Qy	1981	CAGAACCTTCCGACAGAAAGAGAGGCGCGACGCTCACTCCAGGGGTGAAGGACATGTT	2040
Db	1981	CAGAACCTTCCGACAGAAAGAGAGGCGCGACGCTCACTCCAGGGGTGAAGGACATGTT	2040
Qy	2041	CAGCGTGTCAACTACAGACGGGCGCGGCGCCCGGCGCTCTGGGCGCCTCTGTGTGCTGGG	2100
Db	2041	CAGCGTGTCAACTACAGACGGGCGCGGCGCCCGGCGCTCTGTGGCGCCTCTGTGTGCTGGG	2100
Qy	2101	CTTGACGATATCCACAGGCGCTTGCGCACCTTGTGTGTGTGTGGGGCCAGGACCC	2160
Db	2101	CCTGGACGATATCCACAGGCGCTTGCGCACCTTGTGTGTGTGTGGGGCCAGGACCC	2160
Qy	2161	GCCGCTGAGCTGTATCTTTGTCAAGGTGTGAAGTGAACGGGCGCGTACGACACATCTCCCA	2220
Db	2161	GCCGCTGAGCTGTATCTTTGTCAAGGTGTGAAGTGAACGGGCGCGTACGACACATCTCCCA	2220
Qy	2221	GGACAGGCTCAACGAGGTCATCGCCAGCATCAAAACCCCAAGAACAGTATCTGCTGGC	2280
Db	2221	GGACAGGCTCAACGAGGTCATCGCCAGCATCAAAACCCCAAGAACAGTATCTGCTGGC	2280
Qy	2281	TGCGTATCCGCTGGTCCAGAAAGGCGCCCATGGGCAAGTCCGCAAGGCTTCAAGAACCA	2340
Db	2281	TGCGTATCCGCTGGTCCAGAAAGGCGCCCATGGGCAAGTCCGCAAGGCTTCAAGAACCA	2340
Qy	2341	CGTCTTACCTTGAACAGACCTTCAGCCGTATCTGCAAGTTCGTGGCTCACTGTGACGA	2400
Db	2341	CGTCTTACCTTGAACAGACCTTCAGCCGTATCTGCAAGTTCGTGGCTCACTGTGACGA	2400
Qy	2401	GACCAAGCCGCTGAGGGATGCCGTGTATGACAGAGCTCTTCCCTGAATGAGCCAG	2460
Db	2401	GACCAAGCCGCTGAGGGATGCCGTGTATGACAGAGCTCTTCCCTGAATGAGCCAG	2460

QY	2461	AAGTGGGCTCTTGCACGCTTTCCAAAGCTTCAATGAGCAACGAGCCGGTGGCAATCAAGGG	2520
Db	2461	CAGTGGCTCTTGCACGCTTTCTCAAGCTTATGTGCCAACGCGGTGGCAATCAAGGG	2520
QY	2521	CAATCTCACTCCAGTGGCCAGGGGATCCGCGAGGGCTCCATCTCTTCAAGCTGCTCTG	2580
Db	2521	CAATCTCACTCCAGTGGCCAGGGGATCCGCGAGGGCTCCATCTCTTCAAGCTGCTCTG	2580
QY	2581	CAGCTTGCTGTAAGGCGAATGAGAACAGCTGTTTGGGGGAAATTGGGGGAGCGGCT	2640
Db	2581	CAGCTTGCTGTAAGGCGAATGAGAACAGCTGTTTGGGGGAAATTGGGGGAGCGGCT	2640
QY	2641	GCTCTCGCGTTTGGGTGATGATTTCTTTGTTGATGACACTTCACTCAACCCAGGGAAAC	2700
Db	2641	GCTCTCGGTGTTGGTGAATGATTTCTTTGTTGATGACACTTCAACCCAGGGAAAC	2700
QY	2701	CTTCTCTCAGAACCCCTGGTCCGAGGTGTCTCCGATATAGCTGCTGGTGAACCTTGCGAAA	2760
Db	2701	CTTCTCTCAGAACCCCTGGTCCGAGGTGTCTCCGATATAGCTGCTGGTGAACCTTGCGAAA	2760
QY	2761	GACAGTGTGAACCTTCCCTGTGAAGAGAGAGCCCTGGGTGGCAAGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGTAACTTCCCTGTGAAGAGAGAGCCCTGGGTGGCAAGCTTTTGTTCAGAT	2820
QY	2821	GCGGGCCACCGGCTTATTCCTCTGTGTGGCTGTGTGATATCCGGACCTCTGGAGGT	2880
Db	2821	GCCTGGGCCACCGGCTTATTCCTCTGTGTGGCTGTGTGATATCCGGACCTCTGGAGGT	2880
QY	2881	GCAGAGGCACTACCTCCAGCTATGCGCGGACCTCCATCAAGACAGTCTCACTTCAACCG	2940
Db	2881	GCAAGAGGCACTACCTCCAGCTATGCGCGGACCTCCATCAAGACAGTCTCACTTCAACCG	2940
QY	2941	CGGCTTCAAGGCTGGAGGAACATGCGTCCGAAACTCTTTTGGGGTCTTTCGGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGAGGAACATGCGTCCGAAACTCTTTTGGGGTCTTTCGGGCTGAAGTG	3000
QY	3001	TCACAGCTGTTTTCGATTTTGCAGTGTGACAGCTCTCCAGCGGTGTGCACCAATCTA	3060
Db	3001	TCACAGCTGTTTTCGATTTTGCAGTGTGACAGCTCTCCAGCGGTGTGCACCAATCTA	3060
QY	3061	CAAGATCTCTCTGCTGAGGGGTACAGGTTTCAAGCAATGTGCTGACGCTCCCATTTCA	3120
Db	3061	CAAGATCTCTCTGCTGAGGGGTACAGGTTTCAAGCAATGTGCTGACGCTCCCATTTCA	3120
QY	3121	TCAGCAAGTTTGGAAAGAACCCCAATTTTCTCTGGCGTCAATCTCTGACAGGCTCCCT	3180
Db	3121	TCAGCAAGTTTGGAAAGAACCCCAATTTTCTCTGGCGTCAATCTCTGACAGGCTCCCT	3180
QY	3181	CTGTCTACTCAATCTCTGAAGGCCAAGAACGAGGAGATGTGCTGGGGGGCCAAAGGGCGCGC	3240
Db	3181	CTGTCTACTCAATCTCTGAAGGCCAAGAACGAGGAGATGTGCTGGGGGGCCAAAGGGCGCGC	3240
QY	3241	CGGCCCTTCTGCCCTCCGAGGCGCTGCAAGTGTGCTGACCAAGATTTCTGTCTCAAGCT	3300
Db	3241	CGGCCCTTCTGCCCTCCGAGGCGCTGCAAGTGTGCTGACCAAGATTTCTGTCTCAAGCT	3300
QY	3301	GACTGTGAACCGGTGTCACTTACGTGACACTCTCTGGGGGTCACTCAAGAACGCGAAGCGCA	3360
Db	3301	GACTGTGAACCGGTGTGTCACTTACGTGACACTCTCTGGGGGTCACTCAAGAACGCGAAGCGCA	3360
QY	3361	GCTGAGTGTGAAGGCTCCCGGGGAGGAGCTAATGCTCTTGAAGGCGGACCAACCGGCG	3420
Db	3361	GCTGAGTGTGAAGGCTCCCGGGGAGGAGCTAATGCTCTTGAAGGCGGACCAACCGGCG	3420
QY	3421	ACTGCTCTCAAGCTTCAAGAACCATCTGATGTGACACCCGCGCCACACCGAGGCGGA	3480
Db	3421	ACTGCTCTCAAGCTTCAAGAACCATCTGATGTGACACCCGCGCCACACCGAGGCGGA	3480
QY	3481	GAGCAGACACAGAGGCGCTGTACAGCGGGGCTCAAGCTCCAGGGAAGAGGGGGCGCG	3540
Db	3481	GAGCAGACACAGAGGCGCTGTACAGCGGGGCTCAAGCTCCAGGGAAGAGGGGGCGCG	3540

OY		3541	CACACCAGGCGCCGACCCGCTGGGAAGTCAAGGCTCAAGTGAGGTGTTGGCCAGGCCTG	3600
Dd		3541	CACACCAGGCGCCGACCCGCTGGGAAGTCTAAGGCTCAAGTGAGGTGTTGGCCAGGCCTG	3600
OY		3601	CATGTCCGGCTGAAGAAGCTGAGTGTCCGGCTGAAGGCTTAAGCGAAGTGTTCAGCCAAAGGACT	3660
Dd		3601	CATGTCCGGCTGAAGAAGCTGAGTGTCCGGCTGAAGGCTTAAGCGAAGTGTTCAGCCAAAGGACT	3660
OY		3661	GAGTGTCCAGACACCTGCGCGCTTTCACCTTCCCACAAGGCTGGGGCTCCGCTCCACCCCA	3720
Dd		3661	GAGTGTCCAGACACCTGCGCGCTTTCACCTTCCCACAAGGCTGGGGCTCCGCTCCACCCCA	3720
OY		3721	GGGCGACACTTTTCTCACAACGAGGCCGGGCTTCACATCCCCACATAAGAAATAGTCAATCC	3780
Dd		3721	GGGCGACACTTTTCTCACAACGAGGCCGGGCTTCACATCCCCACATAAGAAATAGTCAATCC	3780
OY		3781	CCAGATTGCCCATTTGTTCAACCCCTCGCCCTCGCCCTCTTGTGCTTTCACACCCCAACATCC	3840
Dd		3781	CCAGATTGCCCATTTGTTCAACCCCTCGCCCTCGCCCTCTTGTGCTTTCACACCCCAACATCC	3840
OY		3841	AGGTGAGGAGCCCTGAGAAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTAGCCAAAGGTGTG	3900
Dd		3841	AGGTGAGGAGCCCTGAGAAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTAGCCAAAGGTGTG	3900
OY		3901	CCCTGTACACAGCGGAGAACCTCTGACCTGTGATGGGGTCCCTGTGGCTCAAATTTGGGGG	3960
Dd		3901	CCCTGTACACAGCGGAGAACCTCTGACCTGTGATGGGGTCCCTGTGGCTCAAATTTGGGGG	3960
OY		3961	GAGGTGCTGTGGAGTAGTAATACTAGTAATATATAGATTTTTCAAGTTTTGAATAAAAA	4015
Dd		3961	GAGGTGCTGTGGAGTAGTAATACTAGTAATATATAGATTTTTCAAGTTTTGAATAAAAA	4015

LOCUS	BD218834	4015 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Method and composition for inducing immune response to telomerase antigen.				
ACCESSION	BD218834				
VERSION	BD218834.1	GI:33028604			
KEYWORDS	JP 2002509716-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Gaeta,F.C.A.				
TITLE	Method and composition for inducing immune response to telomerase antigen				
JOURNAL	Patent: JP 2002509716-A 1 02-APR-2002;				
COMMENT	UNIVERSITY TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2002509716-A/1 PD 02-APR-2002 PF 30-MAR-1999 JP 2000541280 PR 31-MAR-1998 US 60/112006 PI FEDERICO C A GAETA PC C12N5/06,A61K35/14,A61K38/43,A61K39/00,A61P35/00,A61P37/00, PC C12N5/10, PC C12N15/09,C12N5/00,A61K37/48,C12N5/00,C12N15/00 CC human telomerase reverse transcriptase (hTERT) FH Key Location/Qualifiers (56). . (3454). FT CDS Location/Qualifiers 1..4015 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
FEATURES					
SOURCE					
ORIGIN	Query Match 100.0%; Score 4015; DB 6; Length 4015; Best Local Similarity 100.0%; Pred. NO. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0.				

DB 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGACGGGCGGTGACACCATCCCGCA 2220
QY 2221 GGAAGGCTCAGAGAGGTATGCGCAGCATCATCAAAACCCAGAACAGTACTGCTGG 2280
DB 2221 GGAAGGCTCAGAGAGGTATGCGCAGCATCATCAAAACCCAGAACAGTACTGCTGG 2280
QY 2281 TCGGATGCGGATGTCAGAAAGGCGCGATGGGCGAGTCCGCAAGGCGCTTCAAGGCA 2340
DB 2281 TCGGATGCGGATGTCAGAAAGGCGCGATGGGCGAGTCCGCAAGGCGCTTCAAGGCA 2340
QY 2341 CGTCTCACTTGAACAGACCTCCAGCGCTGATGACAGAGTTGTTGCTCACTGAGGA 2400
DB 2341 CGTCTCACTTGAACAGACCTCCAGCGCTGATGACAGAGTTGTTGCTCACTGAGGA 2400
QY 2401 GACCAAGCCGCTGAGAGGATGCGCTGATTCAGACAGAGCTCTCTGATGAGGCGAG 2460
DB 2401 GACCAAGCCGCTGAGAGGATGCGCTGATTCAGACAGAGCTCTCTGATGAGGCGAG 2460
QY 2461 GAGTGGCCCTTGAAGCTTCTGAGCTGATGTCAGACAGCGCGCTGAGGAGGAGG 2520
DB 2461 GAGTGGCCCTTGAAGCTTCTGAGCTGATGTCAGACAGCGCGCTGAGGAGGAGG 2520
QY 2521 CAAGTCTTACGTCAGAGCTGAGGAGTCCGAGAGGCTCCATCTCTCCAGCTGCTG 2580
DB 2521 CAAGTCTTACGTCAGAGCTGAGGAGTCCGAGAGGCTCCATCTCTCCAGCTGCTG 2580
QY 2581 GAGCTGCTGCTAAGGAGCATGAGAAAGAGCTGTTGCGGAGATTCGCGGAGCGGCT 2640
DB 2581 GAGCTGCTGCTAAGGAGCATGAGAAAGAGCTGTTGCGGAGATTCGCGGAGCGGCT 2640
QY 2641 GGTCTGCTGCTTGGAGATGATTTCTGTTGGTGAACCTCACTCAACGAGCGGAAAC 2700
DB 2641 GGTCTGCTGCTTGGAGATGATTTCTGTTGGTGAACCTCACTCAACGAGCGGAAAC 2700
QY 2701 CTTCCTCAGAGACCTGAGTCCGAGTGTCCCTGAGTATGCTGCTGATGAGTGGGAA 2760
DB 2701 CTTCCTCAGAGACCTGAGTGTCCCTGAGTATGCTGCTGATGAGTGGGAA 2760
QY 2761 GACAGTGTGAACCTTCCCTGTGAGAGACAGAGCTGCTGAGTGTGAGTGTGAGAT 2820
DB 2761 GACAGTGTGAACCTTCCCTGTGAGAGACAGAGCTGCTGAGTGTGAGTGTGAGAT 2820
QY 2821 GCGGCGGCAAGGCTATTCCTGCTGAGGCGGCTGCTGAGTATGCTGAGTGTGAGAT 2880
DB 2821 GCGGCGGCAAGGCTATTCCTGCTGAGGCGGCTGCTGAGTATGCTGAGTGTGAGAT 2880
QY 2881 GCGAGGCGACTACTCAGCTATGCGGAGCTCTCAGAGCTGAGTGTGAGTGTGAGAT 2940
DB 2881 GCGAGGCGACTACTCAGCTATGCGGAGCTCTCAGAGCTGAGTGTGAGTGTGAGAT 2940
QY 2941 GCGCTTCAAGGCTGAGAGAAACATGCTGCGAAACTCTTTGGGCTTTCGCGCTGAAGTG 3000
DB 2941 GCGCTTCAAGGCTGAGAGAAACATGCTGCGAAACTCTTTGGGCTTTCGCGCTGAAGTG 3000
QY 3001 TCAACAGCTGTTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3060
DB 3001 TCAACAGCTGTTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3060
QY 3061 CAAGATCTCTGCTGAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3120
DB 3061 CAAGATCTCTGCTGAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3120
QY 3121 TCAAGCAAGTTTGAAGAAACCCCATTTTCTGCGCGCTCATCTGAGACGCGCTCCCT 3180
DB 3121 TCAAGCAAGTTTGAAGAAACCCCATTTTCTGCGCGCTCATCTGAGACGCGCTCCCT 3180
QY 3181 CTGCTACTCATCTGAGAAAGCAAGAACGAGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3240
DB 3181 CTGCTACTCATCTGAGAAAGCAAGAACGAGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3240
QY 3241 GCGGCTCTGCGCTGAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3300
DB 3241 GCGGCTCTGCGCTGAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3300

DB 3241 GCGGCTCTGCGCTGAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3300
QY 3301 GACTGAGACCGCTGACCTTACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3360
DB 3301 GACTGAGACCGCTGACCTTACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3360
QY 3361 GCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3420
DB 3361 GCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3420
QY 3421 ACTGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3480
DB 3421 ACTGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3480
QY 3481 GAGCAGACACGAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3540
DB 3481 GAGCAGACACGAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3540
QY 3541 CACACCCAGAGGCGGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3600
DB 3541 CACACCCAGAGGCGGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3600
QY 3601 CATGCTCGGCTGAGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3660
DB 3601 CATGCTCGGCTGAGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3660
QY 3661 GAGTGTGAGACACCTGCTGCTTCACTTCCCAAGGCTGTGAGTGTGAGTGTGAGT 3720
DB 3661 GAGTGTGAGACACCTGCTGCTTCACTTCCCAAGGCTGTGAGTGTGAGTGTGAGT 3720
QY 3721 GGGCCAGCTTCTTCTCAGCAGAGGCGGCTTCCACTCCCAATGAGTGTGAGT 3780
DB 3721 GGGCCAGCTTCTTCTCAGCAGAGGCGGCTTCCACTCCCAATGAGTGTGAGT 3780
QY 3781 CCAGATTCGCAATGTTTCAACCCCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCT 3840
DB 3781 CCAGATTCGCAATGTTTCAACCCCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCT 3840
QY 3841 AGGTGAGACCTTGAAGAGACCTTGGAGCTGTGAGTGTGAGTGTGAGTGTGAGT 3900
DB 3841 AGGTGAGACCTTGAAGAGACCTTGGAGCTGTGAGTGTGAGTGTGAGTGTGAGT 3900
QY 3901 CCTGTGACAGAGGAGGAGCTTGCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3960
DB 3901 CCTGTGACAGAGGAGGAGCTTGCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3960
QY 3961 GAGTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 4015
DB 3961 GAGTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 4015

RESULT 4
E36793 4015 bp DNA linear PART 18-JUN-2001
LOCUS Human telomerase catalytic subunit promoter.
DEFINITION
ACCESSION E36793
VERSION E36793.1 GI:13022756
KEYWORDS JP 199253177-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4015)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 199253177-A 1 21-SEP-1999;
JERON CORP. UNIVERSITY TECHNOLOGY CORP
COMMENT OS unidentified
PN JP 199253177-A/1
PD 21-SEP-1999
PF 15-OCT-1998 JP 199320169
PR 01-OCT-1996 US 08/724,643,18-A
25-APR-1997 US 08/846 017,06-MAY-01

ORIGIN

FEATURES	Location/Qualifiers
source	1. .4015

```
/organism="unidentified"  
/mol_type="genomic DNA"  
/db_xref="taxon:32644"
```

Query Match	100.0%;	Score 4015;	DB 6;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4015; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

[illegible][illegible]

8-1997 US 08/844,419, PR 997 US 08/851,843, PR

Revised
1/1/19

Db	1741	TGTCACGGAGACACAGTTTCAAAAAGAA	CAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1801
QY	1801	CAAGTTGAAAGCATTTGGATATCAGACAGACATTTGAAGGGGTGCAGCTTCGGGAGCTGTCTC		1860
Db	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACAGACATTTGAAGGGGTGACAGCTTCGGGAGCTGTCTC		1860
QY	1861	GGAAGCAGAGGTCAGGCGAGCATTCGGGAAAGCCAGAGCCGGCCCTGGCTGACGTCCAGACTCCG		1920
Db	1861	GGAAGCAGAGGTCAGGCGAGCATTCGGGAAAGCCAGAGCCGGCCCTGGCTGACGTCCAGACTCCG		1920
QY	1921	CTTCATCCCCCAAGCCTGACGGGCTTCGGCCGATTTGTGAAACAATGACATCTACGTCTGTGGAGAC		1980
Db	1921	CTTCATCCCCCAAGCCTGACGGGCTTCGGCCGATTTGTGAAACAATGACATCTACGTCTGTGGAGAC		1980
QY	1981	CAGAAACGTTCCGCAAGAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGGTGAAGGCACTGTT		2040
Db	1981	CAGAAACGTTCCGCAAGAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGGTGAAGGCACTGTT		2040
QY	2041	CAGCGTGTCAACTACAGAGCGGGGGCCGGCCGGCCCTCTGGGGCCGCTGTGGCTGGG		2100
Db	2041	CAGCGTGTCAACTACAGAGCGGGGGCCGGCCGGCCCTCTGGGGCCGCTGTGGCTGGG		2100
QY	2101	CCTGAGCGATATCCACAGAGAGCCTGGCGACCTTCGTGTGCGTGTGCGAGGCCAGAGACC		2160
Db	2101	CCTGAGCGATATCCACAGAGAGCCTGGCGACCTTCGTGTGCGTGTGCGAGGCCAGAGACC		2160
QY	2161	GCCGCGCTGAGCTGTATCTTGTTCAAAGTGTGAATGACGGGCGCGTACGACACATCTCCCA		2220
Db	2161	GCCGCGCTGAGCTGTATCTTGTTCAAAGTGTGAATGACGGGCGCGTACGACACATCTCCCA		2220
QY	2221	GGAAGAGGTCACGGAGGTCATCCGACAGATATCAAAACCCAGAAACAAGTACTGCGTGGC		2280
Db	2221	GGAAGAGGTCACGGAGGTCATCCGACAGATATCAAAACCCAGAAACAAGTACTGCGTGGC		2280
QY	2281	TCGGTATGCGCTGTGTCAGAGAGCCGCCCATATGGGCACTTCGCGAAGGCCCTTCAAGAGCCA		2340
Db	2281	TCGGTATGCGCTGTGTCAGAGAGCCGCCCATATGGGCACTTCGCGAAGGCCCTTCAAGAGCCA		2340
QY	2341	CGTCTCTACCTTGAACAAGCTCTCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA		2400
Db	2341	CGTCTCTACCTTGAACAAGCTCTCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA		2400
QY	2401	GACCAAGCCCGTTGAGAGGATGCCGTCGTATGAGACAGACTTCCTCTGAATGAAGCCAG		2460
Db	2401	GACCAAGCCCGTTGAGAGGATGCCGTCGTATGAGACAGACTTCCTCTGAATGAAGCCAG		2460
QY	2461	CAGTGGCCCTTTCGACAGCTTCCTACGCTTCATGTGGCCACACAGCCGTCGACATCAAGGGG		2520
Db	2461	CAGTGGCCCTTTCGACAGCTTCCTACGCTTCATGTGGCCACACAGCCGTCGACATCAAGGGG		2520
QY	2521	CAAGTCTCACTGTCAGTCCAGTCCAGGGGATCCCGACAGGCTCCATCTCTTCAACGCTGTCTG		2580
Db	2521	CAAGTCTCACTGTCAGTCCAGTCCAGGGGATCCCGACAGGCTCCATCTCTTCAACGCTGTCTG		2580
QY	2581	CAGGCTGTGCTAAGGCGGACATGAGAAACAAGCTGTTTCGGGGATTCGGCGAGACGGGCT		2640
Db	2581	CAGGCTGTGCTAAGGCGGACATGAGAAACAAGCTGTTTCGGGGATTCGGCGAGACGGGCT		2640
QY	2641	GCTCTGCGGTTTGGTGGATGATTTCTTGTTGGTACACCTCACTCAACCCACGGGAAAC		2700
Db	2641	GCTCTGCGGTTTGGTGGATGATTTCTTGTTGGTACACCTCACTCAACCCACGGGAAAC		2700
QY	2701	CTTCCTCAGAGACCTGTGTCAGAGTGTCTCCGATATATGCTGCGTGTGAACTTGCAGAA		2760
Db	2701	CTTCCTCAGAGACCTGTGTCAGAGTGTCTCCGATATATGCTGCGTGTGAACTTGCAGAA		2760
QY	2761	GACAGTGTGAACTTCCCTGTGAAGAAAGACAGAGCCCTGGGTGGCACGGCTTTTGTTCAGAT		2820
Db	2761	GACAGTGTGAACTTCCCTGTGAAGAAAGACAGAGCCCTGGGTGGCACGGCTTTTGTTCAGAT		2820
QY	2821	GCGGCGCCACGGGCGTATTTCCCTGTGTGGGCGTGTGTGTGATATCCCGAGACCTCGAGAGT		2880
Db	2821	GCGGCGCCACGGGCGTATTTCCCTGTGTGGGCGTGTGTGTGATATCCCGAGACCTCGAGAGT		2880

QY	2881	CCAGAGGACCTACCTCCAGCTATGCGCGGACCTCATAGAGCCAGTCTCACTTCAACG	2940
Db	2881	GCAAGGACCTACTTCAGCTATGCGCGGACCTCATAGAGCCAGTCTCACTTCAACG	2940
QY	2941	CGGCTTCAAGGCTGGAGGAACATGCGTGGCAACTTTTGGGCTCTTGGCGGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGAGGAACATGCGTGGCAACTTTTGGGCTCTTGGCGGCTGAAGTG	3000
QY	3001	TCACAGCTGTGTTTGATTTTGGACGTGAACAGGCTTCCAGCGGTGCAACATCTA	3060
Db	3001	TCACAGCTGTGTTTGATTTTGGACGTGAACAGGCTTCCAGCGGTGCAACATCTA	3060
QY	3061	CAAGATCTCTCGTGGAGGCGTACAGTTTACAGCANGTGTGTGAGTCCCATTTTCA	3120
Db	3061	CAAGATCTCTCGTGGAGGCGTACAGTTTACAGCANGTGTGTGAGTCCCATTTTCA	3120
QY	3121	TCAGCAAGTTTGAAGAACCACCATTTTCTGCGGGTCACTCTGTACAAGGCTCCCT	3180
Db	3121	TCAGCAAGTTTGAAGAACCACCATTTTCTGCGGGTCACTCTGTACAAGGCTCCCT	3180
QY	3181	CTGCTACTCCATCTGAAAGCCAAAGAACGAGGATGTGCTGGGGGCCAAAGGCGCGC	3240
Db	3181	CTGCTACTCCATCTGAAAGCCAAAGAACGAGGATGTGCTGGGGGCCAAAGGCGCGC	3240
QY	3241	CGGCGCTTGTGCTCCGAGGCGGTGCACTGAGTGTGCAACAGCATTTCTGTCTCAAGCT	3300
Db	3241	CGGCGCTTGTGCTCCGAGGCGGTGCACTGAGTGTGCAACAGCATTTCTGTCTCAAGCT	3300
QY	3301	GACTCGAACACCGGTGTCACTACGTGGCACTCTGGGGTCACTGAGGACAGGCCAGCGCA	3360
Db	3301	GACTCGAACACCGGTGTCACTACGTGGCACTCTGGGGTCACTGAGGACAGGCCAGCGCA	3360
QY	3361	GCTGAGTCGGAAGCTCCCGGGAGAGAGCGCTGACTGCCCTGAGAGGCGAGCCAACTCCG	3420
Db	3361	GCTGAGTCGGAAGCTCCCGGGAGAGAGCGCTGACTGCCCTGAGAGGCGAGCCAACTCCG	3420
QY	3421	ACTGCGCTCAGACTTCAAGACCATCTGGACTGATGCGCACCGCCACAGCCAGGCCGA	3480
Db	3421	ACTGCGCTCAGACTTCAAGACCATCTGGACTGATGCGCACCGCCACAGCCAGGCCGA	3480
QY	3481	GAGAGAGACACAGAGGCCCTGTCAAGCGCGGGCTTAACTCCAGGGAGGAGGGGCGGCC	3540
Db	3481	GAGAGAGACACAGAGGCCCTGTGTACGCGCGGGCTTAACTCCAGGGAGGAGGGGCGGCC	3540
QY	3541	CACACCCAGGCGCCGACCGCTGGGAGCTGAAGGCTGAAGTGAAGTGTGGCCAGGCGTG	3600
Db	3541	CACACCCAGGCGCCGACCGCTGGGAGCTGAAGGCTGAAGTGAAGTGTGGCCAGGCGTG	3600
QY	3601	CATGTCCGGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGCGAGTGTCAAGCCAAAGGCT	3660
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGCGAGTGTCAAGCCAAAGGCT	3660
QY	3661	GAGTGTCCAGACACTGCGCTTCTCACTTCCCAAGGCTGAGGCGCTGCGCTTCAAC	3720
Db	3661	GAGTGTCCAGACACTGCGCTTCTCACTTCCCAAGGCTGAGGCGCTGCGCTTCAAC	3720
QY	3721	GGGCGAGCTTTTCTTCCACAGAGGCCGGGCTTCCACTCCCACATAGAAAT	3780
Db	3721	GGGCGAGCTTTTCTTCCACAGAGGCCGGGCTTCCACTCCCACATAGAAAT	3780
QY	3781	CCAGATTCCGCAATTGTACACCCCTCGGCTGCGCTCTTTTGC	3840
Db	3781	CCAGATTCCGCAATTGTACACCCCTCGGCTGCGCTCTTTTGC	3840
QY	3841	AGGTGAGAACCTTGAAGAAGACCTTGGGAGCTC	3900
Db	3841	AGGTGAGAACCTTGAAGAAGACCTTGGGAGCTC	3900
QY	3901	CCCTGTACACAGGAGAGACCTG	3960
Db	3901	CCCTGTACACAGGAGAGACCTG	3960

us-10-044-692-1.rge

RESULT 5			
AR182221			
LOCUS	AR182221	4015 bp	DNA
DEFINITION	Sequence 1 from patent US 6337200.		linear PAT 20-APR-2002

ORGANISM

REFERENCE 1 (bases 1 to 4015)

TITLE	HUMAN TELOMERASE CATALYTIC SUBUNIT VARIANTS
DOI	10.1006/jmb.1998.2270
ISSN	0022-270X
PAGE COUNT	10
PRICE	\$10.00
ABSTRACTS AVAILABLE	YES
KEYWORDS	TELOMERASE; HUMAN; CATALYTIC SUBUNIT; VARIANTS
INDEXED	YES
CITED REFERENCES	10
REFERENCES AVAILABLE	YES
REVIEWED	NO
EDITED	NO
COVERED BY	ELSEVIER
COPIES AVAILABLE	10
COPIES ORDERED	0
COPIES SHIPPED	0
COPIES RETURNED	0
COPIES DESTROYED	0
COPIES IN STOCK	10
COPIES ON ORDER	0
COPIES IN TRANSIT	0
COPIES IN PROCESS	0
COPIES IN PROOF	0
COPIES IN REVISION	0
COPIES IN REVIEW	0
COPIES IN ACCEPTANCE	0
COPIES IN PUBLICATION	0
COPIES IN PRESS	0
COPIES IN PRINTING	0
COPIES IN BINDING	0
COPIES IN DISTRIBUTION	0
COPIES IN ARCHIVE	0
COPIES IN LIBRARY	0
COPIES IN COLLECTION	0
COPIES IN DEPOSIT	0
COPIES IN RESERVE	0
COPIES IN SPECIAL COLLECTION	0
COPIES IN SPECIAL ORDER	0
COPIES IN SPECIAL REQUEST	0
COPIES IN SPECIAL DELIVERY	0
COPIES IN SPECIAL HANDLING	0
COPIES IN SPECIAL PACKAGING	0
COPIES IN SPECIAL LABELING	0
COPIES IN SPECIAL MARKING	0
COPIES IN SPECIAL STAMPING	0
COPIES IN SPECIAL SIGNATURE	0
COPIES IN SPECIAL SEALING	0
COPIES IN SPECIAL WRAPPING	0
COPIES IN SPECIAL BOXING	0
COPIES IN SPECIAL TYPING	0
COPIES IN SPECIAL CORRECTING	0
COPIES IN SPECIAL INDEXING	0
COPIES IN SPECIAL CROSS-REFERENCING	0
COPIES IN SPECIAL CITATION	0
COPIES IN SPECIAL SUMMARY	0
COPIES IN SPECIAL ABSTRACT	0
COPIES IN SPECIAL KEYWORD	0
COPIES IN SPECIAL SUBJECT	0
COPIES IN SPECIAL TOPIC	0
COPIES IN SPECIAL FIELD	0
COPIES IN SPECIAL DISCIPLINE	0
COPIES IN SPECIAL BRANCH	0
COPIES IN SPECIAL SECTION	0
COPIES IN SPECIAL PART	0
COPIES IN SPECIAL VOLUME	0
COPIES IN SPECIAL ISSUE	0
COPIES IN SPECIAL SUPPLEMENT	0
COPIES IN SPECIAL ADDENDUM	0
COPIES IN SPECIAL CORRIGENDUM	0
COPIES IN SPECIAL NOTICE	0
COPIES IN SPECIAL ANNOUNCEMENT	0
COPIES IN SPECIAL STATEMENT	0
COPIES IN SPECIAL DECLARATION	0
COPIES IN SPECIAL CERTIFICATE	0
COPIES IN SPECIAL LETTER	0
COPIES IN SPECIAL MEMO	0
COPIES IN SPECIAL REPORT	0
COPIES IN SPECIAL DOCUMENT	0
COPIES IN SPECIAL RECORD	0
COPIES IN SPECIAL JOURNAL	0
COPIES IN SPECIAL MAGAZINE	0
COPIES IN SPECIAL NEWSPAPER	0
COPIES IN SPECIAL BOOK	0
COPIES IN SPECIAL PERIODICAL	0
COPIES IN SPECIAL SERIAL	0
COPIES IN SPECIAL MONOGRAPH	0
COPIES IN SPECIAL THESIS	0
COPIES IN SPECIAL DISSERTATION	0
COPIES IN SPECIAL CONFERENCE	0
COPIES IN SPECIAL SYMPOSIUM	0
COPIES IN SPECIAL SEMINAR	0
COPIES IN SPECIAL MEETING	0
COPIES IN SPECIAL CONGRESS	0
COPIES IN SPECIAL EXHIBITION	0
COPIES IN SPECIAL FAIR	0
COPIES IN SPECIAL FESTIVAL	0
COPIES IN SPECIAL CELEBRATION	0
COPIES IN SPECIAL OCCASION	0
COPIES IN SPECIAL EVENT	0
COPIES IN SPECIAL ACTIVITY	0
COPIES IN SPECIAL PROJECT	0
COPIES IN SPECIAL PROGRAM	0
COPIES IN SPECIAL COURSE	0
COPIES IN SPECIAL CLASS	0
COPIES IN SPECIAL LESSON	0
COPIES IN SPECIAL SESSION	0
COPIES IN SPECIAL WORKSHOP	0
COPIES IN SPECIAL SUMMIT	0
COPIES IN SPECIAL FORUM	0
COPIES IN SPECIAL DEBATE	0
COPIES IN SPECIAL DISCUSSION	0
COPIES IN SPECIAL PRESENTATION	0
COPIES IN SPECIAL DEMONSTRATION	0
COPIES IN SPECIAL PERFORMANCE	0
COPIES IN SPECIAL SHOW	0
COPIES IN SPECIAL EXHIBITION	0
COPIES IN SPECIAL DISPLAY	0
COPIES IN SPECIAL INSTALLATION	0
COPIES IN SPECIAL SETTING	0
COPIES IN SPECIAL ENVIRONMENT	0
COPIES IN SPECIAL SITUATION	0
COPIES IN SPECIAL SCENARIO	0
COPIES IN SPECIAL PLOT	0
COPIES IN SPECIAL STORY	0
COPIES IN SPECIAL NARRATIVE	0
COPIES IN SPECIAL DESCRIPTION	0
COPIES IN SPECIAL ANALYSIS	0
COPIES IN SPECIAL EVALUATION	0
COPIES IN SPECIAL ASSESSMENT	0
COPIES IN SPECIAL SURVEY	0
COPIES IN SPECIAL STUDY	0
COPIES IN SPECIAL RESEARCH	0
COPIES IN SPECIAL INVESTIGATION	0
COPIES IN SPECIAL EXPLORATION	0
COPIES IN SPECIAL DISCOVERY	0
COPIES IN SPECIAL FINDING	0
COPIES IN SPECIAL RESULT	0
COPIES IN SPECIAL CONCLUSION	0
COPIES IN SPECIAL SUMMARY	0
COPIES IN SPECIAL ABSTRACT	0
COPIES IN SPECIAL KEYWORD	0
COPIES IN SPECIAL SUBJECT	0
COPIES IN SPECIAL TOPIC	0
COPIES IN SPECIAL FIELD	0
COPIES IN SPECIAL DISCIPLINE	0
COPIES IN SPECIAL BRANCH	0
COPIES IN SPECIAL SECTION	0
COPIES IN SPECIAL PART	0
COPIES IN SPECIAL VOLUME	0
COPIES IN SPECIAL ISSUE	0
COPIES IN SPECIAL SUPPLEMENT	0
COPIES IN SPECIAL ADDENDUM	0

Location/Qualifiers

```
/mol_type="unassigned DNA"
```

ORIGIN

Query Match	100.0%	Score 4015;	DB 6;	Length 4015;
Best Local Similarity	100.0%	Pred. 0;		
Matches 4015;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

✓

ATC

Dd		1021	GCCGCTTCCTTACTAGCTCTCTC		..UGCTCGAAGCTCTGTGA	1140
Oy		1081	GCCCTTCCTTACTAGCTCTCTC		..UGCTCGAAGCTCTGTGA	1140
Dd		1081	GCCCTTCCTTACTAGCTCTCTG		..AGGCTTACGGCGCTGGAGAGCTCTGTGA	1140
Oy		1141	GACCATTTCTTGSGSTTCAGAGGCCCTGGATGCCAGGGAC		CCCCCGAGAGTTGCCCGGCCT	1200
Dd		1141	GACCATTTCTTGSGSTTCAGAGGCCCTGGATGCCAGGGAC		CTCCCGCAGATTGCCCGGCCT	1200
Oy		1201	GCCCCACGCTACTGCGAAATGCGGCCCTGTTTCTTGAGCTGCTTGGAACAACAGCGCA			1260
Dd		1201	GCCCCACGCTACTGCGAAATGCGGCCCTGTTTCTTGAGCTGCTTGGAACAACAGCGCA			1260
Oy		1261	GTGCTCCCTTAGGGGATGCTCTCTCAAGACGCACATGCGCGCTGCGAGCTTCCGTACCTCCAGC			1320
Dd		1261	GTGCTCCCTTAGCGGGATGCTCTCTCAAGAGCGCACATGCGCGCTGCGAGCTTCCGTACCTCCAGC			1320
Oy		1321	AGCGGATGCTGTATGCCGGGGAGAAGCCCACAGGGCTCTGTGGCGGCCCCCGAGAGAGAGA			1380
Dd		1321	AGCGGATGCTGTATGCCGGGGAGAAGCCCACAGGGCTCTGTGGCGGCCCCCGAGAGAGAGA			1380
Oy		1381	CACAGACCCTCGTGCCTGTGTGACGCTGTTCCGACAGCAACAGACCCCTTGAGCAGTGTAT			1440
Dd		1381	CACAGACCCTCGTGCCTGTGTGACGCTGTTCCGACAGCAACAGACCCCTTGAGCAGTGTAT			1440
Oy		1441	CGGCTTGTGTGGGGGCTTCGCGCCCGGCTGTATGCCCCAGGGCCCTTGAGGGCTCCAAGCA			1500
Dd		1441	CGGCTTGTGTGGGGGCTTCGCGCCCGGCTGTATGCCCCAGGGCCCTTGAGGGCTCCAAGCA			1500
Oy		1501	CAAAGAAAGCGCGTCTCTCAAGAAACACAAGAAATTCATCTCCCTGGGGAGATGACCA			1560
Dd		1501	CAAAGAAAGCGCGTCTCTCAAGAAACACAAGAAATTCATCTCCCTGGGGAGATGACCA			1560
Oy		1561	GCTTCTCGCTGAGAGCTGACGTGGAAGATGAGCTGTGGGATCTGCGTTTGGCTGCGAG			1620
Dd		1561	GCTTCTCGCTGAGAGCTGACGTGGAAGATGAGCTGTGGGATCTGCGTTTGGCTGCGAG			1620
Oy		1621	GAGCCCAAGGGTGTGGCTGTGTTCCGGGCGCAGAACACCGTCTGTGTAGAGGATCTGGGC			1680
Dd		1621	GAGCCCAAGGGTGTGGCTGTGTTCCGGGCGCAGAACACCGTCTGTGTAGAGGATCTGGGC			1680
Oy		1681	CAAGTCTCTGACATGAGCTGATGATGTGTATGNTGTGAGAGTGTCTCAAGTCTTTTCTTTTA			1740
Dd		1681	CAAGTCTCTGACATGAGCTGATGATGTGTATGNTGTGAGAGTGTCTCAAGTCTTTTCTTTTA			1740
Oy		1741	TGTACGAGAGCAACGTTTCAAAAAGAACAGGCTCTTTTTTCTACCGAAGATGTCTGAG			1800

```
1741 TGTACGAGGACACAGGCTTTTCAAAAAGACAGGCTTTTCTACCCGGAAGAGTGTGAG 1800
QY 1801 CAAGTTGCAAGCATTTGGATCAGACAGCATTTGAAGAGGTTGACCTGCGGAGCTGTTC 1860
Db 1801 CAAGTTGCAAGCATTTGGATCAGACAGCATTTGAAGAGGTTGACCTGCGGAGCTGTTC 1860
QY 1861 GGAAGAGAGGTCAAGGACATCGGGAGACCAAGGCGCGCTGCTGACCTGACAGTCCG 1920
Db 1861 GGAAGAGAGGTCAAGGACATCGGGAGACCAAGGCGCGCTGCTGACCTGACAGTCCG 1920
QY 1921 CTTCAATCCCAAGGCTGACGAGGCTGCGGCGCATTTGAAATATGACTACGCTGTGAGAC 1980
Db 1921 CTTCAATCCCAAGGCTGACGAGGCGCGCATTTGAAATATGACTACGCTGTGAGAC 1980
QY 1981 CAGAACTTCCGAGAGAAAGAGGCGCGAGGCTCTACCTTGAGGTTAGAGCACTGTT 2040
Db 1981 CAGAACTTCCGAGAGAAAGAGGCGCGAGGCTCTACCTTGAGGTTAGAGCACTGTT 2040
QY 2041 CAGCGGTCTCACTACGAGCGGGCGGCGCGCGCGCGCTCTGAGGCGCTGCTGTGAG 2100
Db 2041 CAGCGGTCTCACTACGAGCGGGCGGCGCGCGCGCGCTCTGAGGCGCTGCTGTGAG 2100
QY 2101 CTTGAGCATATCAGAGGCGCTGCGGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 CTTGAGCATATCAGAGGCGCTGCGGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
QY 2161 GCGCGCTGAGCTGACTTTTGTCAAGGTGATGATGAGGCGCGCTGAGACATCTCCCA 2220
Db 2161 GCGCGCTGAGCTGACTTTTGTCAAGGTGATGATGAGGCGCGCTGAGACATCTCCCA 2220
QY 2221 GGAAGAGGCTCAGGAGGATGAGGCGCGCATCTCAAAACCCAGAAACAGGACTGCTGAG 2280
Db 2221 GGAAGAGGCTCAGGAGGATGAGGCGCGCATCTCAAAACCCAGAAACAGGACTGCTGAG 2280
QY 2281 TCGGTATGCGGTGCTCAGAAAGGCGCGCATGAGGCGCGCTGCGAGGCTTCAAGAGCA 2340
Db 2281 TCGGTATGCGGTGCTCAGAAAGGCGCGCATGAGGCGCGCTGCGAGGCTTCAAGAGCA 2340
QY 2341 GGTCTTACCTTGAACAGACCTTCAAGCGCTGATGAGCAAGTTGTGTGCTCACTTGAGA 2400
Db 2341 GGTCTTACCTTGAACAGACCTTCAAGCGCTGATGAGCAAGTTGTGTGCTCACTTGAGA 2400
QY 2401 GACAGGCGCGCTGAGGAGTGCCTGCTCAATGAGAGAGGCTCTCTGATGAGGCGAG 2460
Db 2401 GACAGGCGCGCTGAGGAGTGCCTGCTCAATGAGAGAGGCTCTCTGATGAGGCGAG 2460
QY 2461 CAGTGCGCTTCTGAGAGTCTTCTTCAAGCTTCAATGAGAGAGGCTCTCTGAGAGG 2520
Db 2461 CAGTGCGCTTCTGAGAGTCTTCTTCAAGCTTCAATGAGAGAGGCTCTCTGAGAGG 2520
QY 2521 CAAAGTCTTCAAGTCAAGTGCAGAGGAGTCCGAGGCGCTCATCTCTCCACGCTGCTG 2580
Db 2521 CAAAGTCTTCAAGTCAAGTGCAGAGGAGTCCGAGGCGCTCATCTCTCCACGCTGCTG 2580
QY 2581 CAGCGCTTCTGAGGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 2640
Db 2581 CAGCGCTTCTGAGGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 2640
QY 2641 GGTCTGCGTTTGTGATGATTTCTTGTGTGATGATGATGATGATGATGATGATGATGATG 2700
Db 2641 GGTCTGCGTTTGTGATGATTTCTTGTGTGATGATGATGATGATGATGATGATGATGATG 2700
QY 2701 CTTCTCAGAGACCTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAG 2760
Db 2701 CTTCTCAGAGACCTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAG 2760
QY 2761 GACAGGTGAGTTCCTGATGAGAGAGAGGCGCGCTGAGGAGAGAGAGAGAGAGAGAGAG 2820
Db 2761 GACAGGTGAGTTCCTGATGAGAGAGAGGCGCGCTGAGGAGAGAGAGAGAGAGAGAGAG 2820
QY 2821 GCGGCGCGAGGCTTATCCCTGCTGAGGCGCTGCTGAGTACCGGAGCCCTGAGGT 2880
Db 2821 GCGGCGCGAGGCTTATCCCTGCTGAGGCGCTGCTGAGTACCGGAGCCCTGAGGT 2880
QY 2881 GCGAGGCGAGTCTACAGTATGCGGAGCCCTGATCAGAGGCGAGTCTACCTTCAACCG 2940
Db 2881 GCGAGGCGAGTCTACAGTATGCGGAGCCCTGATCAGAGGCGAGTCTACCTTCAACCG 2940
QY 2941 CCGCTTCAAGGCTGAGAGAGATGAGTGCAGAACTTTTGGGGTCTTGGCGCTGAGGTG 3000
Db 2941 CCGCTTCAAGGCTGAGAGAGATGAGTGCAGAACTTTTGGGGTCTTGGCGCTGAGGTG 3000
QY 3001 TCAAGCTGCTTCTGAGTTCAGAGTGAACAGCTTCCAGAGGCTGAGTGCAGTCAATCTA 3060
Db 3001 TCAAGCTGCTTCTGAGTTCAGAGTGAACAGCTTCCAGAGGCTGAGTGCAGTCAATCTA 3060
QY 3061 CAAAGTCTTCTGAGTTCAGAGTGAACAGCTTCCAGAGGCTGAGTGCAGTCAATCTA 3120
Db 3061 CAAAGTCTTCTGAGTTCAGAGTGAACAGCTTCCAGAGGCTGAGTGCAGTCAATCTA 3120
QY 3121 TCAAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGT 3180
Db 3121 TCAAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGT 3180
QY 3181 CTTGCTATCTCATCTGAAAGCCAGAGAGGATGCTGAGGAGGCGCGAGGCGCGC 3240
Db 3181 CTTGCTATCTCATCTGAAAGCCAGAGAGGATGCTGAGGAGGCGCGAGGCGCGC 3240
QY 3241 CCGGCGCTGCGCTGCGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCG 3300
Db 3241 CCGGCGCTGCGCTGCGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCG 3300
QY 3301 GACTGAGACAGGCTGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3360
Db 3301 GACTGAGACAGGCTGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3360
QY 3361 GCTGAGTGCAGAGGCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Db 3361 GCTGAGTGCAGAGGCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
QY 3421 ACTGCGCTGAGCTTCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3480
Db 3421 ACTGCGCTGAGCTTCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3480
QY 3481 GAGAGAGACAGAGAGGCTGCTCAGGCGGAGCTTCAAGTCAAGTCAAGTCAAGTCAAGT 3540
Db 3481 GAGAGAGACAGAGAGGCTGCTCAGGCGGAGCTTCAAGTCAAGTCAAGTCAAGTCAAGT 3540
QY 3541 CACACCCAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
Db 3541 CACACCCAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
QY 3601 CATGTCGCGTGAAGGCTGAGTCCGAGTGAAGGCTGAGGAGAGAGAGAGAGAGAGAGAG 3660
Db 3601 CATGTCGCGTGAAGGCTGAGTCCGAGTGAAGGCTGAGGAGAGAGAGAGAGAGAGAGAG 3660
QY 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGGCTGAGGCTGAGGCTGAGGCTGAG 3720
Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGGCTGAGGCTGAGGCTGAGGCTGAG 3720
QY 3721 GGGCGAGCTTTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
Db 3721 GGGCGAGCTTTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
QY 3781 CCAAGATTCGCAATGTTTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 3840
Db 3781 CCAAGATTCGCAATGTTTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 3840
QY 3841 AGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
Db 3841 AGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
QY 3901 CCGTGTACAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
Db 3901 CCGTGTACAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
```


QY	1	GGAGGCGTGGGCTGCTGCTGCGGACGTTGGGAAAGCCCTGGCCCCGGGCAACCCCGGAGATGCC	60
Db	1	GCAGGCGCTGGCTCTGCTGCGCACTTGGGAAGCCCTGGCCCCGGGCAACCCCGGAGATGCC	60
QY	61	GGGCGCTCCCGGCTGTCGAGACCGGACGCTCCCTGCTGCGACCACTACGGGAGGTCT	120
Db	61	GGGCGCTCCCGGCTGCGGACCGTGGCTCCCTGCTGCGGACCACTACGGGAGGTCT	120
QY	121	GGCGGCTGGCAGGTTCTGTGCGGCGGCTGAGGGGCCCGAGGGGCTGGGCGCTGGTGTGAGCGCGG	180
Db	121	GGCGGCTGGCAGGTTCTGTGCGGCGGCTGAGGGGCCCGAGGGGCTGGGCGCTGGTGTGAGCGCGG	180
QY	181	GGACCCGGGCGGCTTTCCGGCGGCTGGTGGCCAGTGCCTGTGTGTCGTGCTGGGACGC	240
Db	181	GGACCCGGGCGGCTTTCCGGCGGCTGGTGGCCAGTGCCTGTGTGTCGTGCTGGGACGC	240
QY	241	AGGGCGGCGCCCGGCGGCGCCCTCCCTTCGCGCAGGTGTCTGCTGAAAGAGCTGGTGGC	300
Db	241	AGGGCGGCGCCCGGCGGCGCCCTCCCTTCGCGCAGGTGTCTGCTGAAAGAGCTGGTGGC	300
QY	301	CCGAGTGTGCAAGAGCTGTGTGCAACGGCGGCGGCAAGAACGTGTGTGACCTTCCGACTTCG	360
Db	301	CCGAGTGTGCAAGAGCTGTGTGCAACGGCGGCGGCAAGAACGTGTGTGACCTTCCGACTTCG	360
QY	361	GGTGTGCGACGGGGGCGCGGGGGGGCCCCCGGAGAGCCCTTACACACAGCGGTGGGACGTA	420
Db	361	GGTGTGCGACGGGGGCGCGGGGGGGCCCCCGGAGAGCCCTTACACACAGCGGTGGGACGTA	420
QY	421	CTTGCCCAACACGTTGACCGACGCACTGCGGGGGAGCGGGGCGGTGGGGGCTGTGCTGTGCG	480
Db	421	CTTGCCCAACACGTTGACCGACGCACTGCGGGGGAGCGGGGCGGTGGGGGCTGTGCTGTGCG	480
QY	481	CGGCGTGGGCGACGACGTGTGCTGTTCACTGTGTGGACACGCTGGCGGCTCTTGTGTGTGGT	540
Db	481	CGGCGTGGGCGACGACGTGTGCTGTTCACTGTGTGGACACGCTGGCGGCTCTTGTGTGTGGT	540
QY	541	GGCTCTCCAGCTGTGCTTACAGAGTGTGTGGGGCCCGCTGTACAGCTGGGCGCTGCAC	600
Db	541	GGCTCTCCAGCTGTGCTTACAGAGTGTGTGGGGCCCGCTGTACAGCTGGGCGCTGCAC	600
QY	601	TGAGGCGCGGCGCCCGGACACAGCTAGTGACCCCGAAGGCGTCTGGAGATGCCAAGGCG	660
Db	601	TGAGGCGCGGCGCCCGGACACAGCTAGTGACCCCGAAGGCGTCTGGAGATGCCAAGGCG	660

[illegible]

1741 TGTCA CGGAGACAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGGTCTGAG 1800
1741 TGTCA CGGAGACAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGGTCTGAG 1800
1801 CAAGTTGCAGAACATTTGGAATCAGACAGCATTTGAAGAGGTGACAGCTCGGAGCTGTG 1860
1801 CAAGTTGCAGAACATTTGGAATCAGACAGCATTTGAAGAGGTGACAGCTCGGAGCTGTG 1860
1861 GGAAGACAGAGGTCTGAGAGCATCTGGAGAGCCAGGCCCCCTGCTGACCTCCAGACTCCG 1920
1861 GGAAGACAGAGGTCTGAGAGCATCTGGAGAGCCAGGCCCCCTGCTGACCTCCAGACTCCG 1920
1921 CTTCAATCCCAAGCCCTGAGAGGCTGCGCGCATTTGGAACATGGAATAGTGTGGAGAGC 1980
1921 CTTCAATCCCAAGCCCTGAGAGGCTGCGCGCATTTGGAACATGGAATAGTGTGGAGAGC 1980
1981 CAGAAAGTTCCGACAGAAAGAGAGGCGAGGCGCTCTCACTCGAGGAGTGAAGCACTGTT 2040
1981 CAGAAAGTTCCGACAGAAAGAGAGGCGAGGCGCTCTCACTCGAGGAGTGAAGCACTGTT 2040
2041 CAGGCTGCTCACTACAGAGCGGAGCGCGGCCCTCTGAGGCGCTCTGCTGTGGG 2100
2041 CAGGCTGCTCACTACAGAGCGGAGCGCGGCCCTCTGAGGCGCTCTGCTGTGGG 2100
2101 CTTGGAAGATTCACAGAGGCGCGCGCATTTGGAACATGGAATAGTGTGGAGAGC 2160
2101 CTTGGAAGATTCACAGAGGCGCGCGCATTTGGAACATGGAATAGTGTGGAGAGC 2160
2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGAGAGGCGGAGTGAACCATCTCCCA 2220
2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGAGAGGCGGAGTGAACCATCTCCCA 2220
2221 GGAAGAGCTCAGAGAGGTATGCGCAGCATCAAAACCCAGAACCTTACGCTGCG 2280
2221 GGAAGAGCTCAGAGAGGTATGCGCAGCATCAAAACCCAGAACCTTACGCTGCG 2280
2281 TGGGATGCGGTGATCAGAAAGGCGCGCATGGGCGCTCCGCAAGGCTTCAAGAGCA 2340
2281 TGGGATGCGGTGATCAGAAAGGCGCGCATGGGCGCTCCGCAAGGCTTCAAGAGCA 2340
2281 TGGGATGCGGTGATCAGAAAGGCGCGCATGGGCGCTCCGCAAGGCTTCAAGAGCA 2340
2341 GGTCTCTACCTTGAACAGACCTCCAGCGCTATGACAGCATTTGCTGCTCACCTGAGGA 2400
2341 GGTCTCTACCTTGAACAGACCTCCAGCGCTATGACAGCATTTGCTGCTCACCTGAGGA 2400
2401 GACCAAGCCGCTGAGAGGATGCGGTGCTATCGAGCAGAGCTCTCTCCGTAATGAGGCCAG 2460
2401 GACCAAGCCGCTGAGAGGATGCGGTGCTATCGAGCAGAGCTCTCTCCGTAATGAGGCCAG 2460
2461 CAGTGGCCCTTTCAGAGCTTCTTCTACGCTTCAATGACCAAGCCGCTGCTCAAGGAG 2520
2461 CAGTGGCCCTTTCAGAGCTTCTTCTACGCTTCAATGACCAAGCCGCTGCTCAAGGAG 2520
2521 CAAAGTCTACGTCAGTGCAGAGGAGATCCCGCAGGAGCTCACTCTTCCACGCTGCTG 2580
2521 CAAAGTCTACGTCAGTGCAGAGGAGATCCCGCAGGAGCTCACTCTTCCACGCTGCTG 2580
2581 CAGGCTGCTACGTCAGTGCAGAGGAGATCCCGCAGGAGCTCACTCTTCCACGCTGCTG 2640
2581 CAGGCTGCTACGTCAGTGCAGAGGAGATCCCGCAGGAGCTCACTCTTCCACGCTGCTG 2640
2641 GGTCCGCGCTTTCAGAGCTTCTTCTTGTGAGACCTCACTCAAGCCAGGAGAAAC 2700
2641 GGTCCGCGCTTTCAGAGCTTCTTCTTGTGAGACCTCACTCAAGCCAGGAGAAAC 2700
2701 CTTCTCAGAGACCTTGTCCAGAGTGTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG 2760
2701 CTTCTCAGAGACCTTGTCCAGAGTGTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG 2760
2761 GACAGTGTGAACTTCTCTGTAGAGACAGAGGCTCTGGGTGAGCAGCTTTTGTTCAGAT 2820
2761 GACAGTGTGAACTTCTCTGTAGAGACAGAGGCTCTGGGTGAGCAGCTTTTGTTCAGAT 2820

2821 GCCGCCACAGGCTATTATCCCTGAGTGGGCTCTGCTGATGATACCCGAGCCTTGAGGT 2880
2821 GCCGCCACAGGCTATTATCCCTGAGTGGGCTCTGCTGATGATACCCGAGCCTTGAGGT 2880
2881 GCAAGAGCTATCTCAGCTATGCTCCGAGCTTCCATCAGAGCTAGTCTCACTTCAACCG 2940
2881 GCAAGAGCTATCTCAGCTATGCTCCGAGCTTCCATCAGAGCTAGTCTCACTTCAACCG 2940
2941 CCGCTTCAAGGCTGGAGAGAAATGCTGCGAACTCTTTGGGGCTTGGCGCTGAAGTG 3000
2941 CCGCTTCAAGGCTGGAGAGAAATGCTGCGAACTCTTTGGGGCTTGGCGCTGAAGTG 3000
3001 TCACAGCTGTTCTGAGATTTGACAGTGAACAGCTTCCAGAGCTGCTGACCAATCTA 3060
3001 TCACAGCTGTTCTGAGATTTGACAGTGAACAGCTTCCAGAGCTGCTGACCAATCTA 3060
3061 CAAAGTCTCTGCTGAGAGGCTGACAGGCTTCAAGCATGCTGCTGAGCTCCCAATTTCA 3120
3061 CAAAGTCTCTGCTGAGAGGCTGACAGGCTTCAAGCATGCTGCTGAGCTCCCAATTTCA 3120
3121 TCAGCAAGTTTGAAGAACCCCACTTTTCTGGGCGCTCATCTGACACAGGCTCCCT 3180
3121 TCAGCAAGTTTGAAGAACCCCACTTTTCTGGGCGCTCATCTGACACAGGCTCCCT 3180
3181 CTGCTACTCATCTGAAAGCAAGAACAGCAGAGATGCTGCTGGGGCCCAAGGCGCCG 3240
3181 CTGCTACTCATCTGAAAGCAAGAACAGCAGAGATGCTGCTGGGGCCCAAGGCGCCG 3240
3241 CCGGCTCTGCTCCGAGGCGGTGACAGTGTGCTGCTGCAAGCATTTCTGCTCAAGCT 3300
3241 CCGGCTCTGCTCCGAGGCGGTGACAGTGTGCTGCTGCTGCAAGCATTTCTGCTCAAGCT 3300
3301 GACTGACACCGGTGACACTAGTGCACCTCTGGGGTCACTCAGAGACAGCCAGAGCA 3360
3301 GACTGACACCGGTGACACTAGTGCACCTCTGGGGTCACTCAGAGACAGCCAGAGCA 3360
3361 GCTGAGTGGAGAGCTCCCGGAGCGACAGCTGACTCCCTGAGAGCGCAGCCAGCCG 3420
3361 GCTGAGTGGAGAGCTCCCGGAGCGACAGCTGACTCCCTGAGAGCGCAGCCAGCCG 3420
3421 ACTGCTCTGAGCTTCAAGACCATCTGATGAGCCACCGGCCACAGCAGGCGCA 3480
3421 ACTGCTCTGAGCTTCAAGACCATCTGATGAGCCACCGGCCACAGCAGGCGCA 3480
3481 GAGCAGACACAGAGCCCTGCTACAGCGCGGCTCTACGCTCCAGAGGAGAGGCGCGC 3540
3481 GAGCAGACACAGAGCCCTGCTACAGCGCGGCTCTACGCTCCAGAGGAGAGGCGCGC 3540
3541 CACACCCAGGCGCGACAGCTGAGAGTCTGAGGCTGAGAGTGTGCTGAGGAGCTG 3600
3541 CACACCCAGGCGCGACAGCTGAGAGTCTGAGGCTGAGAGTGTGCTGAGGAGCTG 3600
3601 CATGTCGAGTGAAGAGCTGAGTGTCCGCTGAGGCTGAGAGTGTGCTGAGGAGCT 3660
3601 CATGTCGAGTGAAGAGCTGAGTGTCCGCTGAGGCTGAGAGTGTGCTGAGGAGCT 3660
3661 GAGTGTCCAGACACCTGCGCTTCTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3720
3661 GAGTGTCCAGACACCTGCGCTTCTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3720
3721 GGGCCAGCTTTCCTCAACAGAGCCCGGCTTCCATCCCAATAGAAATGCTCATCC 3780
3721 GGGCCAGCTTTCCTCAACAGAGCCCGGCTTCCATCCCAATAGAAATGCTCATCC 3780
3781 CCAAGTTCGCAATTTTCAACCCCTGCGCTGCTCTTGTGCTTCAACCCCAACATCC 3840
3781 CCAAGTTCGCAATTTTCAACCCCTGCGCTGCTCTTGTGCTTCAACCCCAACATCC 3840
3841 AGTGGAGACCTTGAAGAGACCTTGGAGCTCTGGAAATTTGAGTGAACCAAGGTGG 3900
3841 AGTGGAGACCTTGAAGAGACCTTGGAGCTCTGGAAATTTGAGTGAACCAAGGTGG 3900
3901 CCTGTACACAGGCGAGACCTTGCACCTGATGAGGAGTCCCTGTGGGTCAATTTGGGG 3960

Db 3901 CCTGTACACAGCGGAGACCTCTGACCTGTGATGGGGGTCCCTGTGGGTCAATTGGGGG 3960
Qy 3961 GAGGTCTGTGGAGTAATAATGATGATATGAGTTTTCAGTTTGAATAAAAA 4015
Db 3961 GAGGTCTGTGGAGTAATAATGATGATATGAGTTTTCAGTTTGAATAAAAA 4015
RESULT 7
AR226390 4015 bp mRNA linear PRT 20-DEC-2002
LOCUS Sequence 1 from patent US 644650.
DEFINITION AR226390
ACCESSION AR226390
VERSION AR226390.1 GI:27264905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Antisense compositions for detecting and inhibiting telomerase
reverse transcriptase
JOURNAL Patent: US 644650-A 1 03-SEP-2002;
FEATURES
source 1.4015
/organism="unknown"
/mol_type="mRNA"
ORIGIN
Query Match 100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAGCGCTGCTCTCTGTCGACGTCGGAAGCCCTGCCCCCGACCCCGCATGCC 60
Db 1 GCAGCGCTGCTCTCTGTCGACGTCGGAAGCCCTGCCCCCGACCCCGCATGCC 60
Qy 61 GCGGCTCCCGCGCGGAGCGCGTCCCTGCTGCGAGCCACTACCGCAGAGTCT 120
Db 61 GCGGCTCCCGCGCGGAGCGCGTCCCTGCTGCGAGCCACTACCGCAGAGTCT 120
Qy 121 GCGGCTGCGACGTTCTGTCGCGCGCTGCGGAGCCCGCAGGCGCTGCGAGCGCG 180
Db 121 GCGGCTGCGACGTTCTGTCGCGCGCTGCGGAGCCCGCAGGCGCTGCGAGCGCG 180
Qy 181 GAGACCGCGCGCTTCCGCGCGCTGTGTGCCAGTGTGCTGTGCTGTGGAGCGC 240
Db 181 GAGACCGCGCGCTTCCGCGCGCTGTGTGCCAGTGTGCTGTGCTGTGGAGCGC 240
Qy 241 ACGGCGCGCGCGCGCGCGCTCTCTGCGCAGAGTGTCTGCTGAAGAGCTGTGGC 300
Db 241 ACGGCGCGCGCGCGCGCGCTCTCTCTGCGCAGAGTGTCTGCTGAAGAGCTGTGGC 300
Qy 301 CCGAGTCTGACAGAGCTGTGTGCGACGCGCGCGAGAACGTGTGCTTCCGCTTCCG 360
Db 301 CCGAGTCTGACAGAGCTGTGTGCGACGCGCGCGAGAACGTGTGCTTCCGCTTCCG 360
Qy 361 GCTGCTGGAAGCGGCT 420
Db 361 GCTGCTGGAAGCGGCT 420
Qy 421 CCGTCCCAACAGGATGACCGACGACCTGCGGAGGAGCGGAGCGGAGCGGAGCGGAG 480
Db 421 CCGTCCCAACAGGATGACCGACGACCTGCGGAGGAGCGGAGCGGAGCGGAGCGGAG 480
Qy 481 CCGGCTGGGCGACGAGCTGTGTTCACTGTGCGACGCTGCGCGCTTGTGTGTGTGT 540
Db 481 CCGGCTGGGCGACGAGCTGTGTTCACTGTGCGACGCTGCGCGCTTGTGTGTGTGT 540
Qy 541 GCGCTCCAGCTGCGCTTACAGAGTGTGTGGGCGCGCGCGCTGTACAGAGCTGGCGCT 600
Db 541 GCGCTCCAGCTGCGCTTACAGAGTGTGTGGGCGCGCGCGCTGTACAGAGCTGGCGCT 600

Qy 601 TCAGGCGCGGCGCGCGCACAGCTAGTGAACCCGAAAGCGCTGTGGATGCAACGGGC 660
Db 601 TCAGGCGCGGCGCGCGCACAGCTAGTGAACCCGAAAGCGCTGTGGATGCAACGGGC 660
Qy 661 CTGGAACCATAGCGTCAGAGGAGCGCGGCTCCCTGTGGGCTTGCACGCGCGGTGCGAG 720
Db 661 CTGGAACCATAGCGTCAGAGGAGCGCGGCTCCCTGTGGGCTTGCACGCGGTGCGAG 720
Qy 721 GAGGCGCGGAGGAGTGTGACCGGAGCTGCGCTGTGCGCAAGAGGCGCAAGGCTGCGC 780
Db 721 GAGGCGCGGAGGAGTGTGACCGGAGCTGCGCTGTGCGCAAGAGGCGCAAGGCTGCGC 780
Qy 781 TGCCCTGAGCGGAGCGGAGCGCGGCTTGTGGGAGGAGTCTTGGGCGCAACCGCGGAGGAG 840
Db 781 TGCCCTGAGCGGAGCGGAGCGCGGCTTGTGGGAGGAGTCTTGGGCGCAACCGCGGAGGAG 840
Qy 841 GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 841 GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Qy 901 CACCTCTTGTGAGGAGTGTGCTGTGAGCGGCGCACTCCACCATCTCGTGGGCGGCA 960
Db 901 CACCTCTTGTGAGGAGTGTGCTGTGAGCGGCGCACTCCACCATCTCGTGGGCGGCA 960
Qy 961 GCACCAAGCGGCGCGCGCGATCCACATGCGCGGCGCACAGCTGCTGGGACAGCGCTTGTCC 1020
Db 961 GCACCAAGCGGCGCGCGCGATCCACATGCGCGGCGCACAGCTGCTGGGACAGCGCTTGTCC 1020
Qy 1021 CCGGCTGTAAGCGCGGAGACCAAGACTTCTCTACTCTCTGAGCGGCAAGAGGAGCTGCG 1080
Db 1021 CCGGCTGTAAGCGCGGAGACCAAGACTTCTCTACTCTCTGAGCGGCAAGAGGAGCTGCG 1080
Qy 1081 GCGCTCTCTCTACTACTAGCTCTGTGAGGCGCGAGCTGTGAGCGCTGTGAGAGCTGTGGA 1140
Db 1081 GCGCTCTCTCTACTACTAGCTCTGTGAGGCGCGAGCTGTGAGCGCTGTGAGAGCTGTGGA 1140
Qy 1141 GACCATCTTGTGGGTTCCAGGCGCTGATGCGAGGACTCCCGGAGTGTGCGCGCTT 1200
Db 1141 GACCATCTTGTGGGTTCCAGGCGCTGATGCGAGGACTCCCGGAGTGTGCGCGCTT 1200
Qy 1201 GCGCCAGCGCTACTGCGAAATGCGGCGCGCTGTTCTGAGGCTCTTGGAGACACGCGCA 1260
Db 1201 GCGCCAGCGCTACTGCGAAATGCGGCGCGCTGTTCTGAGGCTCTTGGAGACACGCGCA 1260
Qy 1261 GTGCCCTTACGGGAGTCTCTCAAGAGCGACTGCCGCTGCGAGGCTGCAACCGCAGC 1320
Db 1261 GTGCCCTTACGGGAGTCTCTCAAGAGCGACTGCCGCTGCGAGGCTGCAACCGCAGC 1320
Qy 1321 AGCGGATGTGTGCGCGGAGAGCCGAGGCTTGTGTGCGGCGCGCGCGCGCGCGCGCT 1380
Db 1321 AGCGGATGTGTGCGCGGAGAGCCGAGGCTTGTGTGCGGCGCGCGCGCGCGCGCT 1380
Qy 1381 CACAGACCGCGCGCTGTGTGAGTGTGCTCCGCAAGACAGAGGCGCTTGGAGAGTGA 1440
Db 1381 CACAGACCGCGCGCTGTGTGAGTGTGCTCCGCAAGACAGAGGCGCTTGGAGAGTGA 1440
Qy 1441 CCGCTCTGTGCGGAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 1500
Db 1441 CCGCTCTGTGCGGAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 1500
Qy 1501 CAAGGAACCGCGCTTCTCAAGAACCAAGAAATTCACTCTCTGCGGAGACATGCGCAA 1560
Db 1501 CAAGGAACCGCGCTTCTCAAGAACCAAGAAATTCACTCTCTGCGGAGACATGCGCAA 1560
Qy 1561 GCTCTGCTGCGAGAGCTGACAGTGAAGTGAAGCGGAGGAGCTGCGCTTGGCTGCGCAG 1620
Db 1561 GCTCTGCTGCGAGAGCTGACAGTGAAGTGAAGCGGAGGAGCTGCGCTTGGCTGCGCAG 1620
Qy 1621 GAGCCAGAGGAGTGTGCTGTGTTCCGCGCGCGAGAGCAAGCTTGTGAGAGAGATCTGCGC 1680
Db 1621 GAGCCAGAGGAGTGTGCTGTGTTCCGCGCGCGAGAGCAAGCTTGTGAGAGAGATCTGCGC 1680

1681 CAAAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGCTGCTCAGAGTCTTTCTTTTA 1740
1681 CAAAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTTTAA 1740
1741 TGTCAAGGAGACACGCTTTCAAAAAGAACAGAGCTTTTCTTCTACCCGGAAGAGTCTGAG 1800
1741 TGTCAAGGAGACACGCTTTCAAAAAGAACAGAGCTTTTCTTCTACCCGGAAGAGTCTGAG 1800
1801 CAAAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTCTACCCGGAAGAGTCTGAG 1860
1801 CAAAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTCTACCCGGAAGAGTCTGAG 1860
1801 CAAAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTCTACCCGGAAGAGTCTGAG 1860
1861 GGAAGAGAGTGTGAGCAGATGCGAGAGCAGAGCCTGCTGAGAGTCTGAGTCTGAG 1920
1861 GGAAGAGAGTGTGAGCAGATGCGAGAGCAGAGCCTGCTGAGAGTCTGAGTCTGAG 1920
1921 CTTCAATCCCAAGCCTGAGAGGCTGCGAGAGTGTGAGATGAGATGAGTCTGAGAGTCTGAG 1980
1921 CTTCAATCCCAAGCCTGAGAGGCTGCGAGAGTGTGAGATGAGATGAGTCTGAGAGTCTGAG 1980
1981 CAAAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTCTACCCGGAAGAGTCTGAG 2040
1981 CAAAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTCTACCCGGAAGAGTCTGAG 2040
2041 CAGAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTCTACCCGGAAGAGTCTGAG 2100
2041 CAGAGTCTGCACTGAGTATGATGTGATACGTGTCAGAGTCTTCTTCTACCCGGAAGAGTCTGAG 2100
2101 CTTGAGACGATATCCAGAGGCTGAGAGTCTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2160
2101 CTTGAGACGATATCCAGAGGCTGAGAGTCTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2160
2161 GCGAGTCTGAGTATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2161 GCGAGTCTGAGTATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2221 GAGACAGGCTCAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2221 GAGACAGGCTCAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2281 TCGGAT 2340
2281 TCGGAT 2340
2341 GCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
2341 GCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
2401 GAGCAGGCTCAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
2401 GAGCAGGCTCAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
2461 CAGTGGCTCTTCTGAGAGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
2461 CAGTGGCTCTTCTGAGAGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
2521 CAAAGTCTGCACTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
2521 CAAAGTCTGCACTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
2581 CAGAGTCTGCACTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
2581 CAGAGTCTGCACTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
2641 GGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
2641 GGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
2701 CTTCTCAGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
2701 CTTCTCAGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
2761 GACAGTGTGAACTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820

2761 GACAGTGTGAACTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820
2821 GCGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
2821 GCGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
2881 GCGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
2881 GCGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
2941 GCGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
2941 GCGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
3001 TCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
3001 TCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
3061 CAAAGTCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
3061 CAAAGTCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
3121 TCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
3121 TCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
3181 CTTGATCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
3181 CTTGATCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
3241 GCGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
3241 GCGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
3301 GACTGACACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
3301 GACTGACACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
3361 GGTGAT 3420
3361 GGTGAT 3420
3421 ACTGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
3421 ACTGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
3481 GAGCAGACACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
3481 GAGCAGACACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
3541 CACACCCAGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3600
3541 CACACCCAGAGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3600
3601 CATGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660
3601 CATGCTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660
3661 GAGTGTGAGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
3661 GAGTGTGAGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
3721 GGGCAGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
3721 GGGCAGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
3781 CAGAGTGTGAGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840
3781 CAGAGTGTGAGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840
3841 AGTGTGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900


```
Db 1621 GAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACCGCTGTCGTAAGAGATCTTGGC 1680
Qy 1681 CAAAGTTCCTGCACTGGCTGATGATGTGATACGTGCTGAGCTCTCAAGTCTTTT 1740
Db 1681 CAAAGTTCCTGCACTGGCTGATGATGTGATACGTGCTGAGCTCTCAAGTCTTTT 1740
Qy 1741 TGTCAAGAGACCACTTTCAAAAGAACAGAGCTCTTTTCTACCGGAGAGTGTGAG 1800
Db 1741 TGTCAAGAGACCACTTTCAAAAGAACAGAGCTCTTTTCTACCGGAGAGTGTGAG 1800
Qy 1801 CAAAGTTCAAAGCATTGGAATGAGACAGCACTTGAAGAGGTGACAGCTGCGGAGCTG 1860
Db 1801 CAAAGTTCAAAGCATTGGAATGAGACAGCACTTGAAGAGGTGACAGCTGCGGAGCTG 1860
Qy 1861 GGAAGCAGAGGTCTGAGCAGCATTCGGGAACCGAGCCCGCTGCTGACGTCCAGATCCG 1920
Db 1861 GGAAGCAGAGGTCTGAGCAGCATTCGGGAACCGAGCCCGCTGCTGACGTCCAGATCCG 1920
Qy 1921 CTTCAATCCCAAGCCTGAGCGGGCTGCGGCGATTTGTGAACATGACCTACGTGCGGAGC 1980
Db 1921 CTTCAATCCCAAGCCTGAGCGGGCTGCGGCGATTTGTGAACATGACCTACGTGCGGAGC 1980
Qy 1981 CAGAAAGTTCCGACAGAAAGAGAGGCGAGCGTCTACCTGAGGGGTGAAGGCACTGTT 2040
Db 1981 CAGAAAGTTCCGACAGAAAGAGAGGCGAGCGTCTACCTGAGGGGTGAAGGCACTGTT 2040
Qy 2041 CAGCGTGTCTCACTAGACAGGGGCGCGGCGCCCGGCTCTGAGGCGCTCTGTGCTGGG 2100
Db 2041 CAGCGTGTCTCACTAGACAGGGGCGCGGCGCCCGGCTCTGAGGCGCTCTGTGCTGGG 2100
Qy 2101 CCGTGAAGATATCAAGAGGCGCTGAGGCACTTGTGCTGCGGTGTCGGGCGCAGAGACC 2160
Db 2101 CCGTGAAGATATCAAGAGGCGCTGAGGCACTTGTGCTGCGGTGTCGGGCGCAGAGACC 2160
Qy 2161 GCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTGAAGACCAATCCCA 2220
Db 2161 GCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTGAAGACCAATCCCA 2220
Qy 2221 GGAACAGGCTCACGGAGAGTCAATGCGCAGCATCAATCAAAACCCAGAAACCTGCTGG 2280
Db 2221 GGAACAGGCTCACGGAGAGTCAATGCGCAGCATCAATCAAAACCCAGAAACCTGCTGG 2280
Qy 2281 TCGGTATGCGGTGTCCAGAAAGCGCCCATGAGGCACTCCGCAAGGCGCTTCAAGAGCA 2340
Db 2281 TCGGTATGCGGTGTCCAGAAAGCGCCCATGAGGCACTCCGCAAGGCGCTTCAAGAGCA 2340
Qy 2341 CGTCTCTACCTTGACAGACCTCCAGCGCTACATGACAGAGTTCGTGGCTCACTGACAGA 2400
Db 2341 CGTCTCTACCTTGACAGACCTCCAGCGCTACATGACAGAGTTCGTGGCTCACTGACAGA 2400
Qy 2401 GACACAGCCCGCTGAGGAGATGCGGTGCTCATGAGCAGAGCTCTCTCCCTGATAGGCCAG 2460
Db 2401 GACACAGCCCGCTGAGGAGATGCGGTGCTCATGAGCAGAGCTCTCTCCCTGATAGGCCAG 2460
Qy 2461 CAGTGGCTCTTTCAGAGTCTCTCTCACTCATGATGACCAAGCGGTGAGATCAAGGGG 2520
Db 2461 CAGTGGCTCTTTCAGAGTCTCTCTCACTCATGATGACCAAGCGGTGAGATCAAGGGG 2520
Qy 2521 CAAAGTCTACGTCAGATGCGAGGAGATCCCGCAGGGCTCCATCTTCCACGCTGCTCTG 2580
Db 2521 CAAAGTCTACGTCAGATGCGAGGAGATCCCGCAGGGCTCCATCTTCCACGCTGCTCTG 2580
Qy 2581 CAGCGTGTCTACGCGGACATGAGAAACAAGCTGTTGCGGGAGATTCCGGGGAGCCGGCT 2640
Db 2581 CAGCGTGTCTACGCGGACATGAGAAACAAGCTGTTGCGGGAGATTCCGGGGAGCCGGCT 2640
Qy 2641 GCTCCGAGGTTGGTGGATGATTTCTGTTGTGAACACCTCACTCAACCGAGGAAAC 2700
Db 2641 GCTCCGAGGTTGGTGGATGATTTCTGTTGTGAACACCTCACTCAACCGAGGAAAC 2700
Qy 2701 CTTCTCAAGAACCTTGCTCGAGGTGCTCCCTGAGTATGCTGCTGCTGAACTTGGGAA 2760
Db 2701 CTTCTCAAGAACCTTGCTCGAGGTGCTCCCTGAGTATGCTGCTGCTGAACTTGGGAA 2760

Db 2701 CTTCTCAAGAACCTTGCTCGAGGTGCTCCCTGAGTATGCTGCTGCTGAACTTGGGAA 2760
Qy 2761 GACAGTGTGAACCTTCCCTGTGAAGACAGAGGCGCTGGGTGGACAGGCTTTTGTTCAGAT 2820
Db 2761 GACAGTGTGAACCTTCCCTGTGAAGACAGAGGCGCTGGGTGGACAGGCTTTTGTTCAGAT 2820
Qy 2821 GCCGGCCCAAGCCTATTCCTGCTGAGGCTGCTGCTGATGATCCCGAACCTTGAAGT 2880
Db 2821 GCCGGCCCAAGCCTATTCCTGCTGAGGCTGCTGCTGATGATCCCGAACCTTGAAGT 2880
Qy 2881 GCAAGACGATCTACCTGAGTATGCTCGGACCTCCATCAGAGCAGTCTCACTTCAACCG 2940
Db 2881 GCAAGACGATCTACCTGAGTATGCTCGGACCTCCATCAGAGCAGTCTCACTTCAACCG 2940
Qy 2941 CGGCTTCAAGGCTGGAGGAAATGCTGCTGCAAACTTTTGGGGTCTTGGCGTGAAGT 3000
Db 2941 CGGCTTCAAGGCTGGAGGAAATGCTGCTGCAAACTTTTGGGGTCTTGGCGTGAAGT 3000
Qy 3001 TCACAGCCTGTTTCTGATTTGACAGGTGAACAGCTCCAGACGATGTGACCAACATCTA 3060
Db 3001 TCACAGCCTGTTTCTGATTTGACAGGTGAACAGCTCCAGACGATGTGACCAACATCTA 3060
Qy 3061 CAAAGTCTCTGCTGACAGGCTGACAGGTTTCAAGATGTGCTGACAGCTCCATTTCA 3120
Db 3061 CAAAGTCTCTGCTGACAGGCTGACAGGTTTCAAGATGTGCTGACAGCTCCATTTCA 3120
Qy 3121 TCAGCAAGTTGGAGAACCCCAATTTTCTGGGCGCTCATCTGACAGCGGCTCCCT 3180
Db 3121 TCAGCAAGTTGGAGAACCCCAATTTTCTGGGCGCTCATCTGACAGCGGCTCCCT 3180
Qy 3181 CTGCTACTCATCTGAAAGCCAGAACGACAGAGATGTGCTGAGGCGCAAGGCGCGC 3240
Db 3181 CTGCTACTCATCTGAAAGCCAGAACGACAGAGATGTGCTGAGGCGCAAGGCGCGC 3240
Qy 3241 CGGCGCTCTGCGCTCCGAGGCGCTGAGTGTGCTGTGCAACAGCACTTCTGTCAAGCT 3300
Db 3241 CGGCGCTCTGCGCTCCGAGGCGCTGAGTGTGCTGTGCAACAGCACTTCTGTCAAGCT 3300
Qy 3301 GACTGACACGATGTACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Db 3301 GACTGACACGATGTACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Qy 3361 GCTGAGTCCGAAGCTCCCGGAGACGACGCTGACTGCGCTGAGAGCGCAGCCAACTGGC 3420
Db 3361 GCTGAGTCCGAAGCTCCCGGAGACGACGCTGACTGCGCTGAGAGCGCAGCCAACTGGC 3420
Qy 3421 ACTGCGCTCAGACTTCAAGACCATCTGATGATGATGATGATGATGATGATGATGATGAT 3480
Db 3421 ACTGCGCTCAGACTTCAAGACCATCTGATGATGATGATGATGATGATGATGATGATGAT 3480
Qy 3481 GAGCAGACACAGAGGCTGCTGACGCGCGGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3481 GAGCAGACACAGAGGCTGCTGACGCGCGGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Qy 3541 CACACCCAGGCGCGCAGCAGCTGAGTCTGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 3600
Db 3541 CACACCCAGGCGCGCAGCAGCTGAGTCTGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 3600
Qy 3601 CATGTCCGCTGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 3660
Db 3601 CATGTCCGCTGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 3660
Qy 3661 GAGTGTCCAGCACCTGCGCTTCACTTCCCAAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 3720
Db 3661 GAGTGTCCAGCACCTGCGCTTCACTTCCCAAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 3720
Qy 3721 GGGCCAGCTTTTCTCAACAGAGCCCGGCTTCC 3780
Db 3721 GGGCCAGCTTTTCTCAACAGAGCCCGGCTTCC 3780
Qy 3781 CCAAGTTCGCAATGTTCAACCTTCGCG 3840
Db 3781 CCAAGTTCGCAATGTTCAACCTTC 3840
```


1621 GAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACCCGTGTCGTGAGAGATCCTGCGC 1680
1621 GAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACCCGTGTCGTGAGAGATCCTGCGC 1680
1681 CAAGTTCCTGCACTGGCTGATGATGTGTGTAAGTCTGAGCTGCTCAGGTTCTTTCTTTA 1740
1681 CAAGTTCCTGCACTGGCTGATGATGTGTGTAAGTCTGAGCTGCTCAGGTTCTTTCTTTA 1740
1741 TGTCAAGGAGACAGAGTTTCAAAAGACGGCTTTTCTTCTACCCGAAAGAGTCTGAGG 1800
1741 TGTCAAGGAGACAGAGTTTCAAAAGACGGCTTTTCTTCTACCCGAAAGAGTCTGAGG 1800
1801 CAAGTTCGAAAGCATTTGGAATGAAACAGCACTTGAAGAGGTGACAGTCTGCGGAGCTGTC 1860
1801 CAAGTTCGAAAGCATTTGGAATGAAACAGCACTTGAAGAGGTGACAGTCTGCGGAGCTGTC 1860
1861 GGAAGCAGAGGTGACAGCATTCGGGAAAGCCAGGCCCGCTGCTGACGTCACAGACTCCG 1920
1861 GGAAGCAGAGGTGACAGCATTCGGGAAAGCCAGGCCCGCTGCTGACGTCACAGACTCCG 1920
1921 CTTTCATCCCAAGCCCTGACGGGCTGCGGCGAATTGTGAACATGACTAGTGTGAGAGC 1980
1921 CTTTCATCCCAAGCCCTGACGGGCTGCGGCGAATTGTGAACATGACTAGTGTGAGAGC 1980
1981 CAGAAGCTTCCGACAGAAAGAGGCGCAGAGCTCTCAGCTGAGAGGTGAAGCACTGTT 2040
1981 CAGAAGCTTCCGACAGAAAGAGGCGCAGAGCTCTCAGCTGAGAGGTGAAGCACTGTT 2040
2041 CAGCGTGTCTCACTAGAGCGGGCGGCGGCGCCCGGCTCTGAGGCGCTCTGTGTGAGG 2100
2041 CAGCGTGTCTCACTAGAGCGGGCGGCGGCGCCCGGCTCTGAGGCGCTCTGTGTGAGG 2100
2101 CTTGACAGATATCCACAGGGGCTGCGGCGAATTGCTGCTGCGGCGGCGGCGGCGGCGG 2160
2101 CTTGACAGATATCCACAGGGGCTGCGGCGAATTGCTGCTGCGGCGGCGGCGGCGGCGG 2160
2161 GCGGCTGAGCTGTACTTGTGTAAGGTGATGTGACGAGGCGGTGACAGACCATCCCA 2220
2161 GCGGCTGAGCTGTACTTGTGTAAGGTGATGTGACGAGGCGGTGACAGACCATCCCA 2220
2161 GCGGCTGAGCTGTACTTGTGTAAGGTGATGTGACGAGGCGGTGACAGACCATCCCA 2220
2221 GGAAGGCTCAGAGAGTCAATGCGACATCAATCAAAACCCAGAACCTGACTGCGTGGC 2280
2221 GGAAGGCTCAGAGAGTCAATGCGACATCAATCAAAACCCAGAACCTGACTGCGTGGC 2280
2281 TCGGTAATGCGGTCGTCGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
2281 TCGGTAATGCGGTCGTCGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
2341 GGTCTCTACTTGAACAGACCTCAAGCGCTGACATGACAGAGTCTCTCTGATGAGGCGCAG 2400
2341 GGTCTCTACTTGAACAGACCTCAAGCGCTGACATGACAGAGTCTCTCTGATGAGGCGCAG 2400
2401 GACCAAGCCGCTGAGGAGATGCGTGTCTCATGAGAGAGCTCTCTCTGATGAGGCGCAG 2460
2401 GACCAAGCCGCTGAGGAGATGCGTGTCTCATGAGAGAGCTCTCTCTGATGAGGCGCAG 2460
2461 GAGTGGCTCTTCTGAGCT 2520
2461 GAGTGGCTCTTCTGAGCT 2520
2521 CAAGTCTCTACTGTCAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
2521 CAAGTCTCTACTGTCAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
2521 CAAGTCTCTACTGTCAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
2581 CAGCTGTGCTACAGGCGCATGGAAGAACAGCTGTGTGCGGAGATTGCGGCGGAGCGGCT 2640
2581 CAGCTGTGCTACAGGCGCATGGAAGAACAGCTGTGTGCGGAGATTGCGGCGGAGCGGCT 2640
2641 GGTCT 2700
2641 GGTCT 2700
2701 CTTCTCTCAGAGACCTGTCGAGAGTGTCTCTGATGAGTGTGAGTGTGAGTGTGAGTGTG 2760

2701 CTTCTCTCAGAGACCTGTCGAGAGTGTCTCTGATGAGTGTGAGTGTGAGTGTGAGTGTG 2760
2761 GACAGTGTGAACTTCT 2820
2761 GACAGTGTGAACTTCT 2820
2821 GCGGCGCCAGGCGCTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
2821 GCGGCGCCAGGCGCTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
2881 GCGGCGCCAGGCGCTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2940
2881 GCGGCGCCAGGCGCTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2940
2941 GCGGCGCCAGGCGCTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000
2941 GCGGCGCCAGGCGCTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000
3001 TCCAGAGCTGTTCTGGAATTTGAGAGTGAACAGCTCCAGAGAGTGTGACCAATCTTA 3060
3001 TCCAGAGCTGTTCTGGAATTTGAGAGTGAACAGCTCCAGAGAGTGTGTGACCAATCTTA 3060
3061 CAAAGTCTCTCTGCTGACAGGCGTACAGGTTTCAAGCATGTGTGTGACAGCTCCATTTC 3120
3061 CAAAGTCTCTCTGCTGACAGGCGTACAGGTTTCAAGCATGTGTGTGACAGCTCCATTTC 3120
3121 TCCAGAGTGTGGAAGAACCCCACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3180
3121 TCCAGAGTGTGGAAGAACCCCACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3180
3181 CTTGTAATCTCATCTGGAAGAACCCCACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 3240
3181 CTTGTAATCTCATCTGGAAGAACCCCACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 3240
3241 CCGGCT 3300
3241 CCGGCT 3300
3301 GACTGAGACCGGTGTCT 3360
3301 GACTGAGACCGGTGTCT 3360
3361 GCTGAGTGTGGAAGTCT 3420
3361 GCTGAGTGTGGAAGTCT 3420
3421 ACTGCTCTCAGACTTCAAGACCATCTGAGCTGATGAGCAGCCGCGCACAGCCAGGCGCA 3480
3421 ACTGCTCTCAGACTTCAAGACCATCTGAGCTGATGAGCAGCCGCGCACAGCCAGGCGCA 3480
3481 GAGCAGACACAGAGACCT 3540
3481 GAGCAGACACAGAGACCT 3540
3481 GAGCAGACACAGAGACCT 3540
3541 CACACCCAGGCGCGGAGCGCTGAGAGTCTGAGAGCTGAGAGTCTGAGAGTCTGAGAGTCT 3600
3541 CACACCCAGGCGCGGAGCGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCT 3600
3601 CATGTCTCGGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCT 3660
3601 CATGTCTCGGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCT 3660
3661 GAGTGTCTCAGACACTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3720
3661 GAGTGTCTCAGACACTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3720
3721 GGGGAGGCTTTCT 3780
3721 GGGGAGGCTTTCT 3780
3781 CCAAGTGTGCAATGTTTCAACCCCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840

QY	3781	CCAGATTGGCATTGTTCA	CCCTCTGCGCCCTGACCTCTTGTGCTTCCACCCCCACCAATCC	3840
Db	3781	CCAGATTGGCATTGTTCA	CCCTCTGCGCCCTGACCTCTTGTGCTTCCACCCCCACCAATCC	3840
QY	3841	AGGTGGAGACCCCTGAGAAAGACCCCTGGAGCTCTGGGAATTGGAGTGAACCAAGAGTGTG	3900	
Db	3841	AGGTGGAGACCCCTGAGAGACCCCTGGAGCTCTGGGAATTGGAGTGAACCAAGAGTGTG	3900	
QY	3901	CCCTGTACACAGGCGAGGACCCCTGACCTGATGGGGGTCCCTGTGGTCAAAATTGGGGG	3960	
Db	3901	CCCTGTACACAGGCGAGGACCCCTGACCTGATGGGGGTCCCTGTGGTCAAAATTGGGGG	3960	
QY	3961	GAGGTGCTGTGGAGTAAATAATCAATGAATATATGATTTTCAGTTTGAATAAAAA	4015	
Db	3961	GAGGTGCTGTGGAGTAAATAATCAATGAATATATGATTTTCAGTTTGAATAAAAA	4015	

RESULT	12
LOCUS	AR393084
DEFINITION	Sequence from patent US 6617110.
ACCESSION	AR393084
VERSION	AR393084.1
KEYWORDS	G1:40118359
SOURCE	Unknown.

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1 (bases 1 to 4015)				
	Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B., and Andrews, W.H.	Cells immortalized with telomerase reverse transcriptase for use in drug screening	Patent: US 6617110-A 1 09-SEP-2003;	Location/Qualifiers

```
source
1. .4015
/organism="unknown"
/mol type="mRNA"
```

ORIGIN	1	2	3
1	1	1	1
2	1	1	1
3	1	1	1
4	1	1	1
5	1	1	1
6	1	1	1
7	1	1	1
8	1	1	1
9	1	1	1
10	1	1	1
11	1	1	1
12	1	1	1
13	1	1	1
14	1	1	1
15	1	1	1
16	1	1	1
17	1	1	1
18	1	1	1
19	1	1	1
20	1	1	1
21	1	1	1
22	1	1	1
23	1	1	1
24	1	1	1
25	1	1	1
26	1	1	1
27	1	1	1
28	1	1	1
29	1	1	1
30	1	1	1
31	1	1	1
32	1	1	1
33	1	1	1
34	1	1	1
35	1	1	1
36	1	1	1
37	1	1	1
38	1	1	1
39	1	1	1
40	1	1	1
41	1	1	1
42	1	1	1
43	1	1	1
44	1	1	1
45	1	1	1
46	1	1	1
47	1	1	1
48	1	1	1
49	1	1	1
50	1	1	1
51	1	1	1
52	1	1	1
53	1	1	1
54	1	1	1
55	1	1	1
56	1	1	1
57	1	1	1
58	1	1	1
59	1	1	1
60	1	1	1
61	1	1	1
62	1	1	1
63	1	1	1
64	1	1	1
65	1	1	1
66	1	1	1
67	1	1	1
68	1	1	1
69	1	1	1
70	1	1	1
71	1	1	1
72	1	1	1
73	1	1	1
74	1	1	1
75	1	1	1
76	1	1	1
77	1	1	1
78	1	1	1
79	1	1	1
80	1	1	1
81	1	1	1
82	1	1	1
83	1	1	1
84	1	1	1
85	1	1	1
86	1	1	1
87	1	1	1
88	1	1	1
89	1	1	1
90	1	1	1
91	1	1	1
92	1	1	1
93	1	1	1
94	1	1	1
95	1	1	1
96	1	1	1
97	1	1	1
98	1	1	1
99	1	1	1
100	1	1	1

Query Match	100.0%	Score 4015;	DB 6;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4015; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	GCAGCGCTGCATCTCTCTGCGCAGCTGTGGGAAGCCCTCTGGCCCCCGGACCAACCCCGGCAATGGCC	60
Db	1	GCAGCGCTGCATCTCTCTGCGCAGCTGTGGGAAGCCCTCTGGCCCCCGGACCAACCCCGGCAATGGCC	60
QY	61	GGCGCGTCCCGGTGGCGGAGCGGTGGAGTCCCTGCTGGCGAGCACTAACCGAGAGTGTCT	120
Db	61	GGCGCGTCCCGGTGGCGGAGCGGTGGAGTCCCTGCTGGCGAGCACTAACCGAGAGTGTCT	120
QY	121	GGCGCTGGCCAGTTCGTGTGAGGCGCTGTGGGCCCCCAGAGCTGGCGGCTGTGTGACAGCGCG	180
Db	121	GGCGCTGGCCAGTTCGTGTGAGGCGCTGTGGGCCCCCAGAGCTGGCGGCTGTGTGACAGCGCG	180
QY	181	GGAACCCGCGCGCTTTCGCGCGCGTGTGTGAGCCAGATGCTGTGTGCGTCCCTGGAGACG	240
Db	181	GGAACCCGCGCGCTTTCGCGCGCGTGTGTGAGCCAGATGCTGTGTGCGTCCCTGGAGACG	240
QY	241	ACGAGCGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGATGCTCTGGCTGAAGGAGCTGTGTGGC	300
Db	241	ACGAGCGCGCCCCCGCGCGCCCCCTTCCTTCGCGCAGATGCTCTGGCTGAAGGAGCTGTGTGGC	300
QY	301	CCGAGTGTCTGCAAGAGCTGTGTGCCAGCGCGCGGAGAAAGTGTGGCTTTCGAGCTTCG	360
Db	301	CCGAGTGTCTGCAAGAGCTGTGTGCCAGCGCGCGGAGAAAGTGTGGCTTTCGAGCTTCG	360
QY	361	GCTGTGTGAAGGGGCCCCGCGGGGAGCCCCCGAGAGCTTACCAACACAGCTGTGCGCACTA	420
Db	361	GCTGTGTGAAGGGGCCCCGCGGGGAGCCCCCGAGAGCTTACCAACACAGCTGTGCGCACTA	420
QY	421	CTGTGCCAACAAGTGTGACCGACGACTGTGGGGGAGCGGAGCTGTGGGGCTGTGCTTGG	480

Db	421	CTGCCAACA	CGGTGACCGA	CGACGCACTGCGGGGAGCGGGGGGCTGCTGCTGCG	480
Oy	481	CCCGGTGGAG	AGACGAGTGTGATTCACCTGTGGGACGCTGCGGCTCTTGTGTGCTGT	540	
Db	481	CCGGGTGGAG	AGACGAGTGTGATTCACCTGTGGGACGCTGCGGCTCTTGTGTGCTGT	540	
Oy	541	GCTTCCAGTGTGGCTTACAGAGTGTGGGGGCGCGCTGTACAGACTGGGCTGGAC	600		
Db	541	GCTTCCAGTGTGGCTTACAGAGTGTGGGGGCGCGCTGTACAGACTGGGCTGGAC	600		
Oy	601	TCAAGCCCGGCCCCCGCACA	CGCTAGTGAACCCCGAAGGCTCTTGGATGCGAACGGGC	660	
Db	601	TCAAGCCCGGCCCCCGCACA	CGCTAGTGAACCCCGAAGGCTCTTGGATGCGAACGGGC	660	
Oy	661	CTGGAACCAATAGCTGACGGAGGGCGGGGATCCCCCTGGGGCTGGACGCCCGGATGGAG	720		
Db	661	CTGGAACCAATAGCTGACGGAGGGCGGGGATCCCCCTGGGGCTGGACGCCCGGATGGAG	720		
Oy	721	GAGGCGGGGGGCGAGTGTCCAGCCGAAGTCTGCGGTTGCCAAGAGGCCAGGCGTGGCGC	780		
Db	721	GAGGCGGGGGGCGAGTGTCCAGCCGAAGTCTGCGGTTGCCAAGAGGCCAGGCGTGGCGC	780		
Oy	781	TGCCCCCTGAGCCGAGCGGACGCCCGTTGGGGCGGGGCTCTGGGCGCCACCCCGGCGAGAC	840		
Db	781	TGCCCCCTGAGCCGAGCGGACGCCCGTTGGGGCGGGGCTCTGGGCGCCACCCCGGCGAGAC	840		
Oy	841	GCGTGGACCGAGTGAACCGTGGATTTCTGTGTGTGTGATCACTGTGCAGACCCGCGGAAGAAC	900		
Db	841	GCGTGGACCGAGTGAACCGTGGATTTCTGTGTGTGTGATCACTGTGCAGACCCGCGGAAGAAC	900		
Oy	901	CACCTCTTTGGAGGGGTGTGCTCTGTGGACGCGGCACTCCACACCCATCCGTGGGCGCGCA	960		
Db	901	CACCTCTTTGGAGGGGTGTGCTCTGTGGACGCGGCACTCCACACCCATCCGTGGGCGCGCA	960		
Oy	961	GCACCAAGCGGGGCCCCCATCAATGCGGACCAACAAGTCCCTGGGACACAGCTTGTCC	1020		
Db	961	GCACCAAGCGGGGCCCCCATCAATGCGGACCAACAAGTCCCTGGGACACAGCTTGTCC	1020		
Oy	1021	CCCGGTGTAGCCCGAGACAAAGCACTTCTCTTACTCTCAAGGCGACAAGAGCAAGCTGGC	1080		
Db	1021	CCCGGTGTAGCCCGAGACAAAGCACTTCTCTTACTCTCAAGGCGACAAGAGCAAGCTGGC	1080		
Oy	1081	GCCCTCTCTTCTTAATCAAGCTCTCTGAAGGCCAGCTGATCTGGGCGCTGGAGAGCTGTGA	1140		
Db	1081	GCCCTCTCTTCTTAATCAAGCTCTCTGAAGGCCAGCTGATCTGGGCGCTGGAGAGCTGTGA	1140		
Oy	1141	GACCAATCTTCTGTGGTTCAGAGCCCTGGATGCCAGGAACTCCCGCAGGTTGCCCGCCT	1200		
Db	1141	GACCAATCTTCTGTGGTTCAGAGCCCTGGATGCCAGGAACTCCCGCAGGTTGCCCGCCT	1200		
Oy	1201	GCCCCAGGGCTAATGGCAATGGCGGCCCTGTTCTGGAAGTGGTTGAGAAACACAGGCA	1260		
Db	1201	GCCCCAGGGCTAATGGCAATGGCGGCCCTGTTCTGGAAGTGGTTGAGAAACACAGGCA	1260		
Oy	1261	GTGCCCCACAGGGGAGTCTCTCAAGACGCACTGCGCGTGGAGCTGTGATCACCACGC	1320		
Db	1261	GTGCCCCACAGGGGAGTCTCTCAAGACGCACTGCGCGTGGAGCTGTGATCACCACGC	1320		
Oy	1321	AGCCGGTGTCTGTGCCCGGAGAGAGCCCCCAAGGCTCTGTGGCGGCGCCCGAGAGAGGA	1380		
Db	1321	AGCCGGTGTCTGTGCCCGGAGAGAGCCCCCAAGGCTCTGTGGCGGCGCCCGAGAGAGGA	1380		
Oy	1381	CACAGACCCCCCGCTGCTGT	1440		
Db	1381	CACAGACCCCCCGCTGCTGT	1440		
Oy	1441	CGGCTTGTGTGGGGGCTGTGCTGCGCGCGCTGTGTGCCCCAGAGCTCTGGGGCTCACAGCA	1500		
Db	1441	CGGCTTGTGTGGGGGCTGTGCTGCGCGCGCTGTGTGCCCCAGAGCTCTGGGGCTCACAGCA	1500		
Oy	1501	CACGAAAGCGGCTTCTCAAGAAACCAAGAAAGTTCACTTCCCTGGGAAAGATGCCAA	1560		
Db	1501	CACGAAAGCGGCTTCTCAAGAAACCAAGAAAGTTCACTTCCCTGGGAAAGATGCCAA	1560		

Db	3721	GGGCCAGCTTTTCTCTCACAGAGACCGGGCTTCCACTGCCACATATGAAATAGCTCATCC	3780
QY	3781	CCAGATTGCGCATTTGTTTCACTCCCTTGCGCGCCCTCCCTTGGCCTTCCACCCCGACCATCC	3840
Db	3781	CCGATTTGCGCATTTGTTTCACTCCCTTGCGCGCCCTCCCTTGGCCTTCCACCCCGACCATCC	3840
QY	3841	AGGTGAGACCCCTGAGAAAGAACCTCTGGAGCTCTGGGAATTTGGAGTGAACCAAAAGGTGTG	3900
Db	3841	AGGTGAGACCCCTGAGAAAGAACCTCTGGAGCTCTGGGAATTTGGAGTGAACCAAAAGGTGTG	3900
QY	3901	CCCTGTACACAGCGAGAGACCTTGACCTTGAGTGGGGTCCCTGTGGTCAAAATTGGGGGG	3960
Db	3901	CCCTGTACACAGCGAGAGACCTTGACCTTGAGTGGGGTCCCTGTGGTCAAAATTGGGGGG	3960
QY	3961	GAGGTGCTGTGGGAGTAAATCTGAATATATGATTTTTCAGTTTGAATTTGAAAAAAA	4015
Db	3961	GAGGTGCTGTGGGAGTAAATCTGAATATATGATTTTTCAGTTTGAATTTGAAAAAAA	4015

RESULT	13
AR404030	
LOCUS	AR404030 4015 bp mRNA linear PAT 18-DEC-2003
DEFINITION	Sequence 1 from patent US 6627619.
ACCESSION	AR404030
VERSION	AR404030.1 GI:40152014

Source	Unknown.
Organism	Unclassified.

REFERENCE AUTHORS TITLE JOURNAL FEATURES Source
1 (bases 1 to 4015) Cech,T.R., Ligniere,J., Nakamura,T., Chapman,K.B., Morin,G.B., Harley,C.B. and Andrews,W.H. Antisense compositions for detecting and inhibiting telomerase reverse transcriptase Patent: US 6627619-A 1 30-SNP-2003; Location/Qualifiers 1..4015

ORIGIN

Query Match	100.0%;	Score 4015;	DB 6;	length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4015; Conservative	0;	Mismatches	0;	Gaps 0

1 GCACGCTGCGTCTCTGTCGCACGTGGGAAGCCCTGGCCCCGGGCACCCCCCGCATGCC 60

[illegible]

Db 61 GCGCGCTCCCGCTGCCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGAGCT 120

Db 121 GCCGCTGGCCACGTTCTGCGCGGCGCTGGGGCCCGAGGCTGGCGGCTGTCAGCGCGG 180

181 GAGCCCGCGCTTCCGCGCGCTGTGCGCCAGAGCTGTGTGCGTGCCTGGGACGC 240
OY

241 ACGGCGGCCCCCGGCGCCCTTCTCCGCCAGGTGTCCTGCTTGAAGAGACTGTGGC 300

301 CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGGAGAACGTGCTGGCCTTCGGCTTGGC 366
241 ACGGCGGCCCCCGCGCGCGCCCTTCCTTCGCGCAGAGTCTCGCTCGAAGAGACCTGGTGGC 300
Db

Db 301 CCGAGTCTGCACAGGCTGTGCGAGCGCGCGCGAAGACATGCTGGCTTGGCTTGGC 360

QY	421	CTGTGCCCACACGGTGTGACCCAGACGACTCTGCGGGGAGCGGGGGCGTGGGGGAGCGTGGCG	480
Db	421	CTGTGCCCACACGGTGTGACCCAGACGACTCTGCGGGGAGCGGGGGCGTGGGGGAGCGTGGCG	480
QY	481	CCGGGTGAGGCGACGACGTGTGTGTTCACCTGTGTGTGACGCGTGTGTGTGTGTGTGTGTGTGTGT	540
Db	481	CCGGGTGAGGCGACGACGTGTGTGTGTTCACCTGTGTGTGACGCGTGTGTGTGTGTGTGTGTGTGT	540
QY	541	GCGTTCACAGCTGTGCGCCCTAACAGAGGTGTGTGGGCGCGCGCTGTGACAGCGTGGCGGTGCAC	600
Db	541	GCGTTCACAGCTGTGCGCCCTAACAGAGGTGTGTGGGCGCGCGCTGTGACAGCGTGGCGGTGCAC	600
QY	601	TCAGGCGCGGCGCCCGGCACACGCGT	660
Db	601	TCAGGCGCGGCGCCCGGCACACGCGT	660
QY	661	CTGGAACCATATGCGTACAGGAGGCGGGGCTCCCTGTGGGCGTGTGCACGCCGGGTGTGCAG	720
Db	661	CTGGAACCATATGCGTACAGGAGGCGGGGCTCCCTGTGGGCGTGTGCACGCCGGGTGTGCAG	720

721 GAGCGCGGGGAGTGGCCAGCCCAAGTCTGCGCGTTCGCCAAGAGGCGCCAGGCGTGGCGC /80
QY
780

781 TGGCCCTGAGCCGAGCGGACGCCCGTTGGGCAAGGAGTCCCTGGGCCCAACCCGGGACAGAC 840

841 GCGTGAACCGAGTACCGTGGTTCTGTGTGTGTCACCTGCCAGACC CGCGAAGAGC 900
Db 781 TGC CCCCTGAGCGCCGAGCGGACGCCCGTTGGGCAAGGGATCTGGACCTCACCCTCCGACAGAC 874

Db 841 GCCTGACCGAGTACCGTCTTCTGTGTGTGTACCTGCCAGACCGCCGAAGAC 900

QY	901	CACCTCTTTGAGAGGATCGGATCTCTCTGCGACGCGCACTCCGATCCGATCGGCGCA	960
Db	901	CACCTCTTTGAGAGGATCGGATCTCTCTGCGACGCGCACTCCGATCCGATCGGCGCA	960

[illegible]

DG 50 TGCACCAACCGGGCCCCCCCCTCCATCAGGCGA

GQ 1021 CCGGTGTACGCCGAGACCAAGACTTCCTCTACTCCTCAGGCGACAAGAGAGACTGCG 108

Db 1021 CCCGGTGTACGCCGAGACCAAGACTTCCTTACTCCTCAGGCGACAAAGAGACGACTGCG 108

1081 GCCTCCTTCTACTCAGCTCTGTGAGGCCACAGCTGACTGCGCTGGAGGCTGTGGA 114

1141 GACCATCTTTCTGGGTCCAGGCCCGATGACAGGACTCCCGAGGTTGCCCGCCT 120
Oy 1142 GACCATCTTTCTGGGTCCAGGCCCGATGACAGGACTCCCGAGGTTGCCCGCCT 120
1143 GACCATCTTTCTGGGTCCAGGCCCGATGACAGGACTCCCGAGGTTGCCCGCCT 120
1144 GACCATCTTTCTGGGTCCAGGCCCGATGACAGGACTCCCGAGGTTGCCCGCCT 120

1201 GCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGCTGCTTGGGAACCA CGCGCA 126

	1261	GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTC TGAGAGTGCATTGAGAACCCACGCGCA	1289
Db			
	1261	CTGACCCCTTAAGAGATGCTCCTCAAGA GCGCATGCGCGCTGCGAGCTGCGGTCA CCCCAGC	1321

Db 1261 GTGCCCTACGGGGTGTCTCTCTCAAGACGACTGCGCCGGCTGCGAGCTGGCGGTCACCCCAGC 132

OY 1321 AGCCGGTGTCTGTGCCCCGGAGAGACCACAGGCATCCTGTCGCCCTCCCAAGAAAGAACAAA
-280

Pb 1321 AGCCGGTGTCTGTGCCCCGGAGAGACCCACAGGCTCTGTGTCCCGGCCCCCGAAGAGAGAAGA 1386

1381 CACAGACCCCGTCGCTGGTGCAGCTGCTCCGCCAGCACAGACCCCTGGCAGGTGTA 144

[illegible]

Db 1441 CGGCTTCGTGCGAGGCTTGCGGCGGGCTGGTCCCGCCAGGCTCTGGGGCTCCAGGCA 15

Db	3661	GAGTGTCCAGCACACTGCGGCTTTCACCTTCCCAACAGGCTGGGAGCTCGGCTCCACCCCA	3720
OY	3721	GGGCGAGCTTTCCTTCACACAGGAGCCCGGCTTCCTACTCCCAATAGGAATAGTCATCC	3780
Db	3721	GGGCGAGCTTTCCTTCACACAGGAGCCCGGCTTCCTACTCCCAACATAGGAATAGTCATCC	3780
OY	3781	CCAAATTCGCACATTTGTTACACCCCTGGCCCTGACCCCTTTCGCTTCACACCCCAACATCC	3840
Db	3781	CCAAATTCGCACATTTGTTACACCCCTGGCCCTGACCCCTTTCGCTTCACACCCCAACATCC	3840
OY	3841	AGGTGAGACCTTAGAAGAGACCTTGGGAGCTCTGGGAATTTGAGATGACCAAAAGGTGTG	3900
Db	3841	AGGTGAGACCTTAGAAGAGACCTTGGGAGCTCTGGGAATTTGAGATGACCAAAAGGTGTG	3900
OY	3901	CCCTGTACACAGGACGAGACCTGTGACTGTGATGGGGGTCCCTGTGGCTCAAAATTTGGGGG	3960
Db	3901	CCCTGTACACAGGACGAGACCTGTGACTGTGATGGGGGTCCCTGTGGCTCAAAATTTGGGGG	3960
OY	3961	GAGGTGCTGTGGGAGTAAATATCTGAATATATGATTTTTCAGTTTGGAAAAAA	4015
Db	3961	GAGGTGCTGTGGGAGTAAATATCTGAATATATGATTTTTCAGTTTGGAAAAAA	4015

RESULT 14						
AR438403	AR438403	4015 bp	DNA	linear	PAT 20-FEB-2004	
LOCUS						
DEFINITION	Sequence 1 from patent US 6664046.					
ACCESSION	AR438403					
VERSION	AR438403.1	GI:42663256				

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 4015)
TITLE	Chang, S.-Y. P. and Santini, C.D.
JOURNAL	Quantitation of hTERT mRNA expression
FEATURES	Patent: US 6664046-A 16-DEC-2003;
source	location/Qualifiers
	1..4015

```

/organism="unknown"
/mol_type="genomic DNA"

```

ORIGIN	Score 4015;	DB 6;	Length 4015;
Query Match	100.0%;		
Best Local Similarity	100.0%;		
Matches 4015; Conservative	0;	Mismatches	0;
		Indels	0;
		Gaps	0

QY	1	GCAGCGCTCGTCTCTGCTGCGCACGTGGGAAAGCGCTTGAGGCCCGGCCACCCCGCGATGCG	60
Db	1	GCAGCGCTCGTCTCTCTGCTGCGACGTGGGAAAGCGCTTGAGGCCCGGCCACCCCGCGATGCG	60
QY	61	GGCGGCTCCCCGCTGCCGAGCCGTGGGCTTCCCTGCTGCGCAGCACTACCGGAGGTGTCT	120
Db	61	GGCGGCTCCCCGCTGCCGAGCCGTGGGCTTCCCTGCTGCGCAGCACTACCGGAGGTGTCT	120
QY	121	GCGCGTGGCAGCGTTGCTGTCGCGAGCCTGGAGGACCCAGAGGCTGCGGCTGATGACGCGG	180
Db	121	GCGCGTGGCAGCGTTGCTGTCGCGAGCCTGGAGGACCCAGAGGCTGCGGCTGATGACGCGG	180
QY	181	GGAACCCGCGCGCTTTTCGCGCGCTGTGTGCTGCTGATGCTGTGGTGCGCCGAGGAACG	240
Db	181	GGAACCCGCGCGCTTTTCGCGCGCTGTGTGCTGCTGATGCTGTGGTGCGCCGAGGAACG	240
QY	241	ACGAGCGCGCCCGCGCGCCCTCTCTTCCGCAAGTGTCTCTGCTGAGAGAGCTGTGTGC	300
Db	241	ACGAGCGCGCCCGCGCGCCCTCTCTTCCGCAAGTGTCTCTGCTGAGAGAGCTGTGTGC	300
QY	301	CCGAGTGTCTCAAGAGCTGTGTGCGAGCGCGCGGAGAAAGTGTCTTGCGCTTTCG	360
Db	301	CCGAGTGTCTCAAGAGCTGTGTGCGAGCGCGCGGAGAAAGTGTCTTGCGCTTTCG	360
QY	361	GCTGCTGGAAGGAGCGCGCGGAGGCGCCCGCGAGGCTTTCACACCAACAGCTGTGCGAGCTA	420

Db	361	GCCTGCTGACGAGGAGCCCGCGGGGGCCCCCCCCAGAGCTTACACACACAGCTGCGCAGCTA	420
Qy	421	CTGACCACAAACGAGTGAACGACGCACTGCGAGGAGAGCGGAGCGTGGAGCTGCTGCTCG	480
Db	421	CTGTCCCAACACCGGTGACCGACGCACTGCGAGGAGAGCGGAGCGTGGAGCGCTGCTCTCG	480
Qy	481	CCGCGTGGGAGCGACGCTGCTGGTTTCACTGCGTGGAGCGCTGGGCTCTTTGTGCTGAT	540
Db	481	CCGCGTGGGAGCGACGCTGCTGGTTTCACTGCTGGAGCGCTGGGCTCTTTGTGCTGAT	540
Qy	541	GGCTCCGACGTGCGCTTACGAGGTGTGCGGAGCCGCGCTGTACCAAGCTGGGCTTGCAAC	600
Db	541	GGCTTCGACGTGCGCTTACGAGGTGTGCGGAGCCGCGCTGTACCAAGCTGGGCTTGCAAC	600
Qy	601	TCAGGCCCGGCCCCCGCCCAACGCTTATGTGAACCCCGAAGCGCTGTGGATGTGGAAACGGGC	660
Db	601	TCAGGCCCGGCCCCCGCCCAACGCTTATGTGAACCCCGAAGCGCTGTGGATGTGGAAACGGGC	660
Qy	661	CTGGAACATATGCTGACGAGGAGCGGAGGTCCCCCTGGGCTTGCCAGCCCGAGTTCGAG	720
Db	661	CTGGAACATATGCTGACGAGGAGCGGAGGTCCCCCTGGGCTTGCCAGCCCGAGTTCGAG	720
Qy	721	GAGGCGCGGGGAGCAGTGTCAAGCCGAAGTCTTGCCGTTTGCCAAAGGCCCAAGGCTGGGCGC	780
Db	721	GAGGCGCGGGGAGCAGTGTCAAGCCGAAGTCTTGCCGTTTGCCAAAGGCCCAAGGCTGGGCGC	780
Qy	781	TGCCCCATAGCGGAGGAGGAGCGCCGTTGGGACAGGGATCTTGAGGCCAACCCGAGGACAGAC	840
Db	781	TGCCCCATAGCGGAGGAGGAGCGCCGTTGGGACAGGGATCTTGAGGCCAACCCGAGGACAGAC	840
Qy	841	GCGTGGACCGAGTGAACGCTGGTTTCTGTGTGTGTCTTGCTTGCAACCTTGCAACCCGCGGAAAGAC	900
Db	841	GCGTGGACCGAGTGAACGCTGGTTTCTGTGTGTGTCTTGCTTGCAACCTTGCAACCCGCGGAAAGAC	900
Qy	901	CACCTCTTTGAGAGGAGTGGCTCTCGGACGCGGCACTTCCACCCATCCGTGGAGCGGCA	960
Db	901	CACCTCTTTGAGAGGAGTGGCTCTCGGACGCGGCACTTCCACCCATCCGTGGAGCGGCA	960
Qy	961	GACACGCGGAGGCCCCCATCCACATGCGGAGCCACACGTTCCCTGGGACACGCTTGTCTC	1020
Db	961	GACACGCGGAGGCCCCCATCCACATGCGGAGCCACACGTTCCCTGGGACACGCTTGTCTC	1020
Qy	1021	CCCGGTATACGCGGAGACCAAGCACTTCTCTACTCTCAAGGAGCAAGAGGAGGAGCTGCG	1080
Db	1021	CCCGGTATACGCGGAGACCAAGCACTTCTCTACTCTCAAGGAGCAAGAGGAGGAGCTGCG	1080
Qy	1081	GCGCTCTTCTCTACTCAAGCTCTTGAGGAGCCAGGCTGACTGGGCTGTGAGGCTCTGGA	1140
Db	1081	GCGCTCTTCTCTACTCAAGCTCTTGAGGAGCCAGGCTGACTGGGCTGTGAGGCTCTGGA	1140
Qy	1141	GACCATCTTTCTGGGTTTCAAGGCTCTGGAATCCAGAGGACATCCCGGAGAGTTGACCGGCT	1200
Db	1141	GACCATCTTTCTGGGTTTCAAGGCTCTGGAATCCAGAGGACATCCCGGAGAGTTGACCGGCT	1200
Qy	1201	GCCCCAGGCTACTGAGCAATGCGGAGCCCTGTTTCTGAGCTGTGTGGAAACACGCGCA	1260
Db	1201	GCCCCAGGCTACTGAGCAATGCGGAGCCCTGTTTCTGAGCTGTGTGGAAACACGCGCA	1260
Qy	1261	GTCGCCCTTACGAGGTGCTCTTCAAGCACTGCGCGGTGTGAGTGTGGATCCCAAC	1320
Db	1261	GTCGCCCTTACGAGGTGCTCTTCAAGCACTGCGCGGTGTGAGTGTGGATCCCAAC	1320
Qy	1321	AGCGGAGTCTGTGACCCGAGGAGAGGCCCAAGGACTTGTGCGGAGCCCGAGAGAGAGGA	1380
Db	1321	AGCGGAGTCTGTGACCCGAGGAGAGGCCCAAGGACTTGTGCGGAGCCCGAGAGAGAGGA	1380
Qy	1381	CACAGACCCCGCTGCTGTGTGACGTCTCCGACGACACAGACGCCCTTGTGGAGGTGA	1440
Db	1381	CACAGACCCCGCTGCTGTGTGACGTCTCCGACGACACAGACGCCCTTGTGGAGGTGA	1440
Qy	1441	CGGCTTCTGACGAGGAGCTGCGTGGCGCGGCTGGTGTGCGCCCAAGGCTCTGGGCTCCAGGCA	1500
Db	1441	CGGCTTCTGACGAGGAGCTGCGTGGCGCGGCTGGTGTGCGCCCAAGGCTCTGGGCTCCAGGCA	1500

1501 CAAGCAAGCGGCTTCTCAGGAAACCAAGAGTTATCTCCCTGGGGAGCATGCCAA 1560
1501 CAACGAGCGCCCTTCTCAGGAAACCAAGAGTTATCTCCCTGGGGAGCATGCCAA 1560
1561 GCTCTCGCTGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGGCTTGGCTGGCAG 1620
1561 GCTCTCGCTGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGGCTTGGCTGGCAG 1620
1621 GAGCCCAAGGGGTTGGCTGTGTTCGGCCGACAGACACCGTCTGCGAGAGATCTTGGC 1680
1621 GAGCCCAAGGGGTTGGCTGTGTTCGGCCGACAGACACCGTCTGCGAGAGATCTTGGC 1680
1681 CAAGTTCCGCACTGGCTGATGATGTGTATCGTCCGAGCTGCTCAGGCTCTTTCTTTA 1740
1681 CAAGTTCCGCACTGGCTGATGATGTGTATCGTCCGAGCTGCTCAGGCTCTTTCTTTA 1740
1741 TGTCAAGAGACACAGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAGAGTGTGGAG 1800
1741 TGTCAAGAGACACAGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAGAGTGTGGAG 1800
1801 CAAGTTGCAAGCATTTGGAATCAGACAGCATTTGAAGAGGCTGACGCTGGGAGCTGTC 1860
1801 CAAGTTGCAAGCATTTGGAATCAGACAGCATTTGAAGAGGCTGACGCTGGGAGCTGTC 1860
1801 CAAGTTGCAAGCATTTGGAATCAGACAGCATTTGAAGAGGCTGACGCTGGGAGCTGTC 1860
1861 GGAAGCAGAGGTCAGGCAAGCATCGGGAGCAGGCGCCGCTGCTGAGCTGCAAGCTCGG 1920
1861 GGAAGCAGAGGTCAGGCAAGCATCGGGAGCAGGCGCCGCTGCTGAGCTGCAAGCTCGG 1920
1921 CTTCAATCCCAAGCCTGACGAGGCTGGCGCGATTTGGAACATGACATGATCGTGGAGAC 1980
1921 CTTCAATCCCAAGCCTGACGAGGCTGGCGCGATTTGGAACATGACATGATCGTGGAGAC 1980
1981 CAGAAAGTTCCGAGAGAAAGAGAGGCGCAGAGCTCTCAGCTGAGGCTGAAGCACTGTT 2040
1981 CAGAAAGTTCCGAGAGAAAGAGAGGCGCAGAGCTCTCAGCTGAGGCTGAAGCACTGTT 2040
2041 CAGCGGTCACATCTGAGCGGCGCGGCGCGCGCGCGCTCTGAGGCGCTGCTGCTGAG 2100
2041 CAGCGGTCACATCTGAGCGGCGCGGCGCGCGCGCGCTCTGAGGCGCTGCTGCTGAG 2100
2101 CCTGGAAGATATCAGAGGCGCTGAGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTG 2160
2101 CCTGGAAGATATCAGAGGCGCTGAGCGACCTTCTGCTGCTGCTGCTGCTGCTGCTG 2160
2161 GCGGCTGAGCTGATCTTTGTCAAGGTGATGAGCGGCGCTGAGCAACATCCCCA 2220
2161 GCGGCTGAGCTGATCTTTGTCAAGGTGATGAGCGGCGCTGAGCAACATCCCCA 2220
2221 GGAAGGCTCAGGAGGATGATGCGGAGCATCAATCAACCCAGAAACATGATCGCTGGG 2280
2221 GGAAGGCTCAGGAGGATGATGCGGAGCATCAATCAACCCAGAAACATGATCGCTGGG 2280
2281 TCGGATATGCGTGTGTCAGAAAGCGCGCATGAGGCGACGTCGCAAGGCTTCAAGAGCA 2340
2281 TCGGATATGCGTGTGTCAGAAAGCGCGCATGAGGCGACGTCGCAAGGCTTCAAGAGCA 2340
2341 TCGGATATGCGTGTGTCAGAAAGCGCGCATGAGGCGACGTCGCAAGGCTTCAAGAGCA 2340
2341 TCGGATATGCGTGTGTCAGAAAGCGCGCATGAGGCGACGTCGCAAGGCTTCAAGAGCA 2340
2341 GGTCTTCTACCTTGAACAGACCTTCCAGCGTATCATGCAAGTTCGTGGCTCACTGACAGA 2400
2341 GGTCTTCTACCTTGAACAGACCTTCCAGCGTATCATGCAAGTTCGTGGCTCACTGACAGA 2400
2401 GACCAAGCGCGCTGAGGAGATGCGTGTCAATCAGAGCAAGCTCTCTTCAATTAAGGCGCAG 2460
2401 GACCAAGCGCGCTGAGGAGATGCGTGTCAATCAGAGCAAGCTCTCTTCAATTAAGGCGCAG 2460
2461 CAGTGGCTCTTGAAGCTCTTCTTCAAGCTTCAAGTGTGCAAGAGCGCTGCGATCAAGGG 2520
2461 CAGTGGCTCTTGAAGCTCTTCTTCAAGCTTCAAGTGTGCAAGAGCGCTGCGATCAAGGG 2520
2521 CAGTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 2580
2521 CAGTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 2580
2521 CAGTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 2580
2521 CAGTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 2580

2581 CAGCTGTGCTACGCGGCAATGAGAAACAGCTGTTTGGGAGATTCGCGGAGCGGCT 2640
2581 CAGCTGTGCTACGCGGCAATGAGAAACAGCTGTTTGGGAGATTCGCGGAGCGGCT 2640
2641 GCTCTGCGTGTGAGATGATTTCTTGTGTGACACTTCACTTCACTTCAAGCGGAAAC 2700
2641 GCTCTGCGTGTGAGATGATTTCTTGTGTGACACTTCACTTCACTTCAAGCGGAAAC 2700
2701 CTTCTCAAGAACCTTCCGTGAGAGAGAGGCGCTGAGTGCAGGCTTCTTGTTCAGAT 2760
2701 CTTCTCAAGAACCTTCCGTGAGAGAGAGGCGCTGAGTGCAGGCTTCTTGTTCAGAT 2760
2761 GACAGTGTGAACTTCCGTGAGAGAGAGGCGCTGAGTGCAGGCTTCTTGTTCAGAT 2820
2761 GACAGTGTGAACTTCCGTGAGAGAGAGGCGCTGAGTGCAGGCTTCTTGTTCAGAT 2820
2821 GCGGCGCCAGCGCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2821 GCGGCGCCAGCGCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2881 GGAAGGCGAATCTCAGCTATGCGCGGACCTCCATCAGAGCAGTCTCAGCTTCAACCG 2940
2881 GGAAGGCGAATCTCAGCTATGCGCGGACCTCCATCAGAGCAGTCTCAGCTTCAACCG 2940
2941 CCGCTTCAAGGCTGAGGAGAAATGCTGCAAACTCTTGGGAGCTTCTGCGCTGAAATG 3000
2941 CCGCTTCAAGGCTGAGGAGAAATGCTGCAAACTCTTGGGAGCTTCTGCGCTGAAATG 3000
3001 TCACAGCTGTTCTGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 3060
3001 TCACAGCTGTTCTGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 3060
3061 CAAAGTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
3061 CAAAGTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
3121 TCAGCAAGTTGGAAGAACCCCAATTTTCTGCGCGCTCATCTGACAGCGGCTGCT 3180
3121 TCAGCAAGTTGGAAGAACCCCAATTTTCTGCGCGCTCATCTGACAGCGGCTGCT 3180
3181 CTGCTATCTCATCTGAAAGGCAAGAACGAGGAGTGTGCTGAGGAGGAGGAGGAGGAG 3240
3181 CTGCTATCTCATCTGAAAGGCAAGAACGAGGAGTGTGCTGAGGAGGAGGAGGAGGAG 3240
3241 CCGGCTCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3300
3241 CCGGCTCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3300
3301 GACTGACACCGTGTCACTTACGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
3301 GACTGACACCGTGTCACTTACGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
3361 GGTGAGTGGAAAGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
3361 GGTGAGTGGAAAGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
3421 GCTGAGTGGAAAGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
3421 GCTGAGTGGAAAGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
3481 ACTGCGCTTGAAGCTTCAAGACATCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 3540
3481 ACTGCGCTTGAAGCTTCAAGACATCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 3540
3541 GAGCAGACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
3541 GAGCAGACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
3601 CAGTCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3660
3601 CAGTCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3660
3661 GAGTGTCCAGCACACTGCGCTTCTTCACTTCCCAAGGCTGAGGCTGAGGCTTCAACCCA 3720
3661 GAGTGTCCAGCACACTGCGCTTCTTCACTTCCCAAGGCTGAGGCTGAGGCTTCAACCCA 3720

Db 3661 GAGTGTCCAGACACCTGCGCTTACTTCCCAAGGCTGGCTCCAGTCCCA 3720
Qy 3721 GGGCCAGCTTTTCTCTCCAGAGAGCCGGCTTCACTCCCAATAGATGTCATCC 3780
Db 3721 GGGCCAGCTTTTCTCTCCAGAGAGCCGGCTTCACTCCCAATAGATGTCATCC 3780
Qy 3781 CCAGATTCGCCATTTGTTCACTCCCTGGCTCCCTGCTTTCCTTCACTCCCAATCC 3840
Db 3781 CCAGATTCGCCATTTGTTCACTCCCTGGCTCCCTGCTTTCCTTCACTCCCAATCC 3840
Qy 3841 AGGTGAGACCTTGAGAGAGACCTGGAGCTCTGAGAAATTTGAGTGAACAAAGTGTG 3900
Db 3841 AGGTGAGACCTTGAGAGAGACCTGGAGCTCTGAGAAATTTGAGTGAACAAAGTGTG 3900
Qy 3901 CCTGTACACAGGCGAGAGACCTTGACCTTGATGGGGTCTCTGTGGTCAAAATTTGGGG 3960
Db 3901 CCTGTACACAGGCGAGAGACCTTGACCTTGATGGGGTCTCTGTGGTCAAAATTTGGGG 3960
Qy 3961 GAGGTCTGTGGAGTAAATTAAGTAATATGATTTTCACTTTGAAAAAA 4015
Db 3961 GAGGTCTGTGGAGTAAATTAAGTAATATGATTTTCACTTTGAAAAAA 4015

RESULT 15
AX019310 4015 bp DNA linear PAT 07-SEP-2000

LOCUS AX019310
DEFINITION Sequence 10 from Patent WO940221.
ACCESSION AX019310
VERSION AX019310.1 GI:10043297

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Dahm, M.W., Phelps, R.C. and Brockmeyer, C.
TITLE Method for quantitatively analyzing tumor cells in a body fluid and test kits suited therefor
JOURNAL Patent: WO 940221-A 10 12-AUG-1999;
DHM MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)

FEATURES
source 1..4015
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGCGCTGCTGCTGCTGCGACAGTGGAAAGCCCTGGCCCGGACCCCGGATGCC 60
Db 1 GCAGCGCTGCTGCTGCTGCGACAGTGGAAAGCCCTGGCCCGGACCCCGGATGCC 60
Qy 61 GCGGCTCCCGCGCGAGCGCGGCTGCTGCTGCTGCGAGCAGTACCGGAGTGTCT 120
Db 61 GCGGCTCCCGCGCGAGCGCGGCTGCTGCTGCTGCGAGCAGTACCGGAGTGTCT 120
Qy 121 GCGGCTGCGACGTTCTGTGCGGCGCTTGAGGAGCCCAAGGCTGGCGGTGTGACGCGG 180
Db 121 GCGGCTGCGACGTTCTGTGCGGCGCTTGAGGAGCCCAAGGCTGGCGGTGTGACGCGG 180
Qy 181 GAGCCCGGCGCTTTCCGCGCGCTGTGTGCGCCAGTGTGCGTGTGCGCTGTGAGACG 240
Db 181 GAGCCCGGCGCTTTCCGCGCGCTGTGTGCGCCAGTGTGCGTGTGCGCTGTGAGACG 240
Qy 241 AGCGGCGCGCGCGCGCGCGCTCTTCCGCGAGTGTGCGCTGTAAGAGAGCTGTGTGC 300
Db 241 AGCGGCGCGCGCGCGCGCGCTCTTCCGCGAGTGTGCGCTGTAAGAGAGCTGTGTGC 300
Qy 301 CCGAGTGTGAGAGGCTGTGTGAGCGCGGCGAGAGAGTGTGTGCTTGGCTTGC 360

Db 301 CCGAGTGTGAGAGGCTGTGTGAGCGCGGCGAGAGAGTGTGTGCTTGGCTTGC 360
Qy 361 GCTGTGAGACGGAGGCGCGCGGAGGCGCGGAGGCTTTTCAACACAGTGTGTGAGTGA 420
Db 361 GCTGTGAGACGGAGGCGCGCGGAGGCGCGGAGGCTTTTCAACACAGTGTGTGAGTGA 420
Qy 421 CCGGCGCAACAGGTGACGAGACGCTGAGGAGAGCGGAGGCTGTGTGAGTGTGAGTGA 480
Db 421 CCGGCGCAACAGGTGACGAGACGCTGAGGAGAGCGGAGGCTGTGTGAGTGTGAGTGA 480
Qy 481 CCGGCGGAGAGAGAGAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 540
Db 481 CCGGCGGAGAGAGAGAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 540
Qy 541 GGTCTCCAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 600
Db 541 GGTCTCCAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 600
Qy 601 TCAGGCGCGGCGCGCGCGCAACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 660
Db 601 TCAGGCGCGGCGCGCGCGCAACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 660
Qy 661 CTGGAACCATAGCTGTGAGGAGGCGCGGAGTCCCTTGGGCTGTGAGGCGCGGAGTGTGAG 720
Db 661 CTGGAACCATAGCTGTGAGGAGGCGCGGAGTCCCTTGGGCTGTGAGGCGCGGAGTGTGAG 720
Qy 721 GAGGCGCGGAGGAGTGTGAGGAGGCGCGGAGTGTGAGGAGGCGCGGAGTGTGAGGAGG 780
Db 721 GAGGCGCGGAGGAGTGTGAGGAGGCGCGGAGTGTGAGGAGGCGCGGAGTGTGAGGAGG 780
Qy 781 TGCCTCTGAGCGGAGCGGAGCGCGGAGTGTGAGGAGGCGCGGAGTGTGAGGAGGAGGAG 840
Db 781 TGCCTCTGAGCGGAGCGGAGCGCGGAGTGTGAGGAGGCGCGGAGTGTGAGGAGGAGGAG 840
Qy 841 GCGTGTGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 900
Db 841 GCGTGTGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 900
Qy 901 CAGCTTTTGAAGGAGGAGTGTGAGGAGGAGTGTGAGGAGGAGTGTGAGGAGGAGGAGGAG 960
Db 901 CAGCTTTTGAAGGAGGAGTGTGAGGAGGAGTGTGAGGAGGAGTGTGAGGAGGAGGAGGAG 960
Qy 961 GAGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 961 GAGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Qy 1021 CCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Db 1021 CCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Qy 1081 GCGCTCTTCTTCTACTGAGGCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1081 GCGCTCTTCTTCTACTGAGGCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Qy 1141 GAGCATCTTCTGAGGCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1141 GAGCATCTTCTGAGGCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Qy 1201 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Db 1201 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Qy 1261 GTCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db 1261 GTCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Qy 1321 AGCGGAGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Db 1321 AGCGGAGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Qy 1381 CAGAGACCGGCGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1440

Db	1381	CACGAGACCCCCCGTGGCCTGGTGTGACAGCTGCTCCGCGACAGACAGACGCCCTTGCGAGGTGTAT	1440
Qy	1441	CGGCTTCGTGCGGGGCTGCTGCTGCGCGCGGCTGTGTGCTCCCGAGGCTCTTGCGGCTCTCCAGGCA	1500
Db	1441	CGGCTTCGTGCGGGGCTGCTGCTGCGCGCGGCTGTGTGCTCCCGAGGCTCTTGCGGCTCTCCAGGCA	1500
Qy	1501	CAACGAAAGCCGCGCTTCCCTCAGAGAAACCCAAAGATTCACTCCCTGGGGAAGCATGCCCCA	1560
Db	1501	CAACGAAAGCCGCGCTTCCCTCAGAGAAACCCAAAGATTCACTCCCTGGGGAAGCATGCCCCA	1560
Qy	1561	GCTCTCGCTGAGAGAGCTGACGTGGAAATAGCGTGGGGGACTGGCGCTTGGCTGGCGAG	1620
Db	1561	GCTCTCGCTGAGAGAGCTGACGTGGAAATAGCGTGGGGGACTGGCGCTTGGCTGGCGAG	1620
Qy	1621	GAGCCACAGGGGTGTGGCTGTGTTCCGGCCGAGAGACCGCTGCGTGGAGAGATCTGTGC	1680
Db	1621	GAGCCACAGGGGTGTGGCTGTGTTCCGGCCGAGAGACCGCTGCGTGGAGAGATCTGTGC	1680
Qy	1681	CAAGTTCCTGCACCTGAGCTGATGATGATGTGTACGTGTCGACTGCTCAGGTCTTCTTTTA	1740
Db	1681	CAAGTTCCTGCACCTGAGCTGATGATGATGTGTACGTGTCGACTGCTCAGGTCTTCTTTTA	1740
Qy	1741	TGTCACGGAGACACAGCTTCAAAAGAAAGGCTCTTTTCTTCAACGGAAAGATGTCTGGAG	1800
Db	1741	TGTCACGGAGACACAGCTTCAAAAGAAAGGCTCTTTTCTTCAACGGAAAGATGTCTGGAG	1800
Qy	1801	CAAGTTGCAAGCATTTGGATTCAGACAGCATTTGAAAGAGGTGACGCTCGGAGACTGTCTC	1860
Db	1801	CAAGTTGCAAGCATTTGGATTCAGACAGCATTTGAAAGAGGTGACGCTCGGAGACTGTCTC	1860
Qy	1861	GGAAGCAGAGGTCAAGGACGCACTCGGGAAGCCAGGCCCGCTGCTGACCTCAACTTCGCG	1920
Db	1861	GGAAGCAGAGGTCAAGGACGCACTCGGGAAGCCAGGCCCGCTGCTGACCTCAACTTCGCG	1920
Qy	1921	CTTCAATCCCAAGCGCTGACGGGCTGCGGGCCGATTTGTGAACATGACCTACGCTGCGGAGAC	1980
Db	1921	CTTCAATCCCAAGCGCTGACGGGCTGCGGGCCGATTTGTGAACATGACCTACGCTGCGGAGAC	1980
Qy	1981	CAGAACGTTCCGCGACAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGTGAAGGACCTGTT	2040
Db	1981	CAGAACGTTCCGCGACAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGTGAAGGACCTGTT	2040
Qy	1981	CAGAACGTTCCGCGACAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGTGAAGGACCTGTT	2040
Db	1981	CAGAACGTTCCGCGACAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGTGAAGGACCTGTT	2040
Qy	2041	CAGCGTGTCTCAACTGACGCGGGGCGCGGCGCTCTCGGGGCGCTCTGTGCTGTGGG	2100
Db	2041	CAGCGTGTCTCAACTGACGCGGGGCGCGGCGCTCTCGGGGCGCTCTGTGCTGTGGG	2100
Qy	2101	CCTGGAAGATATTCACAAGGGGCTGGCGGACCTTGCTGTGGTGTGGCGGGCCGAGAACCC	2160
Db	2101	CCTGGAAGATATTCACAAGGGGCTGGCGGACCTTGCTGTGGTGTGGCGGGCCGAGAACCC	2160
Qy	2161	GCCGCGCTGAGCTGTACTTTGTCAAGAGGTGATGTGACGGGCGCGTACGACACATCTCCCA	2220
Db	2161	GCCGCGCTGAGCTGTACTTTGTCAAGAGGTGATGTGACGGGCGCGTACGACACATCTCCCA	2220
Qy	2221	GGAACAGGCTCAACGAGGATCATGCGCAGCATCAAAACCCAGAAACAAGTACTGCTGTGCG	2280
Db	2221	GGAACAGGCTCAACGAGGATCATGCGCAGCATCAAAACCCAGAAACAAGTACTGCTGTGCG	2280
Qy	2281	TTCGGTATCCGTGTGTCTGCAAGAGGCGCGCCATATGGGGACGTCCGCAAGGCTTCAAGAGGCA	2340
Db	2281	TTCGGTATCCGTGTGTCTGCAAGAGGCGCGCCATATGGGGACGTCCGCAAGGCTTCAAGAGGCA	2340
Qy	2341	GCTCTCTACCTTGAACAGACTCTCAAGCGGTAATGCGGACAGTTCGTTGCGTCACTGCGAGA	2400
Db	2341	GCTCTCTACCTTGAACAGACTCTCAAGCGGTAATGCGGACAGTTCGTTGCGTCACTGCGAGA	2400
Qy	2401	GACCAAGCCCGCTGAGAGGATGCGCTGTCTATCGAGCAGAGCTCTTCCCTGAATGAGGCGAG	2460
Db	2401	GACCAAGCCCGCTGAGAGGATGCGCTGTCTATCGAGCAGAGCTCTTCCCTGAATGAGGCGAG	2460
Qy	2461	CAGTGGCTCTTTCAGACGTTCTTCTTCAACGCTTCAATGTGCCACACGCGGTGCGCATCAAGGG	2520
Db	2461	CAGTGGCTCTTTCAGACGTTCTTCTTCAACGCTTCAATGTGCCACACGCGGTGCGCATCAAGGG	2520

QY	2521	CAAGTCTTACTAGTCCAGTGGCCAGGGAGATCCCGCAGGGCTCCATATCTTCCAGCGTGTCTGG	2580
Db	2521	CAAGTCTTACTAGTCCAGTGGCCAGGGAGATCCCGCAGGGCTCCATATCTTCCAGCGTGTCTGG	2580
QY	2581	CAGCTGTGTGACAGGGCGACATGGAGAAACAAGCTGTTTGGGGGAGATTCCGCGGGAGCGGGCT	2640
Db	2581	CAGCTGTGTGTACGGCGACATGGAGAAACAAGCTGTTTGGGGGAGATTCCGCGGGAGCGGGCT	2640
QY	2641	GCTTCCTGCGTTTGGTGGATGATTTCTTGTGTGGTGAACCTCACTCACTCACCGACGCGAAAAC	2700
Db	2641	GCTTCCTGCGTTTGGTGGATGATTTCTTGTGTGGTGAACCTCACTCACTCACCGACGCGAAAAC	2700
QY	2701	CTTCTCTCAGAACCTCTGGTCCGAGGTGTCCCTGAGTATGGCTCGGTGTGAATTTCGGGAA	2760
Db	2701	CTTCTCTCAGAACCTCTGGTCCGAGGTGTCCCTGAGTATGGCTCGGTGTGAATTTCGGGAA	2760
QY	2761	GACAGTGTGTAACCTTCCTCGTAAABAACAAGGCGCTGGGTGTGCACGGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGTAACCTTCCTCGTAAABAACAAGGCGCTGGGTGTGCACGGGCTTTTGTTCAGAT	2820
QY	2821	GCCGGCCACAGGCTATATCCCTGTGTGCGAGCTGTGCTGTGAATACCCGAGACCTCTGAGGT	2880
Db	2821	GCCGGCCACAGGCTATATCCCTGTGTGCGAGCTGTGCTGTGAATACCCGAGACCTCTGAGGT	2880
QY	2881	GCAGAGCGACTACTCCAGCTATGCCCCCGGACCTTCATCAGAGCCOAGTCTCACTTCAACCG	2940
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCCCGGACCTTCATCAGAGCCOAGTCTCACTTCAACCG	2940
QY	2941	CGGCTTCAAGGCTGGGAGGAAACAATGGGTGGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGGAGGAAACAATGGGTGGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG	3000
QY	3001	TCAACAGCTGTGTTCTGGAATTTGGAGGTGAACAAGCTCCAGACGGTGTGACCAACATCTA	3060
Db	3001	TCAACAGCTGTGTTCTGGAATTTGGAGGTGAACAAGCTCCAGACGGTGTGACCAACATCTA	3060
QY	3061	CAAGATCTCTCTGTGTCAGGCGGTACAGGTTTCAACGATGTGTCTGACAGTCTCCATTCTCA	3120
Db	3061	CAAGATCTCTCTGTGTCAGGCGGTACAGGTTTCAACGATGTGTCTGACAGTCTCCATTCTCA	3120
QY	3121	TCAGCAAGTTTGGAGAAACCCCAATTTTTCTGTGCGGCTCAATCTCTGACACGGGCTTCCCT	3180
Db	3121	TCAGCAAGTTTGGAGAAACCCCAATTTTTCTGTGCGGCTCAATCTCTGACACGGGCTTCCCT	3180
QY	3181	CTGTCTATCTCCATCTGTGAAGCAAGAACAAGGAGATGTGCTGTGGGGGCAAGGGCGCGCG	3240
Db	3181	CTGTCTATCTCCATCTGTGAAGCAAGAACAAGGAGATGTGCTGTGGGGGCAAGGGCGCGCG	3240
QY	3241	CGGCGCTCTGCGCTCCGAGGCGGTGACGATGGCTGTGCAACCAAGCATTTCTGCTCAAGCT	3300
Db	3241	CGGCGCTCTGCGCTCCGAGGCGGTGACGATGGCTGTGCAACCAAGCATTTCTGCTCAAGCT	3300
QY	3301	GACTTCGACACCGTGTCACTTACCTGTGCACCTCTGTGGGTCACTTCAGGACAGGCCAACAGCA	3360
Db	3301	GACTTCGACACCGTGTCACTTACCTGTGCACCTCTGTGGGTCACTTCAGGACAGGCCAACAGCA	3360
QY	3361	GCTGAGTGTGGAAGTGTCCCGGGGAGCAAGCTGATGTGCTTGAAAGGCGCGCAACCCGGCG	3420
Db	3361	GCTGAGTGTGGAAGTGTCCCGGGGAGCAAGCTGATGTGCTTGAAAGGCGCGCAACCCGGCG	3420
QY	3421	ACTGCGCTCTCAGACTTCAAGAACAATCTCTGGAATGTAGTGGCCACCGCGCCAACGACGAGCGGA	3480
Db	3421	ACTGCGCTCTCAGACTTCAAGAACAATCTCTGGAATGTAGTGGCCACCGCGCCAACGACGAGCGGA	3480
QY	3481	GAGCAGACACCAAGAGCGCTGTACCCCGGGGCTTACATCTCCAGGGAGGGAAGGGCGGCGC	3540
Db	3481	GAGCAGACACCAAGAGCGCTGTACCCCGGGGCTTACATCTCCAGGGAGGGAAGGGCGGCGC	3540
QY	3541	CACACCCAGGCGCGCACCGCTGGGAGCTGTGAAGGCTGATGTGATTTTGGCGGAGGCGGCTG	3600
Db	3541	CACACCCAGGCGCGCACCGCTGGGAGCTGTGAAGGCTGATGTGATTTTGGCGGAGGCGGCTG	3600

```

QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTTGAGCGAGTGTCCAGCCAGGGCT 3660
Db |||||
QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTTGAGCGAGTGTCCAGCCAGGGCT 3660
Db |||||
QY 3661 GAGTGTCCAGCAACCTGCGGTCTTCACTTCCCAACAGGCTGGCGCTCCAGCCCA 3720
Db |||||
QY 3661 GAGTGTCCAGCAACCTGCGGTCTTCACTTCCCAACAGGCTGGCGCTCCAGCCCA 3720
Db |||||
QY 3721 GGGCCAGCTTTTCTCAGCAGAGGCCGGCTTCCACTCCCAATAGAAATAGTCATCC 3780
Db |||||
QY 3721 GGGCCAGCTTTTCTCAGCAGAGGCCGGCTTCCACTCCCAATAGAAATAGTCATCC 3780
Db |||||
QY 3781 CCAAGATTGCGCATTTTCAACCCCTGGCTGCTTCTTGTGCTTCCACCCCAACATCC 3840
Db |||||
QY 3781 CCAAGATTGCGCATTTTCAACCCCTGGCTGCTTCTTGTGCTTCCACCCCAACATCC 3840
Db |||||
QY 3841 AGGTGAGAGACCTGAGAGAGACCTTGGAGACTCTGAGAAATTGAGTGAACAAAGGTGTG 3900
Db |||||
QY 3841 AGGTGAGAGACCTGAGAGAGACCTTGGAGACTCTGAGAAATTGAGTGAACAAAGGTGTG 3900
Db |||||
QY 3901 CCCTGTACACAGGCGAGAGACCTTGCACCTGATGAGGCTTCTGTGGTCAATTGGGGG 3960
Db |||||
QY 3901 CCCTGTACACAGGCGAGAGACCTTGCACCTGATGAGGCTTCTGTGGTCAATTGGGGG 3960
Db |||||
QY 3961 GAGGTGTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4015
Db |||||
QY 3961 GAGGTGTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4015
Db |||||

```

Search completed: October 29, 2004, 20:54:42
 Job time : 16400 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 09:37:01 : Search time 7840 Seconds

(without alignments)
5261.451 Million cell updates/sec

Title: US-10-044-692-2

Perfect score: 5961

Sequence: 1 MPRAPRCANVSLRSHYRE.....TALBAANPAJPSDEKTLID 1132

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_epool/US10044692/runat_28102004_103655_1370/app_query.fasta_1.1287
-DB=EST -QFMT=fastap -SUFFIX=trst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044692_QCGN_1_14804@runat_28102004_103655_1370 -NCPU=6 -ICPU=3
-NO MMAP -LARGEREQUEST -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_hic: *
4: gb_esc3: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2645	44.4	1826	9	AY407349
2	2168	36.4	1584	9	AY407350
3	1805	30.3	1835	9	AY407351
4	1406	23.6	925	4	BM453198
5	1028	17.2	851	5	BU702370
6	875	14.7	851	4	BG917907
7	776	13.0	492	4	BM824748
8	771.5	12.9	664	5	BQ258274
9	682	11.4	1424	3	CR688161

10	667.5	11.2	649	7	CF531069	UI-M-FY0-
11	666.5	11.2	688	1	CF531121	UI-M-FY0-
12	646	10.8	389	7	AA281296	z10802.r
13	610	10.2	599	2	BB618671	BB618671
14	567	9.5	409	7	CN274427	CN274427
15	566	9.5	866	2	BB571943	BB571943
16	554	9.3	614	2	BB651920	BB651920
17	517	8.7	775	4	B1388013	BFL26_002
18	515	8.6	753	5	BU452535	BU452535
19	484.5	8.1	846	7	CN505902	CN505902
20	481.5	8.1	880	5	BU377259	BU377259
21	463	7.8	668	6	CA380121	CA380121
22	457	7.7	724	5	BX889962	BX889962
23	449.5	7.5	632	6	CA353864	CA353864
24	443.5	7.4	715	2	BE396925	BE396925
25	437	7.3	703	5	BX886589	BX886589
26	436	7.3	344	4	CF531258	CF531258
27	425	7.1	409	1	AA311750	AA311750
28	425	7.1	679	2	BE396606	BE396606
29	424	7.1	835	5	BU111946	BU111946
30	422	7.1	649	2	BE514070	BE514070
31	411	6.9	610	2	BE514188	BE514188
32	395.5	6.6	696	5	BU139751	BU139751
33	387	6.5	343	6	BY783093	BY783093
34	384	6.4	338	6	BY784804	BY784804
35	380	6.4	336	6	BY775178	BY775178
36	377	6.3	347	2	AM244516	AM244516
37	374	6.3	326	5	BY149368	BY149368
38	373	6.3	641	8	AZ972318	AZ972318
39	366	6.1	619	7	CK392784	CK392784
40	357.5	6.0	779	2	BE268183	BE268183
41	348.5	5.8	875	5	BU122597	BU122597
42	348.5	5.8	930	7	CO014076	CO014076
43	314	5.3	983	7	CO028055	CO028055
44	307	5.2	1023	7	CO024489	CO024489
45	291.5	4.9	774	7	CF547484	CF547484

ALIGNMENTS

RESULT 1
AY407349
LOCUS
DERIVATION
Homo sapiens TERT gene, 1826 bp
genomic survey sequence.
VIRTUAL TRANSCRIPT, partial sequence.

ACCESSION
AY407349
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..1826

COMMENT
FEATURES
source

gene
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1826
/gene="TERT"
/locus_tag="HCM2861"

ORIGIN

Alignment Scores:

Pred. No.:	4, 89e-173	Length:	1826
Score:	2645.00	Matches:	526
Percent Similarity:	86.66%	Conservative:	0
Best Local Similarity:	86.66%	Mismatches:	81
Query Match:	44.37%	Indels:	0
DB:	9	Gaps:	0

US-10-044-692-2 (1-1132) x AY407349 (1-1826)

```

QY      526 ValGlyCyValProAlaAlaGluHisArgLeuArgGluGluIleLeuAlaIysPheLeu 545
DB      3 GTTGGCTGTGTTCCGGCCGACAGACCCGTCTGAGAGAGATCCCTGGCCAAAGTTCCTG 62
QY      546 HistLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGlu 565
DB      63 CACTGGCTGATGAGTGTGTCGTCTGACGCTCTCAGGCTTTCTTTTATGTCAGGAG 122
QY      566 ThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTTPSerLysLeuGln 585
DB      123 ACCACGTTTCAAAAGACAGGCTCTTTTCTACCGGAGAGATCTGAGCAAGTTGCAA 182
QY      586 SerLysLeuLysLeuArgGlnHisLeuLysArgValGluLeuArgGluLeuSerGluAlaGlu 605
DB      183 AGCATTTGAATCAACACAGCACTTGAGAGAGGTGACGCTGCGAGAGCTTCGGAAGCAGAG 242
QY      606 ValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArgPheIlePro 625
DB      243 GTACGACGACATCCGGAAAGCCAGGCCCGCTGTCGATCCAGATCCGCTTATCCTCCC 302
QY      626 LysProAspGlyLeuArgProIleValAsnMetCaspTyrValValGlyAlaArgThrPhe 645
DB      303 AAGCTGACGGGCGCGCCGATGTGAACTGACATCACTCGGGAGCCAGAACTTC 362
QY      646 ArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeu 665
DB      363 CGCAGAGAAAGAGGGCCGACGCTCTCAGCTCGAGGTCGAGACCTGTCAGGTCCTC 422
QY      666 AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGlyLeuAspAsp 685
DB      423 AACTACGAGCGGGCGCGGCCGCTCTGCGGCCCTCTGCTGGCTGGACGAT 482
QY      686 IleHisArgAlaArgArgThrPheValLeuArgValArgAlaGlnAspProProGlu 705
DB      483 ATCCACAGGGCGCTGGCCGACCTGCTGCTGCGGCGGCCAGAGACCGCCGCTGAG 542
QY      706 LeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGlnAspArgLeu 725
DB      543 CTGTACTTCTTCACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 602
QY      726 ThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCyValArgArgTyrAla 745
DB      603 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 662
QY      746 ValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHisValSerThr 765
DB      663 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 722
QY      766 LeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGluThrSerPro 785
DB      723 TTGACAGACCTCCACCGCATGCGACAGTTCTGCGCTCAGCTCAGAGACCGACCGCG 782
QY      786 LeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSerSerGlyLeu 805
DB      783 CTGAGGAGATGCGCTGCTATCGACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 842

```

```

QY      806 PheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGlyLysSerTyr 825
DB      843 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 902
QY      826 ValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCySerLeuCy 845
DB      903 GTCCAGTGTCCAGGGGATCCCGCAGGCTCCATCTCTCCACGCTGCTCTGAGCCTGTGC 962
QY      846 TyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArg 865
DB      963 TACGCGCACATGAGAGAAACAGCTGTTGGCGGATTCGGCGGAGCGAGCTGCTCTGCGT 1022
QY      866 LeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThrPheLeuArg 885
DB      1023 TTGGTGTGATGATTTCTTGTGTGTGACACTCAGCTCAGCCAGCGGAAACCTTCTCAGG 1082
QY      886 ThrLeuValArgGlyValProGluTyrGlyCyValValAsnLeuArgLysThrValVal 905
DB      1083 ACCCTGTCCTCAGAGGTGTCCTGAGATGCTGCTGCTGAGAACTTGGCGAAGACAGTGTG 1142
QY      906 AsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHis 925
DB      1143 AACTTCCTGTAGAGAGACGAGGCTGGGTGACAGGCTTTGTTCAATGCTCCGCGCCAC 1202
QY      926 GlyLeuPheProTyrCyGlyLeuLeuLeuAspThrArgThrLeuGluValGlnSerAsp 945
DB      1203 GGCCTATTCCTGCTGCGGCTGCTGCTGAGTACCCGACCTGAGAGTGCAGAGCGAC 1262
QY      946 TyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheLys 965
DB      1263 TACTCCAGCTATGCCCGGACCTCCATCAGAGCACTTCACCTTCAACCGGAGCTTCAAG 1322
QY      966 AlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCysHisSerLeu 985
DB      1323 GCTGGAGAGACATGCTGCGCAACTCTTGGGGCTTGGCGCTGAGAGTGCAGCGCTG 1382
QY      986 PheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrLysIleLeu 1005
DB      1383 TTTCTGATTTGCAAGTGAAACAGCTCCAGAGGTGTGACCAACATCTACAAAGTCTCTC 1442
QY      1006 LeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGlnGlnVal 1025
DB      1443 CTGCTGCAGCGGTACAGGTTTCAAGATGTGTGCTGCACTCCATTTCAATCAGCAAGTT 1502
QY      1026 TrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCyTyrSer 1045
DB      1503 TGGAGAAACCCCAATTTTCTGCGCGTCATCTGTGACAGCGCTCCCTGTGTAATCC 1562
QY      1046 IleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyValAlaIleProLeu 1065
DB      1563 ATCCTGAAGCCAAAGACAGGAGATGCTGCGGGGCCAAAGGCGCGCCGCTCTG 1622
QY      1066 ProSerGluAlaValGlnThrLeuCyHisGlnAlaPheLeuLeuLysLeuThrArgHis 1085
DB      1623 CCCTCGAGGCGGTGAGTGTGCTGTCCACCAAGCACTTCTGCTCAAGCTGATCGACAC 1682
QY      1086 ArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGlnLeuSerArg 1105
DB      1683 CTGTGACCTACGTCGACATCTCTGGGGTCATCTCAGACAGCCAGCAGCTGATGCTCG 1742
QY      1106 LysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAlaLeuProSer 1125
DB      1743 AAGCTCCCGGGAGCAGACGCTGACTGCTGGAGCGCGACCAACCGGACTGCTCTCA 1802
QY      1126 AspPheLysThrIleLeuAsp 1132
DB      1803 GACTTCAAGCACTCTGAGAC 1823

```

RESULT 2
AY407350
LOCUS
DEFINITION Pan troglodytes TERT gene, VIRUAL TRANSCRIPT, partial sequence,

ACCESSION genomic survey sequence.
VERSION AY407350
KEYWORDS AY407350.1 GI:39763321
SOURCE GSS.
ORGANISM Pan troglodytes (chimpanzee)
REFERENCE Pan troglodytes
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1584)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.D., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1584)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.D., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source location/Qualifiers
1..1584
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1584
/gene="TERT"
/locus_tag="HCM2861"
ORIGIN
Alignment Scores:
Pred. No.: 5,54e-140 Length: 1584
Score: 2168.00 Matches: 432
Percent Similarity: 82.73% Conservative: 4
Best Local Similarity: 81.97% Mismatches: 91
Query Match: 36.37% Indels: 0
Gaps: 0
US-10-044-692-2 (1-1132) x AY407350 (1-1584)
QY 526 VALGlyCyValProAlaIaIaGluHisArgLeuArgGluGluIleuAlaIysPheLeu 545
DB 3 GTTGCTCTGTTCCGCCGCGCAGAGCACCGTCTGCGAGAGAGATCCTGGCCAAGTTCTTG 62
QY 546 HisTPLeuMeSerValTyRValValGluLeuLeuArgSerPhePheTyRValThrglu 565
DB 63 CACTGGCTGATGAGTGTGTACGTTGTGCGAGCTGCTAGGCTCTTTTATATGTCACGGAG 122
QY 566 ThrThrPheGlnIlyAsnArxglLeuPhePheTyRArgIysSerValTrSerIysLeuGln 585
DB 123 ACCAGGTTTCAGAAAGACGGCTCTTTCTACCGGAAGAGTGTGGAAGAAAGTTGCAA 182
QY 586 SerIleGlyIleArgGlnHisIleuIysAsrValGlnLeuArgGluIleuSerGlnIaIu 605
DB 183 AGCATTTGAAATCAGACAGACATTTGAAGAGGGTGCAGCTCGGAGAGCTGTCGGAAGACAG 242
QY 606 ValArgGlnHisArgGlnIaIaArgProAlaLeuLeuThrSerArgLeuArgPheIlePro 625
DB 243 GTTCAGGACAGCATCAGAAACCCAGGCCGCTGCTGACCTCCAGACTCCGCTTCATCCCC 302
QY 626 LysProAspGlyIleuArgProIleValAsnMetAspTyRValValGlyIleArgTrpPhe 645
DB 303 AAGCTGAGAGGGCTGGCGCGATGTGAACATGACCTACGTCGTGGAGCCAGAACGTTTC 362
QY 646 ArgArgGlnIlyAsrValaIaIuArgLeuThrSerArgValIysAlaLeuPheSerValLeu 665

DB 363 CGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTCAGCGTCTTC 422
QY 666 AsnTyRGIuArgAlaArgArgProGlyLeuLeuGlyAlaSerValIleuGlyLeuAspAsp 685
DB 423 ANNNACGAGCGGGCGCGCGCGCGCTCTGGCGCGCTGTGTCTGTGGCTTGAGCGAT 482
QY 666 IleHisArgAlaATPArgThrPheValIleuArgValArgAlaGlnAspProProGlu 705
DB 483 ATCCACAGGGCGCTGGCGACCTTCGTGCGTGTGGCGGCCAGAGACCCGCGCTGAG 542
QY 706 LeuTyRPhelValIysValAspValThrglyAlaTyRAspThrIleProGlnAspArgLeu 725
DB 543 CTGTACTTTTCACAGNN 602
QY 726 ThrGIuValIleAlaSerIleIleLysProGlnAsnThyTyRValArgArgTyRAla 745
DB 603 NNN 662
QY 746 ValValGlnIysAlaAlaHisGlyHisValArgIysAlaPheLysSerHisValSerThr 765
DB 663 NNN 722
QY 766 LeuThrAspLeuGlnProTyRMetArgGlnPheValAlaHisLeuGlnIuThrSerPro 785
DB 723 TTGACAGACCTCCAGCCGTAACGTGCGACAGCTTCGTGGCTCACCTGACGAGACCGCCA 782
QY 786 LeuArgAspAlaValIleGlnIuInserSerSerLeuAsnGluAlaSerSerGlyLeu 805
DB 783 CTGAGGAGATGCCGTATCATCGACGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 842
QY 806 PheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGlyLysSerTyR 825
DB 843 NNN 902
QY 826 ValGlnCyGlnGlyIleProGlnIySerIleLeuSerThrLeuLeuCySerIleuCyS 845
DB 903 GTCCAGGTGCGAGGGATCCCGCAGGGCTCCACCTGTGTCCACTGCTGCGAGCTGTGC 962
QY 846 TyRGIyAspMetGlnAsnIlyLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArg 865
DB 963 TACGGGACATGAAACAAAGCTGTTGGCGGATTTGGCGGAGACCGGCTGCTCTGCGT 1022
QY 866 LeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaIySerThrPheLeuArg 885
DB 1023 TTGGTGGAGATTTCTTGTGGTGAACCTCACCTCACCCAGCGGAAGCTTCTCCANG 1082
QY 886 ThrLeuValArgGlyValProGluTyRGIyCySValAsnLeuArgIySerThrValVal 905
DB 1083 ACCCTGTCCGAGAGTGTCCCTGAGTATGGCTCGTGTGAACCTTGGAGAGACAGTATG 1142
QY 906 AsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHis 925
DB 1143 AACTTCCCTGTAAGAGTGAAGGCTCGGTGGTGCAGCGCTTTGTTCAGTGGCGGCCAC 1202
QY 926 GlyLeuPheProTyRGIyLeuLeuLeuAspThrArgThrLeuGlnValAlaGlnSerAsp 945
DB 1203 GGCCTATTCCTCGTGTGGCTGCTGCTGCGACACCCGAGCCCTGGAGGTGAGAGCGAC 1262
QY 946 TyRSerSerTyRAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgIyPheIys 965
DB 1263 TACTCAGAGTATGCCCGGACCTCCATCNNNNCCAGCTCACCTTCAACCGCGGCTTCAAG 1322
QY 966 AlaGlyArgAsnMetArgArgIyIleuPheGlyValIleuArgLeuIyCyHisSerLeu 985
DB 1323 GCTGGAGAGAAATCGTGTGCAAACTTTGGGAGCTTGGCGCTGAAGTGCACAGCTTG 1382
QY 986 PheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyRHisIleLeu 1005
DB 1383 TTTTCGATTTTCAGTGAACAGCTCCAGACGGTGTGACCAACATCTCAANNCTCTTC 1442
QY 1006 LeuLeuGlnAlaTyRArgPheHisAlaCySValIleuGlnLeuProPheHisGlnGlnVal 1025
DB 1443 CTGCTGACAGCGTACAGGTTTACCGCATGTGTGTGACAGCTCCCATTCATCAGCAAGTT 1502

B0702370 851 bp mRNA linear EST IS-JUL-2003
 LOCUS UI-M-F10-byx-f-12-0-UI-r1 NIH BMAP_F10 Mus musculus cDNA clone
 DEFINITION IMAGE:6400523 5', mRNA sequence.
 ACCESSION B0702370
 VERSION B0702370.1 GI:23627105
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 851)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyx-5.

FEATURES Location/Qualifiers

1..851
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6400523"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="MDH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_F10"
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 to the protocol of Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CAGCCAGCAGC. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:
 Pred. No.: 3.6e-61 Length: 851
 Score: 1028.00 Matches: 197
 Percent Similarity: 80.85% Conservative: 31
 Best Local Similarity: 69.86% Mismatches: 52
 Query Match: 17.25% Indels: 2
 DB: 5 Gaps: 1

US-10-044-692-2 (1-1132) x B0702370 (1-851)

QY 738 ThrTyrCysValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLys 757
 Db 6 AGCTACTGATATCGCCAGATGCGATGCTCCGAGAGATGACCAAGGCCCAATCCACAG 65
 QY 758 AlaPheLysSerHisAlaSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheVal 777
 Db 66 TCCTTAGAGACAGAGTCCACCAACCTCTCTGACCTCCAGCAATATGCGCAGTCTCTT 125

QY 778 AlaHisLeuGlnGlnThr-----SerProLeuArgAspAlaValAlaIleGlnGlnSer 795
 Db 126 AAGCATTTGACGATTCAGATTCGACATGCACTGAGAACTCCGTTGTCTGACGACAGAG 185
 QY 796 SerSerLeuAsnGlnAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHis 815
 Db 186 ATCTCTATGATGATGAGACACAGCAGCCTGTTGACTCTTCTTGACATCTTCGCTC 245
 QY 816 HisAlaValArgIleArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySer 835
 Db 246 AGTCTCTTAAGATTTGTGTGACAGGTCTATACGACAGTCCAGGGCATCCCCAGGGCTCC 305
 QY 836 IleLeuSerThrLeuLeuLeuCysSerLeuCysTyrGlyAspPheGlnLysLeuPheAla 855
 Db 306 AGCTATTCACCTCTGCTCTGACAGCTGTGTGTGGAACATGAGAAACAAGCTGTTGCT 365
 QY 856 GlyIleArgArgAspGlyLeuLeuLeuLeuValAspAspPheLeuLeuValThrPro 875
 Db 366 GAGGTGCGCGGAGTGGTGTCTTTACGTTTGTGTATACCTTCTGTTGTTGACGCCCT 425
 QY 876 HisLeuThrHisAlaLysThrPheLeuArgThrLeuValArgGlyValProGluTyrGly 895
 Db 426 CACTTGGACCAAGCAAAACCTTCTCAGACACCTGGTCCATGGCGCTTCCGAGTATGGG 485
 QY 896 CysValValaLeuLeuArgLysThrValValaAsnPheProValGluAspGluAlaLeuGly 915
 Db 486 TGCATGATTAACCTTGACAGACAGAGTGTGAACCTTCCCTGTGAGCCTGTTACCTGGCT 545
 QY 916 GlyThrAlaPheValAlaGlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeu 935
 Db 546 GGTGACGCTCCATACACAGCTGCTGCTCTACCTGCTGTTCCCTGTTGGTGGCTTCTGCT 605
 QY 936 AspThrArgThrLeuGlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArg 955
 Db 606 GACACTCAGACTTTGAGAGTGTCTGTGACTACTACAGGTATGCCCAGACTCAATTAAG 665
 QY 956 AlaSerLeuThrPheAsnArgGlyPheLysAlaGlyAsnMetArgArgLysLeuPhe 975
 Db 666 ACAGGCTTCACCTTCAGAGTGTCTTCAGAGTGTGAGGAGACCAAGCAACAGCTCTG 725
 QY 976 GlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnValaAsnSerLeuGln 995
 Db 726 TCGGTCTTCGGTTGAAGTCAAGCTGATATTCTTCAAGCTTGAGAGTGAACAGCTCCAG 785
 QY 996 ThrValCysThrAsnIleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCys 1015
 Db 786 ACAGTCTGATCAATATATACAAAGATCTTCCTTCAGAGCTTCAAGCTTCAATGCAAT 845
 QY 1016 ValLeu 1017
 Db 846 GTGATT 851

RESULT 6
 BG917907 851 bp mRNA linear EST 05-JUN-2001
 LOCUS 602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
 DEFINITION mRNA sequence.
 ACCESSION BG917907
 VERSION BG917907.1 GI:14298383
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 851)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DB: 4 Gaps: 0

US-10-044-692-2 (1-1132) x BM824748 (1-492)

QY 905 ValAsnProValGlnAspGlnAlaLeuGlyGlyThrAlaPheValGlnMetProAla 924
 Db 1 GTGAACCTTCCTGTAAGAAAGACAGAGCCCTGGGTGGACAGCTTTGTTGTCAGATGCCGGCC 60

QY 925 HisGlyLeuPheProThrCysGlyLeuLeuAspThrArgThrLeuGlnValGlnSer 944
 Db 61 CACGGCTATTCCTCCGAGGCGGCTGCTGCTGATACCCGAGCCCTGGAGGTGCAGAGC 120

QY 945 AspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPhe 964
 Db 121 GACTACCTCCAGCATGACCCGAGCCTCCATCAGAGCCAGCTCACTTCAACCGCGCTTC 180

QY 965 LysAlaGlyArgAsnMetArgGlyLeuPheGlyValLeuArgLeuLysCysHisSer 984
 Db 181 AAGGCTGGGAGAACATGCTCCCAACTCTTGGGGCTCTGGAGCTGAAGTGTCAAGC 240

QY 985 LeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrIle 1004
 Db 241 CTGTTTGTGATTTGACGTGAAGCCTCCAGACGGTGTGCACAACTTCAAGATC 300

QY 1005 LeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGln 1024
 Db 301 CTCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGTGAGCTCCCATTTCAACAGCA 360

QY 1025 ValThrLysAsnProThrPheLeuArgValIleSerAspThrAlaSerLeuCysTyr 1044
 Db 361 GTTGGAAAGACCCCAATTTTCTGCGCTCATCTGACAGGCGCTCCCTGCTAC 420

QY 1045 SerIleLeuLysAlaLysAsnAla 1052
 Db 421 TCCATCTCGAAGACCAAGACGA 444

RESULT 8
 BQ258274 664 bp mRNA linear EST 06-MAY-2002
 LOCUS NISC kp11904.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone
 DEFINITION IMAGE:5409222, mRNA sequence.
 BQ258274
 ACCESSION BQ258274.1 GI:20459030
 VERSION BQ258274.1 GI:20459030
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 664)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 CDNA Library Preparation: J. Baker (Stanford University)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 info@image.lnl.gov
 MGI:1645958
 PLACE: LMAN12043 row: N column: 7
 Seg primer: Sp6 primer.
 Location/Qualifiers
 1..664
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /IMAGE:5409222
 /issue_type="embryo, late gastrula"

ORIGIN

/dev stage="embryo, 7.5 dpc"
 /lab_host="XLI-Blue"
 /clone_lib="Baker mouse embryo e7.5"
 /note="vector: pCS105; site_1: NotI; site_2: SalI; cDNA
 made by oligo-dt priming. Directionally cloned into
 SalI/NotI sites using the following 5' adaptor:
 5'-TCACCCACGCGCTCCG-3'. Size-selected for average insert
 size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
 University)."

Alignment Scores:
 Pred. No.: 1,59e-43 Length: 664
 Score: 771.50 Matches: 153
 Percent Similarity: 72.03% Conservative: 17
 Best Local Similarity: 64.83% Mismatches: 45
 Query Match: 12.94% Indels: 21
 DB: 5 Gaps: 2

US-10-044-692-2 (1-1132) x BQ258274 (1-664)

QY 352 ProSerLeuThrGlyAlaArgArgLeuValGlnThrIlePheLeuGlySerArgProTyr 371
 Db 10 CCTAATGACTGGAGGCGAGAGACTGTGTGATATCTTTCTGGGCTCAAGGCTTAG 69

QY 372 MetProGlyThrProArgArgLeuProArgLeuProGlnArgTyrTyrGlnMetArgPro 391
 Db 70 ACATCAGAACACATCTGCAGAGACACACCTCTATCGGCTGATCTGGCAGATGCCGCC 129

QY 392 LeuPheLeuGlnLeuLeuGlyAsnHisAlaGlnCysProTyrGlyValLeuLeuLysThr 411
 Db 130 GTTGTTCACAGCTGCTGCTGTAACCAAGAGAGTCCCAATATGCAACATCTCTAGTCA 189

QY 412 HisCysProLeuArgAlaAla-----ValThrProAlaAlaGlyValCysAlaArg 428
 Db 190 CATTGACAGTTTCCAGACAGAACCAACAGGTGACAGATGCCCTG----- 234

QY 429 GlnLysProGlnGlySerValAlaAlaProGlnGlnGlnAspThrAspProArgArgLeu 448
 Db 235 -----AACCCAGCCACCGCACCTC 255

QY 449 ValGlnLeuLeuArgGlnHisSerSerProTyrGlnValTyrGlyPheValArgAlaCys 468
 Db 256 ATGAGATTGCTCCGCTGCAGACAGCTCCCTGCGAGATATGTTTCTTCGGGCGCTGT 315

QY 469 LeuArgArgLeuValProProGlyLeuTyrGlySerArgHisAsnGlnArgArgPheLeu 488
 Db 316 CTCTGCAAGGTGTGTCTAGTCTCTGGGGGTACAGGACCAATGAGCGCGCTTCTTT 375

QY 489 ArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLysLeuSerLeuGlnLeu 508
 Db 376 AAGAACCTTAAGAGATTCATCTGTGGGGAATACGGCAGACTTCACTGACGAGAACTC 435

QY 509 ThrTyrLeuMetSerValArgAspCysAlaTyrPheArgArgSerProGlyValGlyCys 528
 Db 436 ATGTGAAATGAAATAGATAGATTTGCACTGCTCCGACAGGCCAGGAAAGACCTT 495

QY 529 ValProAlaAlaGlnHisArgLeuArgGlnGlnIleLeuAlaLysPheLeuHisTyrPhe 548
 Db 496 GTCCCGCTGCAGAGACCGTCTGAGGAGAGAGATCTGACGTTCTCTTCTGCGCTG 555

QY 549 MetSerValTyrValAlaGlnLeuLeuArgSerPhePheTyrValThrGlnThrPhe 568
 Db 556 ATGACACATACATGTTGACAGCTGCTTAGGTCACTTTTACATCAGAGACACATTTC 615

QY 569 GlnLysAsnArgLeuPhePheTyrArgLysSerValTyrSerLysLeu 584
 Db 616 CAGAAAGACGCGCTTCTCTACCGTAAAGATGTGAGCAAGCTG 663

RESULT 9
 CR688161 1424 bp mRNA linear HTC 12-AUG-2004
 LOCUS Tetraodon nigroviridis full-length cDNA.
 DEFINITION

ACCESSION	CR688161
VERSION	CR688161.1 GI:51186068
KEYWORDS	HTC; cDNA; full-length; Tetraodon nigroviridis.
SOURCE	Tetraodon
ORGANISM	Tetraodon
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neuteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes; Tetradontoidea; Tetradontidae. 1 (bases 1 to 1424)
AUTHORS	Genoscope.
TITLE	Direct Submision
JOURNAL	Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : seqet@genoscope.cns.fr - Web : www.genoscope.cns.fr) The sequences are based on single pass reads. More information available at http://www.genoscope.cns.fr/tetraodon .
FEATURES	
source	location/Qualifiers 1..1424 /organism="Tetraodon" /mol_type="mRNA" /db_xref="taxon:47144" /cissue_type="Eye"
ORIGIN	
Alignment Scores:	
Pred. No.:	8.77e-37 Length: 1424
Score:	682.00 Matches: 155
Percent Similarity:	58.36% Conservative: 51
Best Local Similarity:	43.91% Mismatch: 140
Query Match:	11.44% Indels: 8
DB:	Gaps: 3 Gaps: 3
US-10-044-692-2 (1-1132) x CR688161 (1-1424)	
Oy	780 LeungGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerLeuAen 799
Dd	21 CTGCAGAAAAAGGAGAATTCACCACCTCAATACTGGTAGACAGCATTTCTTCAGAT 80
Oy	800 GluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArg 819
Dd	81 CTACACAGAAAGATGCACGTGAATTCTTTACTCAATCTTAACGGCGACGCTGTTAAG 140
Oy	820 IleArgGlyLysSerTyrrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThr 839
Dd	141 TTTGGAAAAAAAACATACACAGACAGAGGGGGTTCTCCAGGAGATCTGCTGTACAT 200
Oy	840 LeuLeuCysSerLeuCystyrGlyAspMetGluAsnLysLeuPheAlaGly--IleArg 858
Dd	201 GTGCTTTCCTGCTCTGCTATGCTGTATGAGAAAGTCTCTATTCAGAGACATCATTA 260
Oy	859 ArgAspGlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThr 878
Dd	261 AACAAAGGCTCTTATATGAGACTGGAGTGAGTCTCTCTATATCACCCCTGACCGCG 320
Oy	879 HisAlaLysThrPheLeuArgThrLeuValIAsGglyValProGlnLysGlyCysValAl 898
Dd	321 GACGCACACAGACTTTTGAAGAATCTGCTGCGCGGGGTCCCTCAGATAGTGTTGGGGCT 380
Oy	899 AsnLeuArgLysThrValValAsnDheProValGluAspGluAlaLeuGlyIleThrAla 918
Dd	381 AATCTCGAAGAGATGTGGTCAATTTTGAAGATTTCAGAGACAACACTCTTGCTCGGC 440
Oy	919 PheValGlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArg 938
Dd	441 ATTGCTGTGCTTCCCCTACGCTGCCCTCTTCCCCCTGGTGGAAGCTGCTGLGGAATAC 500
Oy	939 ThrLeuGlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeu 958
Dd	501 AATCTCGACATCTAATAAGACTAATTTCTACTAATGCAACCTGCTTGCGGCTACAGCCTT 560
Oy	959 ThrPheAsnArgGlyPhenylalaGlyArgAsnMetArgArgLysLeuDeuNeglyValLeu 978

[illegible]

/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	2,696-36	Length:	649
Score:	667.50	Matches:	153
Percent Similarity:	46.32%	Conservative:	17
Best Local Similarity:	41.69%	Mismatches:	32
Query Match:	11.20%	Indels:	165
DB:	7	Gaps:	3

US-10-044-692-2 (1-1132) x CF531069 (1-649)

```

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
DB 42 ATGACCGCGCTCTGCTGCGCGCGCTCTCTGCTGCGCGCGCGCGCGCGCGAG 101
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPargLeuValGln 40
DB 102 GTGGGCGCGCTGGAGACCTTGCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCG 161
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 162 CCGCGGAGCGGAGATCAACCGCATTTGGTTGCCAATGGCTCAGTGTGCATGCACCTGG 221
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnAlaSerCysLeuValArgLeu 80
DB 222 GGCTCAGCGCTCCACCTGCGCGCGCTCTTCCACACGAGGTGATCCCTGAAAGACTG 281
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyValArgGlyAlaValAsnValLeuAlaPheGly 100
DB 282 GTGGCGCGGTTGGCAGAGCTCTGCGAGGCGAAGAGAAAGCGTGGCGTTTGGC 341
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrSerValArg 120
DB 342 TTGAGCTGCTTAACGAGCGCAGAGCGCGGCTCCCATGGCTTCACCTAGTAGCGTGGC 401
QY 121 SerTyrLeuProAlaThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
DB 402 AGCTACTTGGCCCACTGTTATTTGAGACCTGCGGTGTCAGTGTGATGATGATCTCTG 461
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 462 TTGACCGCAGTGGGAGACGACCTGCTGTCTACCGTGGCAGACCTGGCTTTATCTT 521
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 522 CTGGTGGCCCCCAGCTGTGCTTAC----- 545
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 545 ----- 545
QY 201 ArgAlaTyrPasnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 545 ----- 545
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuArgProArgArg 240

```

```

DB 545 ----- 545
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 546 ----- 557
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaAlaProAlaGlu 280
DB 557 ----- 557
QY 281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 557 ----- 557
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrPasnPro 320
DB 558 ----- 569
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
DB 569 ----- 569
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 570 ---AAACCTCATTTCTACTCAGCANCTCCAGCTTAACCTGACCTGGCGCCAGAGACTG 626
QY 361 ValGluThrIlePheLeuGly 367
DB 627 GTGAGATCATCTTTCTGGGC 647

```

RESULT 11

CF531121 688 bp mRNA linear EST 12-SEP-2003
 UI-M-FY0-CGP-m-21-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
 IMAGE:30355988 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Seq primer: pYX-5,

Location/Qualifiers

1..688

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30355988"

/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-vec vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGCAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemmi Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	3,456-36	Length:	688
Score:	666.50	Matches:	154
Percent Similarity:	46.34%	Conservative:	17
Best Local Similarity:	41.73%	Mismatches:	32
Query Match:	11.18%	Indels:	166
	7	Gaps:	2

US-10-044-692-2 (1-1132) x CF531121 (1-688)

```

Oy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTryrArgIu 20
Db 79 ATGACCCGGCTCTCTGTTGCCCGGGTGGCTCTCTCTCTGCGAGCCGATACCGGGAG 138

Oy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTryrArgLeuValGln 40
Db 139 GTGTGGCCGCTGGCAACCTTTGTGGCGCCCTGGGGCCCGAGGGCGGGCTTGTGCA 198

Oy 41 ArgGlyAerProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTr 60
Db 199 CCGGGGAGCCCAAGATCTACCGCACTTTGTGGCCATGCTTACTGTCATGCACTGG 258

Oy 61 AspaIaArgProProAlaAlaProSerPheArgGlnValSerCysLeuGlyLeu 80
Db 259 GGCTACAGCTCCACCTGCTTCTTCCACAGAGTGTCACTCCCTGAAGAGCTG 318

Oy 81 ValAlaArgValLeuGlnArgLeuGlyCysGlyValAlaAsnValLeuAlaPheGly 100
Db 319 GTGGCCAGGTTGTGAGAGCTGCGAGCCGACGAGAGAAACCTGTGCTTTGGC 378

Oy 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrHisSerValArg 120
Db 379 TTGAGCTGCTTACAGAGCCAGAGGGGGCTCCATGCTTCACTAGTACGCTGCT 438

Oy 121 SerTyLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValaTrpGlyLeuLeu 140
Db 439 AGCTACTTGGCCCAACCTGTATTGAGACCTGCGCTGTCAGTGTGTCATGCTACTG 498

Oy 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 499 TTGAGCCGAGTGGGCGACGACGCTGCTGCTTACCTGCTGCGACACCTGCTTATCTT 558

Oy 161 LeuValAlaProSerCysAlaTrpGlnValCysGlyProProLeuTrgInLeuGlyAla 180
Db 559 CTGGTGGCCCGCCACGCTGCTTAC----- 582

Oy 181 AlaTrgInAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
Db 582 ----- 582

Oy 201 ArgAlaTrpAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 582 ----- 582

Oy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProlyAsnArgProArgArg 240
Db 582 ----- 582

Oy 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTrpAlaHisProGln 260
Db 583 ----- 598

```

```

Oy 260 YArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
Db 598 ----- 598

Oy 280 uGlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGln 300
Db 598 ----- 598

Oy 300 YArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAsnThrPr 320
Db 598 ----- 598

Oy 320 cCysProProValTyrAlaGlnThrIleHisPheLeuTrpSerSerGlyAspLeuGlnGln 340
Db 599 ----- 603

Oy 340 nLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLe 360
Db 604 TCTAAACCCCTCATCTCTACTGAGCAGCTCAGCCTTAAGTGAAGGCGCAGAGACT 663

Oy 360 uValGlnThrIlePheLeuGlySer 368
Db 664 GGTGGAGATCATCTTTCTGGGCTCA 688

RESULT 12
AA281296 389 bp mRNA linear EST 14-NOV-1997
z108g02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
mRNA sequence.
AA281296 GI:1924194
AA281296.1
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2187 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 385.
Location/Qualifiers
1..389
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:712562"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
/note="vector: pT73-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCATCTGAAGTGGAGCGCGCCCTCATTTTCTTTTCTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

ORIGIN

Db	295	GGCTCAGACGCTCCACCTGCGGACCTTTCCTTCCACACAGTGTATCCCTTAAGAGCTG	354
QY	81	Val1AaargVal1LeuGlnAargLeuCySGluAargGlyAlaIyAaenVal1LeuAlaPheGly	100
Db	355	GTGGCCAGGGGTGTGTGCAGAGACTGCTGCAGCGCAACAGAGAAACGTGTGGCTTTGGC	414
QY	101	PheAlaLeuLeuAaPbGlyAlaAargGlyGlyProProGua1AlaPheThThSerValAarg	120
Db	415	TTTAAAGCTGCTTAACAGGAGCGAGGCGGGGCTCCCATGCGCTTCACTAGTAAGCGTGCT	474
QY	121	SerTyLeuProAenThVal1ThAaPbAlaLeuAargGlySerGlyAlaATrGlyLeuLeu	140
Db	475	AGCTACTTGCCCAACACCTGTTATTGAGACCTGCGTGTCACTGTGTGATGTGATGCTACTG	534
QY	141	LeuAargAargValGlyAaPbAargVal1LeuAlaIyAaenVal1AargCySAlaLeuPheVal	160
Db	535	TTGAGCGGAGTGGGGGAGACGACTGTGTCTTACCTGCTGACACTGTGACTCTTATCTT	594
QY	161	Leu	161
Db	595	CTG	597
RESULT 14			
LOCUS	CN274427	409 bp	mRNA linear EST 16-MAY-2004
DEFINITION	17000531326763 GRN_ES Homo sapiens CDNA 5', mRNA sequence.		
ACCESSION	CN274427		
VERSION	CN274427.1	GI:47290841	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 409)		
AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Rang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.M.		
JOURNAL	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation		
COMMENT	Nat. Biotechnol. 22 (6), 707-716 (2004)		
FEATURES	Contact: Brandenberger R		
source	Regenerative Medicine		
	Genon Corporation		
	230 Constitution Drive, Menlo Park, CA 94025, USA		
	Tel: 650 473 8658		
	Fax: 650 473 7760		
	Email: rbrandenberger@genon.com		
	Insert Length: 409 Std Error: 0.00.		
	Location/Qualifiers		
	1..409		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"		
	/clone_lib="GRN ES"		
	/note="Oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p13), H7 (p25), and H9 (p26) maintained in feeder-free conditions"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1,286-29	Length:	409
Score:	567.00	Matches:	108
Percent Similarity:	99.08%	Conservative:	0
Best Local Similarity:	99.08%	Mismatches:	1
Query Match:	9.51%	Indels:	0
DB:	7	Gaps:	0
US-10-044-692-2 (1-1132) x CN274427 (1-409)			
QY	1	MeCPROA1GALAPROA1GYSa1gAlaValA1ArgSerLeuA1ArgSerH1eTyA1ArgGlu	20

Dn		82	ATGCGGGCCCTCCCCCTCCAGCGGTGCCTCCTGCTGCCAGCACTACCGGAG	141
Qy		21	VallieuProLeuAlathrPheValArgArgUeuGlyProGlnGlyTTPArgLeuValGln	40
Dn		142	GTCGTGCGCTGGCCAGTGTCGTGCGCGCGCTGGCGGCCAGAGCTGCGCTGTGTCAG	201
Qy		41	ArgGLysAProAlaaIaphenArgAlaleuValaaGlnCysLeuValCysValProThr	60
Dn		202	CGCGGGAGACC GGCGGCTTTCCGGCGCCTGTGTGCCAGGTCCGTGTGTGCTCCCTGG	261
Qy		61	AspAlaArgProPProfoAlaaIaProSerPheArgGlnValSerCysLeuYSGluLeu	80
Dn		262	GACGACGCGCGCCCCCGCGCCCTCTCTCCGACAGGTGTCTGCTGAAGAAGACTG	321
Qy		81	ValAlaArgValleuGlnArgLeuCysGluArgGlyAlalaYsaenValleuAlaPheGly	100
Dn		322	GTGGCCGAGTGTGTGACAGAGGTGTGTGAGAGCGCGCGAAGAACGTGTGCTGCCTTACGC	381
Qy		101	PheAlaLeuLeuAspGlyAlaArgGly	109
Dn		382	TTCGCTGTGTGACGAGCGCGCGCGG	408

RESULT 15						
LOCUS	BE371943	866 bp	mRNA	linear	EST 21-JUL-2000	
DEFINITION	60121772BF1 NCI CGAP Lu29 Mus musculus cDNA clone IMAGE:3586614 5'					
ACCESSION	BE371943					
VERSION	BE371943.1 GI:9317215					
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)					
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov					
JOURNAL	Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.jnl.gov					
COMMENT	Plate: LHAM6748 row: h column: 07 High quality sequence stop: 639. Location/Qualifiers					

FEATURES	
source	1..866
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="CZECH II"
	/db_xref="taxon:10090"
	/clone="IMAGE:3586614"
	/tissue type="spontaneous tumor, metastatic to mammary."
	stem cell origin."
	/lab_host="DH10B"
	/clone_id="NCI_CGAP_Lu29"
	/note="Organ: lung; Vector: pCMV-SPORT6, Site 1: SalI, Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

Alignment Scores:			
Pred. No.:	4,72e-29	Length:	866
Score:	566.00	Matches:	108
Percent Similarity:	82.31%	Conservative:	13
Best Local Similarity:	73.47%	Mismatches:	26
Query Match:	9.50%	Indels:	0

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 10:30:52 ; Search time 7841 Seconds
(without alignments)
5260.780 Million cell updates/sec

Title: US-10-044-692-2
5961
Sequence: 1 MPRAPRCRAVSLRSHYRE.....TALSAANPALPSDFKTLTD 1132

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_plus_p2n.model -DEV-xlh
-O=/cgn2.1/USPTO_epool/US10044692/runat_28102004_113043_5483/app_query.fasta_1.1287
-DB=EST -QFMT=fastp -SUFFIX=trc -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45
-DOCALL=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=trc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044692@cgn2.1 1.14804@runat_28102004_113043_5483 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_esc1:*
2: gb_esc2:*
3: gb_hic:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2645	44.4	1826	9	AY407349
2	2168	36.4	1584	9	AY407350
3	1805	30.3	1835	9	AY407351
4	1406	23.6	925	4	BM453198
5	1028	17.2	851	5	BU702370
6	875	14.7	851	4	BC917907
7	776	13.0	492	4	BM824748
8	771.5	12.9	664	5	BO258274
9	682	11.4	1424	3	CR688161

10	667.5	11.2	649	7	CF531069	CF531069	UI-M-FY0-
11	666.5	11.2	688	7	CF531121	CF531121	UI-M-FY0-
12	646	10.8	389	1	AA281296	AA281296	UI-M-FY0-
13	610	10.2	599	2	BB618671	BB618671	UI-M-FY0-
14	567	9.5	409	7	CN274427	CN274427	170005313
15	566	9.5	866	2	BB371943	BB371943	601217728
16	554	9.3	614	4	BB651920	BB651920	BB651920
17	517	8.7	775	4	B1388013	B1388013	BFL26_002
18	515	8.6	753	5	BU452535	BU452535	603767927
19	484.5	8.1	846	7	CN505902	CN505902	AGENCOURT
20	481.5	8.1	880	5	BU377259	BU377259	603811228
21	463	7.8	668	6	CA380121	CA380121	659344 NC
22	457	7.7	724	5	BA889962	BA889962	BA889962
23	449.5	7.5	632	6	CA353864	CA353864	625449 NC
24	443.5	7.4	715	2	BE396925	BE396925	601290610
25	437	7.3	703	5	BE331258	BE331258	BE331258
26	436	7.3	344	7	CF531258	CF531258	UI-M-FY0-
27	425	7.1	409	1	AA311750	AA311750	EST182469
28	425	7.1	679	2	BE396606	BE396606	601289077
29	424	7.1	835	5	BU111946	BU111946	603127372
30	422	7.1	649	2	BE514070	BE514070	601316575
31	411	6.9	610	2	BE514188	BE514188	601316376
32	395.5	6.6	696	5	BU139751	BU139751	603134527
33	387	6.5	343	6	BY783093	BY783093	BY783093
34	384	6.4	338	6	BY784804	BY784804	BY784804
35	380	6.4	336	6	BY755178	BY755178	BY755178
36	377	6.3	347	2	AM244516	AM244516	BR ENDOCB
37	374	6.3	346	5	BY149368	BY149368	BY149368
38	373	6.3	641	8	AM2972318	AM2972318	2M0246P07
39	366	6.1	619	7	CK392784	CK392784	K0850A03-
40	357.5	6.0	779	2	BE268183	BE268183	601125261
41	348.5	5.8	875	5	BU122597	BU122597	603148441
42	348.5	5.8	930	7	CO014076	CO014076	EST802411
43	344	5.3	983	7	CO028055	CO028055	EST806439
44	307	5.2	1023	7	CO024489	CO024489	EST802873
45	291.5	4.9	774	7	CF547884	CF547884	AGENCOURT

ALIGNMENTS

RESULT 1
AY407349
LOCUS
DEFINITION
Homo sapiens TERT gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION
AY407349.1 GI:39763320
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 1826)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D., Adams, M.D. and Cargill, M.
Infering nonneutral evolution from human-chimp-mouse orthologous gene trios

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 1826)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT
FEATURES
source
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
1..1826

gene
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..1826
 /gene="TERT"
 /locus_tag="HCM2861"

ORIGIN

Alignment Scores:

Pred. No.:	4,896-173	Length:	1826
Score:	2645.00	Matches:	526
Percent Similarity:	86.66%	Conservative:	0
Best Local Similarity:	86.66%	Mismatches:	81
Query Match:	44.37%	Indels:	0
DB:	9	Gaps:	0

US-10-044-692-2 (1-1132) x AY407349 (1-1826)

```

QY      526 ValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnIleLeuAlaLysPheLeu 545
DB      3 GTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGAGAGATCCTGGCCAAAGTTCTCG 62
QY      546 HisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhePheTyrValThrGlu 565
DB      63 CACTGGCTGATGATGTTGTAAGTCTGTCGAGCTGCTCAGGCTCTTTTATATGTCAGGAG 122
QY      566 ThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGln 585
DB      123 ACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGAAGATGTCTGGAGCAAGTTGCA 182
QY      586 SerTleGlyTleArgGlnHisLeuLysArgValGlnLeuArgGlnLeuSerGlnAlaGlu 605
DB      183 ACATATGGAATCAGACAGACATTGAAGAGGTGCACCTCGGAGCTGTCCGAGACAGAG 242
QY      606 ValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArgLeuArgPheIlePro 625
DB      243 GTACGACAGCATCTGGAGAACAGGCGCCGCTGCTACGTCAGACTCCGCTTCATCCCC 302
QY      626 LysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlnAlaArgThrPhe 645
DB      303 AAGCTGACGGGCTGGCGCGCATTTGGAACATGACATTAAGTCTGTGGAGCCAGAACGTTTC 362
QY      646 ArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAlaLeuPheSerValLeu 665
DB      363 CCACAGAAAGAGGCGCCAGCGCTCTCACCTCGAGGGTGAAGCACTGTTCAAGCGTCTC 422
QY      666 AsnTyrGlnArgAlaArgArgProGlyLeuLeuGlnAlaSerValLeuGlyLeuAspArg 685
DB      423 AACTACGAGCGGGCGCGCGCCCGGCTCTCGGCGCTCTGTGCTGGGCTCGAGCGAT 482
QY      686 IleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspProProGln 705
DB      483 ATCCACAGGGCGCTGGGCACTTTCGTGCTGCGGTGCGGGCCAGAGACCCGCGCTGAG 542
QY      706 LeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGlnAspArgLeu 725
DB      543 CTGTACTTTGTCAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 602
QY      726 ThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArgArgTyrAla 745
DB      603 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 662
QY      746 ValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHisValSerThr 765
DB      663 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 722
QY      766 LeuThrAspLeuGlnProTyrThrCargLysPheValAlaHisLeuGlnGlnLysSerPro 785
DB      723 TTGACAGACCTCCAGCGTACATGACAGAGTTCTGTGCTCACCTGCAGAGACAGCCCG 782
QY      786 LeuArgAspAlaValValIleGlnGlnSerSerSerLeuAsnGlnAlaSerSerGlyLeu 805
DB      783 CTGAGGAGTGGCTGTCTCATCGAGCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 842

```

```

QY      806 PheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGlyLysSerTyr 825
DB      843 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 902
QY      826 ValGlnCysGlnGlyIleProGlnLysSerIleLeuSerThrLeuLeuCysSerLeuCys 845
DB      903 GTCCAGTGGCAGGGGATCCCGCAGGGGCTCATCTCTCCACGCTGCTGCAGCGCTGTGC 962
QY      846 TyrGlyAspMetGlnAsnLysLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArg 865
DB      963 TACGGCGCATGGAAGAACAGGCTGTTGGGGGATTCGGGGAGCGGCTGCTCTGCGCT 1022
QY      866 LeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThrPheLeuArg 885
DB      1023 TTGGTGGAGATTTCTTGTGGTGAACCTCACCTCACCCACGCAAAACCTTCTCCAGG 1082
QY      886 ThrLeuValArgGlyValProGlnTyrGlyCysValValAsnLeuArgLysThrValVal 905
DB      1083 ACCCTGATCCGAGAGTGTCCCTGATGAGTGTGCTGCTGTAACCTTGCGAAGACAGTGTG 1142
QY      906 AsnPheProValGlnAspGlnAlaLeuGlnGlyThrAlaPheValGlnMetProAlaHis 925
DB      1143 AACTTCCCTGTAGAAAGACAGGCTCTGGGTGGACAGGCTTTGTTCAGATGCCGAGCCAC 1202
QY      926 GlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGlnValGlnSerAsp 945
DB      1203 GGCCTATTCCCTGGTGGCGGCTGCTGCTGATACCCGACCTGAGAGTGCAGAGCGAC 1262
QY      946 TyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheLys 965
DB      1263 TACTCCAGCTATGCCCGGACCTCCATCAGAGCACTGTCACCTTCAACCGCGCTTCAAG 1322
QY      966 AlaGlyArgAsnMetArgArgLysLeuPheGlyValIleuArgLeuLysCysHisSerLeu 985
DB      1323 GCTGGAGAGAACATCGTGGCAAACTTTTGGGGCTTGGGCTTAAGTGTACAGCTTG 1382
QY      986 PheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrLysIleLeu 1005
DB      1383 TTCTCGAATTCAGATGTAAGAGCTCCAGACGGTGTGACCAACATCTACAAAGATCTTC 1442
QY      1006 LeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGlnGlnVal 1025
DB      1443 CTGCTGACGGCGCTACAGGTTTCCAGCATGTGTGTCAGCTCCCATTCATCAGCAAGTT 1502
QY      1026 TrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCysTyrSer 1045
DB      1503 TGGAAAGAACCCACATTTTCTGCGCGTCACTCTGACACGGCTTCCCTCTGCTACTCC 1562
QY      1046 IleLeuLysAlaLysAsnAlaGlyMetSerLeuGlnAlaLysGlyAlaAlaGlyProLeu 1065
DB      1563 ATCTGAAAGCCAAAGAACAGAGATGTGCTGGGGGCGCAAGGGCGCGCGCCCTCTG 1622
QY      1066 ProSerGlnAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeuThrArgHis 1085
DB      1623 CCTCCGAGGCGGTCCAGGTGTCGACCAAGAGATTCCTGCTCAGAGTGCAGCAC 1682
QY      1086 ArgValThrTyrValProLeuLeuGlySerLeuAcgTTrpAlaGlnThrGlnLeuSerArg 1105
DB      1683 CGTGTACCTACGTGCTCACTCTGGGGTCACTCAGAGACAGCCCAAGCAGCTGAGTGG 1742
QY      1106 LysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsnProAlaLeuProSer 1125
DB      1743 AAGCTCCCGGGAGCAGACGCTGCTGCGGAGGCGCGAGCCCAACCCGAGCACTGCCCTCA 1802
QY      1126 AspPheLysThrIleLeuAsp 1132
DB      1803 GACTTCAAGACCATCTGTGAC 1823

```

RESULT 2
 LOCUS AY407350 1584 bp DNA linear GSS 15-DEC-2003
 DEFINITION Pan tiroglydyes TERT gene, VIRUTAL TRANSCRIPT, partial sequence,

genomic survey sequence.
 AY407350 GI:39763321
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 1 (bases 1 to 1584)
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1584)
 AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment
 FEATURES
 source 1..1584
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..>1584
 /gene="TERT"
 /locus_tag="HCM2861"
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,54e-140 Length: 1584
 Score: 2168.00 Matches: 432
 Percent Similarity: 82.73% Conservative: 4
 Best Local Similarity: 81.97% Mismatches: 91
 Query Match: 36.37% Indels: 0
 Gaps: 0
 US-10-044-692-2 (1-1132) x AY407350 (1-1584)
 QY 536 ValGlyCyValProAlaIaGluHisArgLeuArgGluGluIleuAlaLysPheLeu 545
 DB 3 GTTGGCTGTTCCGCCGCGACGACCGCTGCGAGAGATCTGGCCAAAGTTCTTG 62
 QY 546 HisTPLeuMetSerValIytrValValIGluLeuLeuArgSerPhePheTytrValThrGlu 565
 DB 63 CACTGGCTATGATGAGTGTGTACGTTGTTCGAGCTGCTCAGGCTCTTTTATATGTCAGCGAG 122
 QY 566 ThrThrPheGlnLysAsnArgLeuPhePheTytrArgLysSerValTrpSerLysLeuGln 585
 DB 123 ACCACGCTTTCAGAAAGACAGGCTCTTTCTACCGGAAGAGTGTGAGCAAGTTGCAA 182
 QY 586 SerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluIaGlu 605
 DB 183 AGCATTTGGAATCAGACAGACCTTGAAGAGGCTGCACCTCGGAGAGCTGTGGAAGACAG 242
 QY 606 ValArgGlnHisArgGluIaArgProAlaLeuLeuThrSerArgLeuArgPheIlePro 625
 DB 243 GTTCAGGCAATCAGAAAGCCAGGCGCGCTGCTACCTCCAGACTCCGCTTCATCCCC 302
 QY 626 LysProAsnGlyLeuArgProIleValAsnMetAspTytrValValGlyIaArgThrPhe 645
 DB 303 AAGCTGACGGGCTGGCGGATGTGAACATGAGACTACGTCGTGGAGCCAGAAAGTTTC 362
 QY 646 ArgArgGluLysArgIaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeu 665

DB 363 CGCAGAGAAAGAGGCGGAGCGTCTCACCTCGAGGGTGAAAGCACTGTTACGCGTGC 422
 QY 666 AsnTytrGluArgAlaArgArgProGlyLeuLeuGlnValaSerValLeuGluLysAsnAsp 685
 DB 423 ANNNACGAGGCGGCGGCGGCGGCGGCTCTGGGCGCTGTGTGTGGGCTTGAGCAT 482
 QY 686 IleHisArgAlaTrpArgThrPheValaLeuArgValaArgAlaGlnAspProProGlu 705
 DB 483 ATCCACAGGCGCTGCGGACCTTGCTGCTGCGGTGGCGGCGGCGGCGGCGGCTGAG 542
 QY 706 LeuTytrPheValaLysValaSerValThrGlyAlaTytrAspThrIleProGlnAspArgLeu 725
 DB 543 CTGTACTTTCCTCAAGNN 602
 QY 726 ThrGluValIleAlaSerIleIleLysProGlnAsnThrTytrCysValArgArgTytrAla 745
 DB 603 NNN 662
 QY 746 ValValGlnLysAlaAlaHisGlyHisValaArgLysAlaPheLysSerHisValaSerThr 765
 DB 663 NNN 722
 QY 766 LeuThrAspLeuGlnProTytrThrArgGlnPheValaAlaHisLeuGlnGluThrSerPro 785
 DB 723 TTGACAGACCTTCACGCGGATGACAGACAGTTCGTGGCTCACCTGACAGAGACAGCCCA 782
 QY 786 LeuArgAspAlaValaValIleGlnGlnSerSerSerLeuAsnGluLysSerGlyLeu 805
 DB 783 CTGAGGAGATGCCGTATCATCGACGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 842
 QY 806 PheAspValPheLeuArgPheMetCysHisAlaValaArgIleArgGlyLysSerTytr 825
 DB 843 NNN 902
 QY 826 ValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCysSerLeuCys 845
 DB 903 GTCCAGTGCAGGAGATCCCGCAGGAGCTTCATCTGTCCACGCTGCTGCAGCGCTGTGC 962
 QY 846 TytrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArg 865
 DB 963 TACGGGAGATGAGAAAGAGCTGTTGTGGGAGATTCGGGAGAGCGGCTGCTCCGCG 1022
 QY 866 LeuValaAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThrPheLeuArg 885
 DB 1023 TTGGTGAGATTTCTGTGTGTGACACTCACCTCACCCAGCGGAAAGCTTCCTCANG 1082
 QY 886 ThrLeuValaArgGlyValaProGluTytrGlyCysValaAsnLeuArgLysThrVala 905
 DB 1083 ACCCTGTCCGAGAGTGTCCCTGATGAGCTGCTGCTGTAACCTTGCGGAAGACAGTAGTG 1142
 QY 906 AsnPheProValaGluAsnGluAlaLeuGlyIleThrAlaPheValaGlnMetProAlaHis 925
 DB 1143 AACTTCCCTGTGAAGATAGGAGCCCTGGGTGACAGGCTTTGTTACGTGCGGCGCAC 1202
 QY 926 GlyLeuPheProTytrCysGlyLeuLeuLeuAspThrArgThrLeuGluValaGlnSerAsp 945
 DB 1203 GGCCTATTCCCTGTGTGCGGCTGCTGCTGACACCCGAGACCTGAGAGGTGACAGCGAG 1262
 QY 946 TytrSerSerTytrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheLys 965
 DB 1263 TACTCCAGGTATGCCGAGACTCCATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1322
 QY 966 AlaGlyArgAsnMetArgArgLysLeuPheGlyValaLeuArgLeuLysPheHisSerLeu 985
 DB 1323 GCTGGAGAGAAATGCTGCGAAACTTTTGGAGTCTTGGGCTGAAGTCAAGCTCG 1382
 QY 986 PheLeuAspLeuGlnValaAsnSerLeuGlnThrValaCysThrAsnIleTytrLysIleLeu 1005
 DB 1383 TTTCGTGATTTCAAGTGAACAGCTTCAGAGCGGTGTGACCAACATCAANNATCCCTC 1442
 QY 1006 LeuLeuGlnAlaTytrArgPheHisAlaCysValaLeuGlnLeuProPheHisGlnGlnVal 1025
 DB 1443 CTGTGACAGGCTACAGGTTTACGCGATGTGTGTCAGACTGCTCATATTCATGACAGAGTT 1502

QY 1026 TrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerIleuCysTyrSer 1045
DB 1503 TGGAAAGACCCCACTTTTCCGGCCATCATCTCGACACGGCCCTCTCTCTCTCC 1562
QY 1046 IleLeuAlaAlaLysAsnAla 1052
DB 1563 ATCTGAAAGCCAAAGACGCA 1583
RESULT 3
AY407351
LOCUS AY407351 1835 bp DNA linear GSS 15-DEC-2003
DEFINITION Mus musculus TERT gene, VIRTUAL TRANSCRIPT, partial sequence,
AY407351
ACCESSION AY407351
VERSION AY407351.1 GI:39763322
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1835)
AUTHORS Clark,A.G., Gdanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniatsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1835)
AUTHORS Clark,A.G., Gdanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniatsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..1835
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1835
/gene="TERT"
/locus_tag="HCM2861"
gene
ORIGIN
Alignment Scores:
Pred. No.: 1.17e-114 Length: 1835
Score: 1805.00 Matches: 373
Percent Similarity: 69.56% Conservative: 52
Best Local Similarity: 61.05% Mismatches: 176
Query Match: 30.28% Indels: 11
Gaps: 3
DB: 9
US-10-044-692-2 (1-1132) x AY407351 (1-1835)
QY 529 ValProAlaAlaGluHisArgLeuArgGluGluIleLeuAlaLysPheLeuHisTrpLeu 548
DB 12 GTCCCGCGTCGACAGACCGCTCTGAGGAGAGGATCTGCTACGTTCTCTCTGGCG 71
QY 549 MetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGlnThrThrPhe 568
DB 72 ATGGACACATACGCTGCTACAGCTGCTTACGTCATTCTTTACATCACAGAGGCACATT 131
QY 569 GlnTyrAsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGlnSerIleGly 588
DB 122 CAGAGAAACAGGCTCTTCTTACCGTTAGAGTGTGTGAGCAGAGTGCAGACATTGGA 191
QY 589 IleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluAlaGluValArgGln 608

DB 192 GTACGACCAACCACTTGAGAGAGTGGGCTACCGGAGCTGTACAGAGAGAGTCCAGCAT 251
QY 609 HisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArgPheIleProLysProLys 628
DB 252 CACAGAGACCTGGCTAGCCATGCCCATCTGCACATCGCGCTTATCCCAAGCCCAAC 311
QY 629 GlyLeuArgProIleValAsnMetAspTyrValValGlyAlaArgThrPheArgGlu 648
DB 312 GGCCTGGGCCCATTTGTGAATGAGTTTATGACATGGTATCCAGAGCTTTGGCGAGAG 371
QY 649 Lys-ArgAlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeuAsnTyrG 668
DB 372 AAGCAGGGCCGACATTACACCGACGTCCTCAAGACTCTCTTACAGATGCTCAATGTA 431
QY 668 ValArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGlyLeuAspAspIleHisAr 688
DB 432 GCGGACAAACATCTTCACCTTATGGGCTTCTGTACTGGGTATGATGACATCTACG 491
QY 688 GAlATrPArgThrPheValIleuArgValArgAlaGlnAspPropProGluLeuTyrPh 708
DB 492 GACCTGGCGGCTTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
QY 708 eValLysValAspValThrGlyAlaTyrAspThrIleProGlnAspArgLeuThrGluVa 728
DB 552 TGTAAAGNN 611
QY 728 IleAlaSerIleIleLysProGlnAspThrTyrCysValArgArgTyrAlaValAlaGl 748
DB 612 NNN 671
QY 748 nLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHisValSerThrLeuThrAs 768
DB 672 NNN 731
QY 768 PleuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGluThr-----SerProLe 786
DB 732 CCTCAGACATACATGAGGCGCAGTCTTACAGATCTGCAGATTCAGATGCAGTGCAC 791
QY 786 ValArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSerSerGlyLeuPh 806
DB 792 GAGGAATCCGTTGTTCATCGACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 851
QY 806 eAspValPheLeuArgPheMetCysHisHisAlaValArgLysGlyLysSerTyrVa 826
DB 852 NNN 911
QY 826 GlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCysSerLeuCysTyr 846
DB 912 GCAGTGCAGGCGCATCCCCCAGGCGCTCCAGCTATCCACCTGCTCAGCTGTGT 971
QY 846 rGlyAspMetGluValLysLysPheAlaGlyIleArgArgAspGlyLeuLeuArgLe 866
DB 972 CAGAGACATGGAGAACAGAGCTGTGTGCTGAGAGCGGAGATGGGTGTCTTTACGTT 1031
QY 866 uValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThrPheLeuArgTh 886
DB 1032 TGTGATGACTTTCTGTGTGTGAGCGCTCACCTGGACCAAGAAACCTTCTCAGAC 1091
QY 886 rLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLysThrValValAs 906
DB 1092 CCTGTTCATGCGCTTCTGTGATGAGGTGATGATGAATGAACCTTGCAAGAGACAGTGTGA 1151
QY 906 nPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHisG 926
DB 1152 CTTCCTGTGAGCTGTGTACCTGGTGTGCTGACCTCATACCAAGCTGCTGCTCAGT 1211
QY 926 yLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluValGlnSerAspTyr 946
DB 1212 CCGTTTCCCGGT 1271
QY 946 rSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheLysAl 966

BU702370 851 bp mRNA linear EST 15-JUL-2003
 LOCUS UI-M-FIO-byx-f-12-0-UI-r1 NIH BMAP_FIO Mus musculus cDNA clone
 DEFINITION IMAGE:6400523 5', mRNA sequence.
 ACCESSION BU702370
 VERSION BU702370.1 GI:23627105
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 851)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIN at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyx-5.
 Location/Qualifiers
 1..851
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6400523"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_FIO"
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CAGCCACGAC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemm Chiu, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 3,6e-61 Length: 851
 Score: 1028.00 Matches: 197
 Percent Similarity: 80.85% Conservative: 31
 Best Local Similarity: 69.86% Mismatches: 52
 Query Match: 17.25% Indels: 2
 DB: 5 Gaps: 1

US-10-044-692-2 (1-1132) x BU702370 (1-851)

QY 738 ThrTTCGValAlaArgTyrAlaValAlaGlnlyAlaAlaHisGlyHisValArglys 757
 Db 6 ACGTACTGATGATCGGATGAGTGGCCGAGAGATGACCAAGGCCAAATTCACAAAG 65
 QY 758 AlaPheLysSerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheVal 777
 Db 66 TCCTTTAGAGACAGGTCAACCCCTCTGTGACTTCGAGCCATACATGGCCAGATTCTT 125

QY 778 AlaHisLeuGlnGluThr-----SerProLeuArgAspAlaValValIleGlnGlnSer 795
 Db 126 AAGCATTCGACAGATTTCAGATCCAGTCAGTACAGAGAACTCCGTGTGATCAGACAGAGC 185
 QY 796 SerSerLeuArgGlnValAspSerGlyLeuPheAspValPheLeuArgPheMetCysHis 815
 Db 186 ATCTCTATGAAATGAGAGACAGACAGCCGTGTGACTTCTTCCTCAGACTTCTGCGCTCAC 245
 QY 816 HisAlaValArgGlnGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlnSer 835
 Db 246 AGTGTGCTGAATGATGTCAGACAGTCTATACGACGTGCGAGGATCCCGAGGAGCTCC 305
 QY 836 IleLeuSerThrLeuLeuCysSerLeuCysTyrGlyAspMetGluAlaLysLeuPheAla 855
 Db 306 ACCCTATCACCCTGCTCTGCGAGTGTGTGTTGCGAGACATGAGAACAGAGCTGTTGGCT 365
 QY 856 GlyIleAlaGArgArgGlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrPro 875
 Db 366 GAGGTGACGCGGAGATGGGTGCTTTTACGTTTGTGTGATGACTTCTGTGTGACGCGCT 425
 QY 876 HisLeuThrHisAlaLysThrPheLeuArgThrLeuValArgGlyValProGlnTyrGly 895
 Db 426 CACTTGACCAAGCAAAAACCTTCTCAGACACCTGCTCATGCGCTTCTGAGATGAGG 485
 QY 896 CysValValAsnLeuArgLysThrValValAsnPheProValGluAspGluAlaLeuGly 915
 Db 486 TGCATGATTAACCTTCGACAGACAGTGGTGAACCTCCGTGGAGCCGTGATCCCTGGGT 545
 QY 916 GlyThrAlaPheValGlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeu 935
 Db 546 GGTGACGCTCCATACACACCTGCTCTCAGCTGCTTCCGTGTGGCTGTGCTGTG 605
 QY 936 AspThrArgThrLeuGlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArg 955
 Db 606 GACACTCAGACTTTCGAGAGTGTCTGTGACTACTAGGTATGCCCAACCTCAATTAAAG 665
 QY 956 AlaSerLeuThrPheAsnArgLysGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPhe 975
 Db 666 ACGAAGCTCAACCTTCAGAGTGTCTTTCANAGCTGGAGAACCATCGGAACANGCTCTG 725
 QY 976 GlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGln 995
 Db 726 TCGGTCTTGGCGGTGAAGTGCACGCTTATTTCTTACGCTTGACAGGTAAACAGCTCCAG 785
 QY 996 ThrValCysThrAsnIleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCys 1015
 Db 786 ACGTCTGCATCAATATATACAAATCTTCTGCTTCANGCTCAGAGTTCATCATGT 845
 QY 1016 ValLeu 1017
 Db 846 GTGATT 851

RESULT 6

BG917907 851 bp mRNA linear EST 05-JUN-2001
 LOCUS 602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:494987 5',
 DEFINITION mRNA sequence.
 ACCESSION BG917907
 VERSION BG917907.1 GI:14298383
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 851)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DB: 4 Gaps: 0

US-10-044-692-2 (1-1132) x BQ258274 (1-492)

QY 905 ValAsnProValGlnAspGluAlaLeuGlyValThrAlaPheValGlnMetProAla 924

Db 1 GTGAACCTTCTGTAAAGACAGAGCCCTGGGGGACGACCTTTGTTCAATGCCGCC 60

QY 925 HisGlyLeuPheProTyrCysGlyLeuLeuAspThrArgThrLeuGluValGlnSer 944

Db 61 CAGGCGCTATTCCTCGTGGGCTGCTGCGATACCCGAGCCCTGGAGGTGCAAGC 120

QY 945 AspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPhe 964

Db 121 GACTACTCCAGCATATCCCGAGACCTTCATCAGGCGCATCTCAACCGCGCTTC 180

QY 965 LysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLysCysHisSer 984

Db 181 AAGGCTGGAGGAACATGCTCCGAACTTTGGGGCTCTGGGCTGAAGTGCACAGC 240

QY 985 LeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrLysIle 1004

Db 241 CTGTTCTGATTTGACAGGTGAACAGCTCCAGCGGTGCAACAATCTTACAGATC 300

QY 1005 LeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGln 1024

Db 301 CTCCTGCTGACGAGCTACAGGTTTCAAGCATGTGTCTGACGCTCCCATTTATCAGCA 360

QY 1025 ValTyrPheAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCysTyr 1044

Db 361 GTTTGGAAGAACCCCAATTTTCTGCGGTATCTGACAGCGGCTCCCTGCTAC 420

QY 1045 SerIleLeuLysAlaLysAsnAla 1052

Db 421 TCATCTCTGAAGCCAGAAAGCA 444

RESULT 8

LOCUS BQ258274 664 bp mRNA linear EST 06-MAY-2002

DEFINITION NISC_Kp11g04.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone

ACCESSION IMAGE:5409222, mRNA sequence.

VERSION BQ258274

KEYWORDS BQ258274.1 GI:20459030

SOURCE EST.

ORGANISM Mus musculus (house mouse)

REFERENCE NISC_Kp11g04.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

COMMENT Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: csgbbs-remail.nih.gov

cDNA Library Preparation: J. Baker (Stanford University)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CCAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

info@image.lnl.gov

MGI:1845958

Plate: LLM12043 row: N column: 7

Seq primer: SP6 primer:

Location/Qualifiers

1..664

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CD-1"

/db_xref="taxon:10090"

/clone="IMAGE:5409222"

/tissue_type="embryo, late gastrula"

/dev stage="embryo, 7.5 dpc"

/lab_host="XLI-Blue"

/clone_lib="Baker mouse embryo e7.5"

/note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA

made by oligo-dT priming. Directionally cloned into

SalI/NotI sites using the following 5' adaptor:

5'-TCGACCCAGCGCTCCG-3'. Size selected for average insert

size 1.8-1.9 kb. Library constructed by J. Baker (Stanford

University)."

ORIGIN

Alignment Scores:

Pred. No.: 1.65e-43 Length: 664

Score: 771.50 Matches: 153

Percent Similarity: 72.03% Conservative: 17

Best Local Similarity: 64.83% Mismatches: 45

Query Match: 12.94% Indels: 21

DB: 5 Gaps: 2

US-10-044-692-2 (1-1132) x BQ258274 (1-664)

QY 352 ProSerLeuThrGlyValArgArgLeuValGluThrIlePheLeuGlySerArgProTyr 371

Db 10 CCTAATGACTGAGGCGAGAGACTGTGAGATCATCTTTCTGGGCTCAAGGCTAGG 69

QY 372 MetProGlyThrProArgArgLeuProArgLeuProGlnArgTyrTyrGlnMetArgPro 391

Db 70 ACATGAGACCACTCTGAGAGACACCGTCTACGCTGATCTGGAGATGCGGCC 129

QY 392 LeuPheLeuGluLeuLeuGlyValAsnHisAlaGlnCysProTyrGlyValLeuLeuLysThr 411

Db 130 GTTGTCCAAAGCTGCTGTGTGACCATGACAGAGGCAATATGTCAGACTCTAGGTCA 189

QY 412 HisCysProLeuArgAlaAla-----ValThrProAlaAlaGlyValCysAlaArg 428

Db 190 CATTGACAGTTTCAGACAGCAACCAACAGGTGACAGTGCCTG----- 234

QY 429 GluLysProGlnGlySerValAlaIleProGluGluGluAspThrAspProArgArgLeu 448

Db 235 -----AACACCAGCCCAAGCCGACCTC 255

QY 449 ValGlnLeuLeuArgGlnHisSerSerProTyrGlnValTyrGlyPheValArgAlaCys 468

Db 256 ATGGAATTTGCTCGCTGCTGACAGCATGCTCCGAGGATATGTTTCTTCGGGCTGCT 315

QY 469 LeuArgArgLeuValProProGlyLeuTyrGlySerArgHisAsnGluArgArgPheLeu 488

Db 316 CTCTGCAAGGTGTGTCTGCTAGTCTGAGGGTACCAAGCAATGACGCGCTTCTTT 375

QY 489 ArgAsnThrLysPheIleSerLeuGlyLysHisAlaLysLeuSerLeuGlnGluLeu 508

Db 376 AAGAACTTAAAGATTCATCTGTTGGGAAATCGGCAAGCTATCTCGAGAACTG 435

QY 509 ThrTyrLysMetSerValArgAspCysAlaTyrPheLeuArgSerProGlyValGlyCys 528

Db 436 ATGTGGAAGATGAAGATAGATGATCCACTGCTCCGAGAGCCAGGAGAAAGACGT 495

QY 529 ValProAlaAlaGlnHisArgLeuArgGluGluIleLeuAlaLysPheLeuHisTyrPhe 548

Db 496 GTCCCGCTGACAGACCGCTGAGGAGAGAGATCTGGCTACAGTCTCTGTTGGGCTG 555

QY 549 MetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGluThrPhe 568

Db 556 ATGACACATACGTGTACAGCGCTGCTAGGTCAATCTTTTATCATCAGAGAGCATTC 615

QY 569 GlnLysAsnArgLeuPhePheTyrArgLysSerValTyrSerLysLeu 584

Db 616 CAGAGAGACAGGCTCTTCTTACCGTAAAGAGTGTGAGCAAGCTG 663

RESULT 9

LOCUS CR688161 1424 bp mRNA linear HTC 12-AUG-2004

DEFINITION Tetradon nigroviridis full-length cDNA.

/note="Organ: Brain; Vector: pYX-Asc; Site 1: Bcor 1; Site 2: Not 1; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Bcor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	2,69e-36	Length:	649
Score:	667.50	Matches:	153
Percent Similarity:	46.32%	Conservative:	17
Best Local Similarity:	41.69%	Mismatches:	32
Query Match:	11.20%	Indels:	165
DB:	7	Gaps:	3

US-10-044-692-2 (1-1132) x CF531069 (1-649)

```

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
DB 42 ATGACCCGGGCTCTGTCGCCCCGGGGGCGCTCTCTCTGCGACCGCATACCGGGAG 101
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPargLeuValGln 40
DB 102 GTGTGGCGCTGGCAACCTTTGTGGCGCGCTGGGCGCCGAGGGGAGGGGCTGTGGCA 161
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 162 CCGGGGACCCAGAGATCAACGCACTTGTGCCCAATGCTATGTGCACTGCACTGG 221
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuGluLeu 80
DB 222 GGCTACACGCTCCACCTCCGACCTTCTTCACCAAGGTGTCATCCCTGAAAGCTG 281
QY 81 ValAlaArgValLeuGlnArgLeuGlyCysGluArgGlyAlaLeuValLeuAlaPheGly 100
DB 282 GTGGCCAGGCTGTGTGAGAGACTCTGCGAGCGCAAGAGAAACGTGCTGGCTTTGGC 341
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 342 TTGAGCTGCTTAACGAGGCCAGAGCGGGGCTCCCATGGCTTCATGATGCGCTGGC 401
QY 121 SerTyrLeuProAlaThrAlaPheAlaLeuArgGlySerGlyValAlaTyrGlyLeuLeu 140
DB 402 AGCTACTTCCCAACACTGTATTGAGACCTGCGGTGAGTGAGTGAGTGCATGACTGCTG 461
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 462 TTGAGCCGAGGTGGGAGACGCTGCTGTCTACTGCTGGCAACGTGCTCTTATCTT 521
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 522 CTGGGTGCCCCCAGCTGCTGCTAC----- 545
QY 181 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 545 ----- 545
QY 201 ArgAlaTyrPasnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 545 ----- 545
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProValArgProArgArg 240

```

```

DB 545 ----- 545
QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 546 ----- 557
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGln 280
DB 557 ----- 557
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 557 ----- 557
QY 301 ArgGlnHisLeuAlaGlyProProSerThrSerArgProProArgProTyrPasnThrPro 320
DB 558 ----- 569
QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 569 ----- 569
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 570 ---AAACCTCATTCCTACTCAGCANNCTCCAGCTTACTGAGGGCCAGAGACTG 626
QY 361 ValGluThrIlePheLeuGly 367
DB 627 GTGAGATCATCTTCTGGGC 647

```

RESULT 11

CF531121 688 bp mRNA linear EST 12-SEP-2003
 UI-M-FY0-GSP-W-21-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:3035598 5', mRNA sequence.

DEFINITION

LOCUS

CF531121

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Seg primer: pYX-5.
 Location/Qualifiers
 1..688
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:3035598"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (TI phage resistant)"
 /clone_lib="NIH BMAP FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: Bcor 1; Site 2: Not 1; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGCAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
3.45e-36	666.50	688	154
Percent Similarity:	46.34%	Conservative:	17
Best Local Similarity:	41.73%	Mismatches:	32
Query Match:	11.18%	Indels:	166
	7	Gaps:	2

US-10-044-692-2 (1-1132) x CF531121 (1-688)

```

OY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyraArgGlu 20
DB 79 ATGACCCGGGCTCTGTTGCCCGGGTGGCGCTCTCTCTCGCAGCCGATACCGGGAG 138

OY 21 ValLeuProLeuAlaThrValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
DB 139 GTGTGGCCGCTGGCAACCTTGTGGCGCCCTGGGGCCCGAGGCGCGGCTTGTGCAA 198

OY 41 ArgGlyAspProAlaAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 199 CCGGGGACCCCAAGATCTACCCGCACTTGTGGCCATGCTTACTGTGCATGCACTGG 258

OY 61 AspaAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB 259 GGCTCAGACCTCCACCTGCTTCTTCCACAGGTGTGCATCCTGAAAGAGCTG 318

OY 81 ValAlaArgValLeuGlnArgLeuGlyArgGlyAlaLeuAsnValLeuAlaPheGly 100
DB 319 GTGGCGAGGTTGTGAGAGACTGTGGCGGCAAGAGAAACGTGTGCTTTTGGC 378

OY 101 PheAlaLeuLeuAspGlyAlaArgGlyProProGluAlaPheThrThrSerValArg 120
DB 379 TTGAGCTGCTTAAACAGGCGCAGAGCGGCGCTCCCATGCTTCACTAGTACGCTGCT 438

OY 121 SerTyrLeuProAsnThrValThrAspaAlaLeuArgGlySerGlyAlaTyrPheLeuLeu 140
DB 439 AGCTACTTGGCCCAACACTGTATTGTAGACCTGCGGTGTCAGTGGTGCATGCTGCTG 498

OY 141 LeuAlaArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 499 TTGAGACCGAGTGGGAGACACCTGCTGTCTACCTGCTGGCACACTGTCTTTATCTT 558

OY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 559 CTGGTGGCCCGCCAGCTGTCTTAC----- 582

OY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 582 ----- 582

OY 201 ArgAlaTyrPheAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 582 ----- 582

OY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 582 ----- 582

OY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyr-AlaHisProGlu 260
DB 583 ----- 598

```

CAGGGGAGATGCCAN-----

```

OY 260 YArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
DB 598 ----- 598

OY 280 UGlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlu 300
DB 598 ----- 598

OY 300 YArgGlnHisAlaGlyProProSerThrSerArgProProAlaProTyrPheThrPr 320
DB 598 ----- 598

OY 320 OCysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLeuGluGlu 340
DB 599 ----- 603.

OY 340 nLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLe 360
DB 604 TCTAAACCCCTCATTCCTACTCAGCANCCTCAGCCTTAATTGACTGGGCGCAGAGACT 663

OY 360 UValGluThrIlePheLeuGlySer 368
DB 664 GTTGAGATCATCTTTCTGGGCTCA 688

RESULT 12
AA281296 389 bp mRNA linear EST 14-AUG-1997
LOCUS z108902.r1 NCI_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
DEFINITION mRNA sequence.
AA281296.1 GI:1924194
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 2187 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence srop: 385.
Location/Qualifiers
1. 389
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Caxon:9606"
/clone="IMAGE:712562"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_GCAP_GCB1"
/notes="Vector: pT73D-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Altman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTACCAATCTGAAGTGGAGCGCGCGCTCATTTTCTTTTCTT-3'
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

ORIGIN

Db	295	GGCTCAGAGCTCCACCTCGCCGACCTTTCTTCACCAACGAGTGTATCCCTTAAGAGCTG	354
Qy	81	Val11aargVal1Leug1nargLeuCyag1uaarg1yala1uysaenVal1leu1a1phe1y	100
Db	355	GTGGCCAGGGTTGTGCAGAGACTCTGGCAGGCGCAAGAGAAACGTGCTGCTTTGGC	414
Qy	101	Phe1aleu1leu1aarg1yala1arg1ygl1ytrp1rogl1ual1a1peth1rTh1Ser1Val1Arg	120
Db	415	TTTTAGCTGCTTTAAACGAGGCCAGAGCGCGGCTCCATGCGCTTCACATGACGCGTGGCT	474
Qy	121	Ser1Yleu1P1roAanTh1Val1Th1Asp1a1leu1narg1y1Ser1yala1Trp1Gly1Leu1	140
Db	475	AGCACTTGCCCAACACTGTTATTGACCCCTGGTGTCAAGTGGGACGTGATGCTACTG	534
Qy	141	Leu1aarg1Val1G1y1Asp1Asp1Val1leu1Val1His1leu1leu1a1aarg1Cy1a1a1leu1Phe1a1	160
Db	535	TTGAGCGGAGTGGGCGACGACCTGCTGTCTTACTGCTGACACTGTGCTTTATCTT	594
Qy	161	Leu 161	
Db	595	CTG 597	
RESULT 14			
LOCUS	CN274427	409 bp	mRNA linear EST 16-MAY-2004
DEFINITION	17000531326763 GRN_ES Homo sapiens CDNA 5', mRNA sequence.		
ACCESSION	CN274427		
VERSION	CN274427.1	GI:47290841	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 409)		
AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. M.		
JOURNAL	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation		
COMMENT	Nat. Biotechnol. 22 (6), 707-716 (2004)		
FEATURES	Contact: Brandenberger R		
source	Regenerative Medicine		
	Geron Corporation		
	230 Constitution Drive, Menlo Park, CA 94025, USA		
	Tel: 650 473 8658		
	Fax: 650 473 7760		
	Email: rbrandenberger@geron.com		
	Insert Length: 409 Std Error: 0.00.		
	location/Qualifiers		
	1..409		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"		
	/clone_11b="GRN ES"		
	/note="Oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p3), H7 (p25), and H9 (p26) maintained in feeder-free conditions"		
ORIGIN			
Alignment Scores:			
Score: 1.28e-29	Length: 409		
Percent Similarity: 567.00	Matches: 108		
Best Local Similarity: 99.08%	Conservative: 0		
Query Match: 99.08%	Mismatches: 1		
DB: 9.51%	Indels: 0		
	Gaps: 0		
US-10-044-692-2 (1-1132) x CN274427 (1-409)			
Qy	1	MetProba1g1a1Pro1a1Cy1a1r1g1a1Val1a1r1g1Ser1Leu1a1r1g1Ser1Hi1Ty1a1r1g1u	20

Dd		82	ATGCCGGCCGCTCCCCCTCCAGCGGTGCCTCCTGCTGCACCACTACCGGAG	141
Oy		21	ValleuProleuaIatrhPhevalAargArgLeuGIYProGInGIYTPaArgLeuValGln	40
Dd		142	GTCGTGC CGCTGC GCA GGTTC GTGTC GCAG CCGCTGC GGAG CCCCA GGGACTGC GGTGTGC AG	201
Oy		41	ArgGIAspPrPCoAlaAlaPheAargAlaLeuValAlaGInCySLeuValCYsValProTrp	60
Dd		202	CGCGGGAAcCCGGGGGCTTTCCTCCGGCGCTGAGTGGCCAGAGTCCGTGATGTCGTCCTGG	261
Oy		61	AspAlaArPPoPpCoAlaAlaAProSerPheArgGInValSerCYsLeuYSGLIleu	80
Dd		262	GACCACAGGCGCGCCCCCGCCGCCCTCTTCGCGCACAGGTGTCTCTGTGAAGGACTG	321
Oy		81	ValAlaArValleuGInAargLeuCYsGIuAArgGIYAlaYSaenValLeuAlaPheGIY	100
Dd		322	GTGCGCCGAGTGCTGCAGAAGGCTGTGTGAAGCGCGCGGCGAAGAACGTGTGCTTCAGC	381
Oy		101	PheAlaLeuLeuAaspGIYAlaArgLY	109
Dd		382	TTCGCGCTGTGCAGCGGGCGCGCGGG	408
RESULT 15				
BE371943		866 bp	mRNA	linear EST 21-JUL-2000
LOCUS		601217728BP1	NCI CGAP Lu29 Mus musculus cDNA clone IMAGE:3586614 5'	
DEFINITION			mRNA sequence.	
ACCESSION		BE371943		
VERSION		BE371943.1	GI:9317215	
KEYWORDS		EST.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Mus musculus		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE		1 (bases 1 to 866)		
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
		Contact: Robert Strausberg, Ph.D.		
		Email: cgabbs-remail.nih.gov		
		Tissue Procurement: Gilbert Smith, Ph.D.		
		cDNA Library Preparation: Life Technologies, Inc.		
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
		DNA sequencing by: Incyte Genomics, Inc.		
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:		
		http://image.lnl.gov		
		Plate: LLM8748 row: h column: 07		
		High quality sequence stop: 639.		
FEATURES		Location/Qualifiers		
source		1..866		
		/organism="Mus musculus"		
		/mol_type="mRNA"		
		/strain="CZECH II"		
		/db_xref="taxon:10090"		
		/clone="IMAGE:3586614"		
		/tissue.type="spontaneous tumor, metastatic to mammary.		
		Stem cell origin."		
		/lab_host="DH10B"		
		/clone_lib="NCI CGAP Lu29"		
		/note="Organ: lung; Vector: pCMV-SPORT6, Site.1: SalI,		
		Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.		
		library constructed by Life Technologies. Investigator		
		providing samples: Gilbert Smith, NIH"		
ORIGIN				
Alignment Scores:				
Pred. No.:	4.72e-29	Length:	866	
Score:	566.00	Matches:	108	
Percent Similarity:	82.31%	Conservative:	13	
Best Local Similarity:	73.47%	Mismatches:	26	
Query Match:	9.50%	Indels:	0	

VERSION	BT452535.1	GI:25941846
KEYWORDS	EST.	
SOURCE	Gallus gallus (chicken)	
ORGANISM	Gallus gallus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	
	Phasianinae; Gallus.	
REFERENCE	1 (bases 1 to 753)	
AUTHORS	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,	
	Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.	
	A Comprehensive Collection of Chicken CDNAS	
	Curr. Biol. 12 (22), 1965-1969 (2002)	
TITLE	12445392	
JOURNAL	22335534	
MEDLINE		
PUBMED		
COMMENT	Contact: Simon Hubbard Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST) PO Box 88, Manchester, M60 10D, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@umist.ac.uk.	
FEATURES	Location/Qualifiers	
source	1..753	
	/organism="Gallus gallus"	
	/mol_type="mRNA"	
	/strain="Layer"	
	/db_xref="taxon:9031"	
	/clone="CHEST696F"	
	/sex="Female"	
	/dev_stage="adult"	
	/lab_host="DH10B"	
	/clone_idb="CSQRBN14"	
	/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:	
	ECORI; Site_2: NotI; This normalized library was	
	constructed from 1 million independent clones. cDNA	
	synthesis was initiated using an oligo(dT) primer, using	
	methyated C in the first strand synthesis reaction.	
	Following this first strand reaction, double-stranded cDNA	
	was blunted, ligated to NotI adapters, digested with	
	ECORI, size-selected, and cloned into the NotI and EORI	
	compatible sites of a custom modified MCS of the	
	pBluescript (KS+) vector. The library was normalized in 2	
	rounds using conditions adapted from Soares et al., PNAS	
	(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6	
	(1996): 791, except that a significantly longer	
	reannealing hybridization was used."	
ORIGIN		
Alignment Scores:	1.34e-25	length: 753
Pred. No.:	515.00	Matches: 100
Score:	74.55%	Conservative: 23
Percent Similarity:	60.61%	Mismatches: 42
Best Local Similarity:	8.64%	Indels: 0
Query Match:	5	Gaps: 0
DB:		
US-10-044-692-2 (1-1132) x BU452535 (1-753)		
Oy	668 ArgAsmMeArGArgysleupheglVallleuAglLeuYcShisSerieuPheleu	987
Db	5 AAAAAGCTGAATGCAAAATGACTGCAAGTCCTCAAACTGAATGCGATCTTACTCTT	64
Oy	988 AsPleuGlnValnsenSerleuGlnTtTtValGysTtThAsnllTtYtIsllleuenu	1007
Db	65 GACTTAAGTGAACAGCCCTTCAGACAGTCTTAATTAACATCTACAGATATTTTACTT	124
Oy	1008 GtAlAtATyArGrPheHsAlaCySValleuGlnLeuProPheHsIsgInValTtPyS	1027
Db	125 CAGGCTTACGGTTCATCGCTGTGTTCTTCACCTTCATTCAACAGAAAGTTAGAAAT	184
Oy	1028 AspProThrPhePheLeuA-gValllIsesrAspThAlSerleuCyStYrSerllleu	104

Db	185	AACTCGATTCTTCTCTAAGATCATCTCTGATACCTGTCATGCTGCTATTATATCCTG	244
Oy	1048	LYSALAATASASALAGIYwEterSeuEnGyAlaLySGyAlaAlaAGIyProleuProser	1067
Oy	245	AAAGCTAAATAATCCAGAGATTCTTTAGTATGCAAAAGATGATCTGTATGTCCTCTTT	304
Db	1068	GUAlaValaGlntPrleuCySHIsgInaLpHeLeuLySLeuThArXhIaRyVal	1087
Oy	305	GAGGCGACGAATGGCTGTCTTCAACATGCTTCATTCGTAACATGTCCAACACAAAGTT	364
Oy	1088	ThTyValpJroLeuLeuGySerLeuArXhIaGlntRnLpLeuSerArXyLeu	1107
Db	365	ATTACAAATGCTACTTAAAGCCCTTAAAGTCTAAAGATGATGATCTGTTGGGAAGATC	424
Oy	1108	ProGlyThThLeuThrAlaLeuGluAlaAlaAlaProAlaLeuProSerAspHe	1127
Db	425	CCAAGGATATCTATGAACTGCTGAAGACGGTACGGAACCAATCGCTTGTCAAGATTTC	484
Oy	1128	LyEThrIleLeuAsp	1132
Db	485	AAAACATATCTGAC	499
RESULT 19			
CNS05902		846 bp	mRNA
LOCUS			linear
DEFINITION	AGNCNCURJ 2243746 NIH_ZGC_7 Danio rerio cdna clone IMAGE:7267941		EST 28-APR-2004
ACCESSION	CNS05902		
VERSION	5', mRNA sequence.		
KEYWORDS	CNS05902.1 GI:46818526		
SOURCE	EST.		
ORGANISM	Danio rerio (zebrafish)		
REFERENCE	Danio rerio		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;		
JOURNAL	Cypriniformes; Cyprinidae; Danio.		
COMMENT	1 (bases 1 to 846)		
	NIH-MGC http://mgs.nci.nih.gov/.		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Daniela S. Gerhard, Ph.D.		
	Office of Cancer Genomics		
	National Cancer Institute / NIH		
	Bldg. 31 Rm10A07 Bethesda, MD 20892		
	Email: dsgrahp@remail.nih.gov		
	Tissue Procurement: Len Zon, Harvard		
	Tissue Library Preparation: Open Biosystems		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: L1AM15246 row: h column: 19		
	High quality sequence start: 21		
	High quality sequence stop: 756.		
FEATURES			
source			
	1. 846		
	/organism="Danio rerio"		
	/mol_type="mRNA"		
	/db_xref="taxon:7955"		
	/clone="IMAGE:7267941"		
	/tissue_type="whole body"		
	/lab_host="DH10B"		
	/clone_id="NIH_ZGC_7"		
	/note=vector: pExpress1, Site_1: NotI, Site_2: EcoRV,		
	Bulk tissue was collected from a whole adult individual		
	from the Tuebingen strain, 1st strand cDNA was primed with		
	a Not I - oligo (dT) primer, double-stranded cDNA was		
	cloned into the Not I and EcoRV sites of pExpress-1.		
	Library was size-selected for >1 kb fragments and		
	normalized. A non-normalized version of this library is		
	also available (NIH_ZGC_10). Library was constructed by		
	Open Biosystems (Huntsville, AL)"		

ORIGIN

ORIGIN


```

Db      234 GAATATGAAGAGGTTTGCATGCGAGAGTATATGCTTACTATCATCAGATCAAG 293
Oy      957 rleuthrPheleuAarglyPheleuAalaglyAarghmetAarglyLeuPhegLyA 977
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      294 TCTTTCTTCAATCAAGTAGAATAGCTGGAAACATGAAATGCAATTCATCAGT 353
Oy      977 lLeuAarglyCyshiSerleuPheleuAarglyAalaglyAalSerleuGlnThVa 997
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      354 CCAACATGAATAGCATCTTACTTCTTGAATTAAGATCAACAGCTTCACAGACGT 413
Oy      997 lCystrAmetllyrlyllylLeuLeuGlnAalAlyrAarghPheHisaCyValle 1017
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      414 TCTAATTAACATCAAGATATTTTACTTCAGGCTTACAGGTTTCATGCTGCTTCT 473
Oy      1017 uGlnLeuProPheHisiGlnInValTrrlyAseProtrhPheleuAargValIleSe 1037
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      474 TCAAGCTTCATTCACAGAAAGTGAATATCTGATTCCTTCTTCAAGATCATCTC 533
Oy      1037 rAepthAalSerleuCystrSerlLeuLyAalAlyAarghAalGlymetSerleuG 1057
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      534 TGATACGCTTCATGCTGCTATTTTATCTGAAGCTTAATAATCCAGAGGTTCTTAGG 593
Oy      1057 yAlaLyGlyAlaAlaglyProleuProserGlnAalAalGlnTrpleuCyshiGlnA 1077
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      594 TAGCAAAAGATGATCTGGCAT-GTCCCTTGAGGCGAGCAAGATGCTGTGATACATG 652
Oy      1077 aPheleuLeuLySerleuThrAarghAargValThrValProleuGlnGlySerleuA 1097
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      653 CTTGATGTCAAACTGTGCCAACAACAAAGTTATTCAAAAGCTTACTTAAGCCCTTA 712
Oy      1097 gThAlaGlnThrGlnLeuSerAarglyLeuProGlyThrThreuthAalLeuGlnA 1117
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      713 AAGCTATAGATGATCTGTGGGAAAGATCCAGGATCTTAAGGAACGTGTGAAG 772
Oy      1117 aAlaAlaAsnProAlaLeuProSerAepPheLyS 1128
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      773 CGGAGCGCAACCATCGCTGTGTCAGAAATTCAA 806

```

RESULT 21
CA380121 668 bp mRNA linear EST 06-NOV-2002
LOCUS 659344 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT49P11_B_H06 5',
DEFINITION mRNA sequence.
ACCESSION CA380121.1 GI:24701509
VERSION CA380121.1 GI:24701509
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 668)
Rexroad, C.B. 3rd, Lee, Y., Keele, J.W., Karanicheva, S., Brown, G.,
Koop, B., Gahr, S.A., Paili, Y. and Quakehush, V.
Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
Cytogenet Genome Res. 102 (1-4), 347-354 (2003)
JOURNAL Contact: Rexroad CE
COMMENT USDB, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_aln option. Vector identified by
cross match v0.990329.
Seq primer: AGCGATTAACAATTTCACACAGA.
Location/Qualifiers
1..668
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT49P11_B_H06"

```

ORIGIN
Alignment Scores:
Pred. No.: 4.57e-22 Length: 668
Score: 463.00 Matches: 102
Percent Similarity: 58.19% Conservative: 33
Best Local Similarity: 43.97% Mismatches: 85
Query Match: 7.77% Indels: 12
Db: 6 Gaps: 4

US-10-044-692-2 (1-1132) x CA380121 (1-668)
Oy      451 LeuLeuAargGlnHisiSerSerProTrrGlnValTrrlyPheValAargAlyLeuAarg 470
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      7 CTCCTGCCCGCAGCAGACGTGACCTCACCGGCTGATCTTGTGCAGAGTCCCTCAAC 66
Oy      471 AargLeuValProProGlyLeuTrrlySerAargHisiAargGlnAargAargAarg 490
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      67 GCGGTGTCCTCCCTCGAGGTTCTGGGGGTCCGACCATTAACGATTAATTCCTGTCCGA 126
Oy      491 ThrlySerPheHisiSerleuGlyLyshiAalAlySerleuGlnGlnLeuThrTrp 510
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      127 GTCAGAACTTCCTGTCATGGGCAAGTTTGAAGAGATGATCATGTGCTGAGATGTGG 186
Oy      511 LysMetSerValAargAepCyAalTrrpleuAargSerProGlyValGlyCyValPro 530
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      187 AAGATGAAGGTGAATGACTGTGATTTGGCTGAAGATCGCAAG--ACGGGCGGTGCCG 243
Oy      531 AlaAlaGlnHisiAargLeuAargGlnGlnLeuLeuAlySerPheLeuHisiTrpleuMetSer 550
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      244 CCAAGTGAAGCTGTGCTATTCGACCGGGGTCTTAGGCAAGCTCCGTGGCTGGCTGAT 303
Oy      551 ValTrrValAalGlnLeuLeuAargSerPhePheTrrValThrGlnThrPheGlnLyS 570
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      304 GGTATGTGCTAGGCTGTGAGGCTATGTTTCTACGTCACAGAGAGATGGACAGAG 363
Oy      571 AanaAargLeuPhePheTrrAargLySerValTrrSerLySerleuGlnSerllyleGlyleA 590
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      364 AACGCACTGGCTTCTACAGATACCAAGTCTGGGCAAGCTTCAGAGCTGGCTTCACT 423
Oy      591 GlnHisiLeuLyAargValGlnLeuAargGlnLeuSerGlnAalAalAargGlnHisiA 610
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      424 GGTCACTCTCTTAAGGTCAAGTGCAGAGTTGACCTGGCCCAAGTG-----ACG 474
Oy      611 GlnAalAargProAlaLeuLeuThrSerAargLeuAargPheHisiProLyProAalLyLeu 630
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      475 TCGCTCCCAAAACCACTGTCCCTCCCGCTCCCTTCATCCCAAGACCAAGAGGATG 534
Oy      631 AargProIleValAasMetAaspTrrValAalGlyAalAargThrPheAargGlnLyAarg 650
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      535 AGACCATCACACAG-----GTCAAGGGGCT-----GACGCCAA 570
Oy      651 AlaGlnAargLeuThrSerAargVallyAalAlySerleuValLeuAasTrrGlnAarg 670
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      571 ACAAGGTTCACAGACCGGTGAAGAGCGTTGAAGATGCTAGGTCTGTGTACG 630
Oy      671 AargAargProGlyLeuLeuGlyAalSerValleuGly 682
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      631 TCTCTCTCTCTCTCTGAGCTCTCAAGTGTGGGG 666

```

RESULT 22
BX889962 724 bp mRNA linear EST 27-JUL-2004
LOCUS BX889962 tcdk Oncorhynchus mykiss cDNA clone tcdk0041c.i.20 5prim,
DEFINITION mRNA sequence.
ACCESSION BX889962
VERSION BX889962.2 GI:43411444

KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 724)
AUTHORS Goyorum,M., Guiguen,Y. and Le Gac,F.
TITLE Construction and primary characterization of normalized cDNA
libraries in rainbow trout, *Oncorhynchus mykiss*
JOURNAL Unpublished (2003)
COMMENT On Dec 18, 2003 this sequence version replaced gi:40140362.
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0041 row: i column: 20
Seq primer: M13R.
Location/Qualifiers
1..724
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="cdk041c.1.20"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="cdk"
/note="Vector: pT73D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Ressource centre. Francois PLOMI,
Francois Pluimel@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Alignment Scores:
Pred. No.: 1.35e-21 Length: 724
Score: 457.00 Matches: 106
Percent Similarity: 58.47% Conservative: 39
Best Local Similarity: 42.74% Mismatches: 89
Query Match: 7.67% Indels: 15
DB: Gaps: 5
US-10-044-692-2 (1-1132) x BX889962 (1-724)

OY 486 ArgPheLeuAArgAAnThrLyLeysPheIleSerLeuGlyLyshIaLalysLeuSerLeu 505
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 2 AAATTCCTGTCGCGACGTACGAATCTTCCTGCATGCGCAAGTTGAGAGATGTCATG 61
OY 506 GInGluLeuThrTrpLyMetSerValaArgAAspCyalaTrpLeuAArgSerProGly 525
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 62 GCTGAGCTGATGTGAAGATGAAGTGAATGACTGATTGCTGAAGATCGCAAG--- 118
OY 526 ValGlyCyValProAlaIaGluHisArgLeuAArgGluGluIleLeuAlaLysPheLeu 545
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 119 ACAGCCCGTGCCTCCCGACGTAGCTGTGTCATCCGACCGGGGTGTAGCCACGCTCCG 178
OY 546 HisTrpLeuMetSerValTrpValaGluLeuLeuAArgSerPhePheTrpValThrGlu 565
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 179 GCTTGCTGCTGCTGATGCTATGCTAGGCTGCTGATGCTATGCTTCACTCAACAGAG 238
OY 566 ThrTrpPheGlnIlyAsaAArgLeuPhePheTrpArgGlySerValTrpSerIlyLeuGln 585
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 239 AGCATGGACACAAAGAACCCACTGCGCTTCTACAGATACAGGCTGCGCCAAAGCTGCG 298
OY 586 SerIleGlyIleArgGlnHisLeuysAArgValaGlnLeuAArgGluLeuSerGluIaGlu 605

Db 299 GAGCTGCTTTCAGTGTCTACCTCTCTAAAGCTCAGAGTGCAGAGTTCACCTGCGCCAG 358
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
OY 606 ValAArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuAArgPheIlePro 625
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 359 GGG-----ACGTGCTCCGCCCAAAACACACTGCCCTCCGCTCGCTCATATCCCC 409
OY 626 LysProAAspGlyLeuAArgProIleValaSerMetAAspTrpValaIleAlaArgThrPhe 645
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 410 AAGACCGAAGGATAGACCATTCACAGG-----GTCTATGGGGCT----- 451
OY 646 ArgAArgGluLysAArgAlaGluAArgLeuThrSerAArgValIlyAlaLeuPheSerValLeu 665
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 452 -----GAGCGCAAAACAAGGTTGTTCCAGACCCCTGTGAAGAGACTGTATGATGTCTA 505
OY 666 AAspTrpGluAArgAlaAArgAArgProGlyLeuLeuGlyAlaSerValaLeuAAspAArg 685
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 506 GGTGTCTGTGTACGGTCTCTCTCTCTCTCTGAGCTGTACAGTGGGGGTGTGACCGAC 565
OY 686 ILeHisAArgAlaTrpAArgThrPheValaLeuAArgValaArgAlaGlnAAspProAArgProGly 705
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 566 ATCCACAGATCTCTCTCTCC-----ATCACCCCTGCTCAGAAAGACAAACACACGCG 619
OY 706 LeuTrpPheValIlyValaAspValaThrGlyAlaTrpAAspTrpIleProGlnAAspAArgLeu 725
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 620 CTCTACTTGTTCAGATGATGTGATGAGTGGGGCTGTAGACGTACCCAC-ACACAGCTC 678
OY 726 ThrGluValIleAlaSerIleIle 733
|||||:::|||||:::|||||:::|||||
Db 679 TTGAGAGTGAATGTCATGATGCTCTG 702

RESULT 23
CA353864 632 bp mRNA linear EST 05-NOV-2002
LOCUS 625469 NCCGWA 1RT Oncorhynchus mykiss cDNA clone 1RT74012_C_H06 5',
DEFINITION mRNA sequence.
ACCESSION CA353864
VERSION CA353864.1 GI:24599035
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 632)
AUTHORS Rexroad,C.B. 3rd, Lee,Y., Keele,J.W., Karaycheva,S., Brown,G.,
Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.
TITLE Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
COMMENT Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim.alt option. Vector identified by
cross match v0.990329.
Seq primer: AGCGATACCAATTTCACACAGCA.
FEATURES
source
1..632
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT74012_C_H06"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCGWA 1RT"
/note="Vector: pCMV SPOR6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN

Alignment Scores:

Pred. No.: 3,64e-21 Length: 632
 Score: 449.50 Matches: 102
 Percent Similarity: 55.978 Conservative: 34
 Best Local Similarity: 41.988 Mismatches: 68
 Query Match: 7.54% Indels: 40
 Gaps: 2

US-10-044-692-2 (1-1132) x CA353864 (1-632)

QY 773 MetArgGlnPheValAlaHisLeuGlnGluThrSerProLeuArgAspAlaValIle 792
 Db 17 ATGAAGAGGCTTGTAGTGTCTGCAAGAGAGGCAAGAGTTCCAGATCCACTGCGG 76
 QY 793 GlnGlnSerSerSerLeuGlnGlnAlaSerSerGlyLeuPheAspValPheLeuArgPhe 812
 Db 77 GAGCAGCATTTCTCCACAGATATTCATGGCAAGACGCTTGGAGGCTTGACCCAGATG 136
 QY 813 MetCysHisHisAlaValAlaArgGlyLeuSerValGlnGlySerGlnGlyIlePro 832
 Db 137 CTCTCTAGCTGAGTTCAGCTTCGGAGAAATCGTTCGTCAGGAGGTCAGGGATTCCT 196
 QY 833 GlnGlnSerIleLeuSerThrLeuLeuCysSerLeuCysTyrGlyAspMetGlnSerLys 852
 Db 197 CAGGAGTCCCGGAGAGTGTCTGCTGGCTGCTCTGTTACGGGCAATGGAGAACCTT 256
 QY 853 LeuPheAlaGlyIle--ArgArgAspGlyLeuLeuLeuArgLeuValAspAspPheLeu 871
 Db 257 CTGTTCTTCAACGTCAGACGGCGAGGAGGAGGTCGTGATGAGCTGATGACATTCCTC 316
 QY 872 LeuValThrProHisLeuThrHisAlaLeuThrPheLeuArgThrLeuValArgGlyVal 891
 Db 317 CTCTACCTCTGACCTGAGCAGGACAGACAGCTTCTCTCAAGCCTGATGGCGGGGTA 376
 QY 892 ProGlnTyrGlyCysValAlaAsnLeuArgLeuValAlaAsnPheProValGluAsp 911
 Db 377 CCACGGTACGGGTGTGTGAGAACCCCAAGAGGTGCTTAACCTTCCCTTT-GAC--- 432
 QY 912 GluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHisGlyLeuPheProTyrCys 931
 Db 432 ----- 432
 QY 932 GlyLeuLeuLeuAspThrArgThrLeuGlnValGlnSerAspTyrSerSerTyrAlaArg 951
 Db 433 -----TACGCTGGC 441
 QY 952 ThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheIleValAlaGlyAsnMetArg 971
 Db 442 CTATCCCTGCGCTACAGCTGACGCTAGCTCCCTCCACTGCGGGGCGAACAAACGAG 501
 QY 972 ArgGlyLeuPheGlyValLeuLeuArgLeuLeuCysHisSerLeuPheLeuAspLeuVal 991
 Db 502 AGGAAGCTCATGTCATCTTATGATTCAAGTGCACGCCCTCTTCTCTGACCTCAGAAC 561
 QY 992 AsnSerLeuGlnThrValCysThrAsnIleTyrIleLeuLeuLeuGlnAlaIleTyrArg 1011
 Db 562 AACTCCCTGAGAGCGCTGATAGCAACGTCACAGTATGTTGCTGACAGCGCTCAGG 621
 QY 1012 PheHisAla 1014
 Db 622 TTCATGCTCC 630

RESULT 24
 BE396925 715 bp mRNA linear EST 21-JUL-2000
 LOCUS 601290610F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621050 5',
 DEFINITION mRNA sequence.

ACCESSION BE396925
 VERSION BE396925.1 GI:9342290
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbs-rxmail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc
 Clome distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM294 row: C column: 03
 High quality sequence stop: 634.

FEATURES

source
 1..715
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3621050"
 /issue_type="Burkitt Lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: Lymph; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN

ORIGIN

Alignment Scores:
 Pred. No.: 1.15e-20 Length: 715
 Score: 443.50 Matches: 98
 Percent Similarity: 90.09% Conservative: 2
 Best Local Similarity: 88.29% Mismatches: 6
 Query Match: 7.44% Indels: 5
 Gaps: 1

US-10-044-692-2 (1-1132) x BR396925 (1-715)

QY 525 GlyValGlyCysValProAlaAlaGluHisArgLeuArgGlnIleLeuAlaIlePhe 544
 Db 373 GGGGTGGCTGTGTTCCGGCCGACAGACACGCTGTGCTGAGAGATCTGGCAAGTTC 432
 QY 545 LeuHisThrPheMetSerValTyrValValGluLeuLeuArgSerPhePhe-TyrValThr 564
 Db 433 CTGCACTGGCTATGATGATGTGATGCTGTCGACGCTGCTCAGGTCTTTTATATGTCAC 492
 QY 564 rgiuThrThrPheGlnLysAsnArgLeuPheTyrArgGlySerValTyrPheIle 584
 Db 493 GGAACCAAGTTCAAAAGAACAGAGGCTTTTTCACCGAAGAGTGTCTGAGCAAGTT 552
 QY 584 uginserIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlnLeu-SerGlnVal 604
 Db 553 GCAAGCATTGGATGACAGACGACTTGAAAGGGTGCAGCTGCGGAGACTGATGGAGAG 612
 QY 604 laciValArgGlnHisArg--GluAlaArgProAlaLeuLeuThrSerArgLeuArgPhe 623
 Db 613 CAGAGGTCAAGGACGATCCGGGAAACCAAGGCCCTGCTGATGACGTCACAC---TCCGT 669
 QY 623 eileProLysProAspGlyLeuArg 631
 Db 670 TCATCCCAAGCTGAAGGGGCTGGCG 694

RESULT 25
 EX886589 703 bp mRNA linear EST 27-JUL-2004
 LOCUS EX886589
 DEFINITION EX886589 tcdk Oncorhynchus mykiss cDNA clone tcdk0036c.p.02 5prim,

ACCESSION BX886589
 VERSION GI:42819050
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 703)
 Govoroun, M., Guiguen, Y. and Le Gac, F.
 Construction and primary characterization of normalized cDNA libraries in rainbow trout, *Oncorhynchus mykiss* unpublished (2003)
 On Dec 18, 2003 this sequence version replaced gi:40135983.
 COMMENT
 JOURNAL
 TITLE
 AUTHORS
 REFERENCE
 1 (bases 1 to 703)
 Govoroun, M., Guiguen, Y. and Le Gac, F.
 Construction and primary characterization of normalized cDNA libraries in rainbow trout, *Oncorhynchus mykiss* unpublished (2003)
 On Dec 18, 2003 this sequence version replaced gi:40135983.
 CONTACT: Guiguen Y
 INRA - SCRIBE
 Campus de beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.
 Plate: 0036 row: p column: 2
 Seq primer: M13R.
 FEATURES
 SOURCE
 1.703
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="tcdbk0036c.p.02"
 /tissue_type="multi-tissues"
 /dev_stage="from embryos to adults"
 /lab_host="DH10B"
 /clone_1lb="tcdbk"
 /note="Vector: pT7T3D-pac; AGENAE Rainbow trout multi-tissues - normalized + 2 subtractions; Clone distribution: AGENAE Resource centre, Francois PUMI, Francois Plumiojouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (UREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.17e-20 Length: 703
 Score: 437.00 Matches: 95
 Percent Similarity: 64.29% Conservative: 31
 Best local Similarity: 48.47% Mismatches: 70
 Query Match: 7.33% Indels: 1
 DB: 5 Gaps: 0
 US-10-044-692-2 (1-1132) x BX886589 (1-703)
 QY 935 LeuAAPTrrArXThrLeuGluValGlnSerAspTyrSerSerTyrAlaAthrghSerile 954
 DB 1 CTGAATACACACACCTGAGCTCTA-CACAACACAGCCAGCTAGCCTGCTATCCCTG 59
 QY 955 ArgAlaSerLeuThrPheAsnArgGlyPheValAGlyArgAsnMetArgArgTyrLeu 974
 DB 60 CGCTACAGCTGACCGCTAGGCTCCGCCACCTCGCGGCGGACCAATGAGAGAGAGCTC 119
 QY 975 PheGlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeu 994
 DB 120 ATGTCCATCTTCAAGTTCAGTGCACCGCTCTTCTTGACCTCAAAACCAACTCCCTG 179
 QY 995 GlnThrValCysThrAsnLeuTyrLysLeuLeuLeuGlnAlaTyrArgPheHisAla 1014
 DB 180 GAGGCTGTATATGACACTTCAATGTTAGTGTGCTCAGACGCTTCAAGTCCATGCC 239
 QY 1015 CysValLeuGlnLeuProPheHisGlnGlnValTrrPlyAsnProThrPhePheLeuArg 1034

DB 240 TGTGCACAGAGTTTGCCTTTGTCAGAAAGTGGCGGAAACCACTGACTTCTCAAT 299
 QY 1035 VallieserApThrAlaSerLeuCystrSerileLeuLysAlaLysAsnAlaGlyMet 1054
 DB 300 CTGATCTGGAGCTTGGCCGAGTACCAACCATCTAGTCAGACTTGCACAAAGGTG 359
 QY 1055 SerLeuGlyAlaLysGlyAlaAlaGlyProLeuProSerGlyAlaValGlnTrpLeuCy 1074
 DB 360 TCTTAGGCTTGAAGCTTAAACAGTACCTTCAAGTATGAGGAGCTGAAGTATATAC 419
 QY 1075 HisGlnAlaPheLeuLeuLysLeuThrArgHisArgValThrTyrValProLeuLeuGly 1094
 DB 420 TGTCTGGCTCTCTGTTGTTCTGTCTGTCCCTGATCCCTCTACTACCATCTCTGCT 479
 QY 1095 SerLeuArgThrAlaGlnThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAla 1114
 DB 480 CCGCTACGACACGTTAAGAGAGCTGAGAGGAGAGCTGAGAGGTTTGAGATGGCCCA 539
 QY 1115 LeuGlnAlaAlaAlaAsnProAlaLeuProSerAspPheLysThrile 1130
 DB 540 ATCAGACAGGCTGCCACACCCAAATGCTGAAGCTTCAAGGCCATC 587
 RESULT 26
 CF531258 344 bp mRNA linear EST 12-SEP-2003
 LOCUS UI-M-FY0-GSP-h-01-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 DEFINITION IMAGE:30355848 5', mRNA sequence.
 ACCESSION CF531258
 VERSION CF531258.1 GI:34583222
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousef1.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: PYX-5.
 FEATURES
 SOURCE
 1.344
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355848"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_1lb="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: PYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National

ORIGIN Institute of Mental Health (NIMH), Hemm Chinn, Ph.D.,
program coordinator."

Alignment Scores:

Pred. No.: 1,25e-20 Length: 344
Score: 436.00 Matches: 85
Percent Similarity: 79.82% Conservative: 6
Best Local Similarity: 74.56% Mismatches: 23
Query Match: 7.31% Indels: 0
DB: 7 Gaps: 0

US-10-044-692-2 (1-1132) x CF531258 (1-344)

QY 904 ValValaAspPheProValaGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetPro 923
DB 1 GGGGTAACTTCCTCCCTGGAGCCTGGTACCTGGGGTGGGACGCTCCATACAGAGCTGCT 60
QY 924 AlaHieGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluValGln 943
DB 61 GCTCACTGCTGCTTCCCTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 944 SerAspTyrSerSerTyrAlaArgThrSerTyrAlaSerLeuThrPheAsnArgGly 963
DB 121 TGTGACTACTACAGGTTATGCCCGACCTCAATTAAAGACGACCTCACTTCCAGAGTGTTC 180
QY 964 PheValAlaGlyArgAsnMetArgGlyValLeuPheGlyValLeuPheLeuGlyCysHis 983
DB 181 TTCAGAGCTGGGAGACCATGGGAAACAAGCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGT 240
QY 984 SerLeuPheLeuAspPheGluValaSerLeuGlnThrValCysThrAsnIleTyrLys 1003
DB 241 GGTCTATTCTTCTACACTTGGAGGTCGAAACAGCTTCAAGAGCTGATCANTATATACAG 300
QY 1004 IleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeu 1017
DB 301 ATCTTCCTGCTTACAGGCTTACAGGTTCCATGATGTGATT 342

RESULT 27 409 bp mRNA linear EST 19-APR-1997
AA311750
LOCUS EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
DEFINITION
ACCESSION AA311750
VERSION AA311750.1 GI:1964077
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 409)

TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE
PUBMED 96026280
75606098

COMMENT

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@igf.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers

FEATURES

source 1..409
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):158964"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/clone_id="Jurkat T-cells VI"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Alignment Scores:
Pred. No.: 9.44e-20 Length: 409
Score: 425.00 Matches: 80
Percent Similarity: 97.56% Conservative: 2
Best Local Similarity: 97.56% Mismatches: 0
Query Match: 7.13% Indels: 0
DB: 1 Gaps: 0

US-10-044-692-2 (1-1132) x AA311750 (1-409)

QY 866 LeuValaAspAspPheLeuLeuValThrProHisLeuThrHisAlaLeuThrPheLeuArg 885
DB 3 TTGGTGGATGATTCTTGTGTGTACACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 62
QY 886 ThrLeuValaGlyValaProGluTyrGlyCysValaValaLeuAspLysThrValaVal 905
DB 63 ACCCTGTCGAGGAGTCCCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122
QY 906 AsnProValaGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHis 925
DB 123 AACTTCCCTGTAAGAGACGAGCCTGGGTGGACAGGCTTTTNTTCAAGTCCGAGCCAC 182
QY 926 GlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluValaGlnSerAsp 945
DB 183 GGCNTATTCCCTGATGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 242
QY 946 TyrSer 947
DB 243 TACTCC 248

RESULT 28 679 bp mRNA linear EST 21-JUL-2000
BE396606
LOCUS 601289077F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619674 5',
DEFINITION
ACCESSION BE396606
VERSION BE396606.1 GI:9341882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 679)

TITLE NIH-MGC <http://mgi.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L1CM290 row: i column: 19
High quality sequence start: 2
High quality sequence stop: 656.

ORIGIN

[illegible]

US-10-044-692-2 (1-1132) x BE396606 (1-679)

Oy	525	GLYVALGTCYRVALPRALG-ALAGLNIHISARGIENURGIUGIULIEUALALYEPH	544
Dd	372	GGGGTGGCTGTGTTCGGGCTGCAGACACCGTGTGCTAGAGATCTGGCCAAATT	431
Oy	544	eleuHISrTp-LeuMeSeSeValTYrValValGIuLeuLeuARgSePhePheTYrValT	564
Dd	432	CTTCGACATGCTCTATATGATGTGTACGTGTGTGAGCTGTCAAGCTTCTTTATATGCA	491
Oy	564	hrGIuThrThr-PheGIuLYSaSaNaRgLeuPhePheTYrARgLYSeSeValITPSeTLYSL	584
Dd	492	CGAGAGACACGCTTTCAAAAGAAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAGACAGT	551
Oy	584	eugInSeITileGLYrILEArGGINHISLeuLYSArValGIuLeuARgLIuLeuSeRGIuA	604
Dd	552	TGCAAAGCATTTGSAATCAGACAGCACCTTGAAGAAGGGTGCAGCTGGGAGAGCTGTGGAAAG	611
Oy	604	IaGIuValARgGIuHISARGIuIArARgPPro	614
Dd	612	CAGAGGTGCGGACGATCTGGAGACCGGCCG	643
RESULT 29			
LOCUS	BU111946	835 bp	mRNA
DEFINITION	601217372r1 CSEQCHL13 Gallus gallus CDNA clone ChEST59p18 5', mRNA		linear
ACCESSION	BU111946		
VERSION	BU111946.1	GI:25315846	
KEYWORDS	EST.		
SOURCE	Gallus gallus (chicken)		
ORGANISM	Gallus gallus		
REFERENCE			
AUTHORS	Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Butt,D.W., Bosch,E.,		
TITLE	Fong,W.T., Rickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.U.		
	A Comprehensive Collection of Chicken cDNAs		

JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE	22335534
PUBMED	12445392
COMMENT	Contact: Simon Hubbard

FEATURES

Alignment Scores:	
Pred. No.:	3.3e-19
Score:	424.07
Percent Similarity:	50.90%
Best Local Similarity:	38.63%
Query Match:	7.11%
GB:	5
	Gaps:
	2
	Length:
	835
	Matches:
	107
	Conservative:
	34
	Mismatches:
	74
	Indels:
	63
	Gaps:
	2

US-10-044-692-2 (1-1132) X BU11946 (1-835)

QY	592	HisLeuLysArgValGlnLeuArgGluLeuSerGluValIaGluValArgGlnHisArgGlu	611
Db	184	CATTTCGCCAAGTCACTACGTACGTCCTTGCTTCAGAGGAATGGAAGTCATCCGTCAA	243
QY	612	AlaArgProAlaLeuLeuThrSerArgLeuArgPheIleProLysProAspGlyLeuArg	631
Db	244	AAAAGTATTTTCCATTGCATCAAGGCTCCGGTTCATTCCTTAAGAATGATGTTTAAGA	303
QY	632	ProIleValAsnMetAspTryValValGlyVala-ArgThrPheArgArgGluLysArgAl	651
Db	304	CCCGTGTGAACCTAAGCCGGCTGTTGTAAGAGACAGAACTCACCAAGGAACAGACAGAGA	363
QY	651	ArgIuArgLeuThrSerArgValLysAlaLeuPheSerValLeuAsnTryGluArgAlaAr	671
Db	364	AAAG-----	367
QY	671	GArgProGlyLeuLeuGlyAlaSerValLeuGlyLeuAspAspIleHisArgAlaTrpAr	691
Db	367	-----	367
QY	691	GThrPheValLeuArgValAlaGlnAspProProGluLeuUtryrPheValLysVa	711
Db	368	-----	372
QY	711	IAspValThrGlyAlaTryAspThrIleProGlnAspArgLeuThrGluValIleAlaSe	731
Db	373	TGATGTATCCAGAGCTTTGATATACCATTCCTCACAGAAGATCTGTGAAAGCATATCACA	432
QY	731	rllellellyPro-----GlnAsnThrTryCysValAlaArgArgTryrAlaValValGlnly	749

Db 433 GGCTTGAACCTGAGAGCAACCTGTATGAAATTAAGTGTATGCAATGATATGAT 492
 QY 749 salalahlslgylhlsvalarjlyalaahelyserhlsvalserthrleuthrasple 769
 Db 493 TACCCCACTGAGAAAGCAGAGAACTCATATAGAGACATGTTCTACTTTCAGAGATT 552
 QY 769 uqlnprorymetarjlnphevalalahlslenglnlurthrserproleuargaspal 789
 Db 553 TATTCACAGACATGAGACATGTTGTGTCCAAAGCTTCAGAGCACTTCATTAGAAAGTC 612
 QY 789 aalvalallieglnlserSerSerleuansnglnlaserSerjlyleupheaspvalph 809
 Db 613 AATAGATGTGACACAGCTGCTTACTTAAATGGAACAGATTCCACCTGTTACTTCTT 672
 QY 809 eleuargpmetcyshlsishlsalavalargjlyleargjlyserjlyvalglnCysgl 829
 Db 673 TCTTCAAGTTCATCATATATACATCTCGAGATTTGGCACAGTACTATATACAGTCTC 732
 QY 829 nglylleproglnglyserlileuserthrleuleucysserleucyetyrjlyasphe 849
 Db 733 TGGAAATCCACAGAGGCTCCATTGTGC--AACTTACTTTCAGCTTATGCTACGAGACAT 790
 QY 849 tgluan-lyslau-phealaglyleargargaspjlyleuleu 863
 Db 791 GGAAACCAATTAATCTCTGTGGATCCAGAGATGGAGTCTA 835

RESULT 30
 BE514070 649 bp mRNA linear EST 07-AUG-2000
 LOCUS BE514070 601316575F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634962 5',
 DEFINITION mRNA sequence.
 ACCESSION BE514070
 VERSION BE514070.1 GI:9721282
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 649)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LLCM330 row: f column: 19
 High quality sequence stop: 628.

FEATURES

source

1..649
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3634962"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN

Alignment Scores:
 .Pred. No.: 3.09e-19 Length: 649

Score: 422.00 Matches: 87
 Percent Similarity: 95.74% Conservative: 3
 Best Local Similarity: 92.55% Mismatches: 2
 Query Match: 7.08% Indels: 2
 DB: 2 Gaps: 0

US-10-044-692-2 (1-1132) x BE514070 (1-649)

QY 525 GLYVALGICYSVALPRCAALAGLHLSARGLHUGLHLEUALALYSPHE 544
 Db 368 GGGGTGGCTGTGTCCGCCGACACACGCTGCTGATGAGATCTCGCCAACTTC 427
 QY 545 Leu-HisThrLeuMetSerValjlyvalglnleuleuargserpheepryvalth 564
 Db 428 CTGCACTGGCTATGATGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTATGTCCAC 487
 QY 564 rgluthrthrphelglnlyasnaargleu-pheprerjlyarglysserValTrpSerlysl 584
 Db 488 GGAGACCAAGCTTCAGAAAGACAGGCTCTTTTCTACCCGAGAGATGTCTGGAGCAAGT 547
 QY 584 euglnserlleglyllearglnhlsleuysargvalglnleuargjlyleuargjlyua 604
 Db 548 TCGAAGGATTTGAAATTCAGACACACTTTCAGAGAGGCTCGAGCTCGGAGACTGTCCGAG 607
 QY 604 laglvalargjlnhlsargjlnlaargproalaleu 616
 Db 608 CAGAGTCAGGACGATCGGAGACAGGCCCGCTGATG 645

RESULT 31
 BE514188 610 bp mRNA linear EST 07-AUG-2000
 LOCUS BE514188 601316376F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634987 5',
 DEFINITION mRNA sequence.
 ACCESSION BE514188
 VERSION BE514188.1 GI:9721400
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 610)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LLCM330 row: g column: 20
 High quality sequence stop: 610.

FEATURES

source

1..610
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3634987"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN

Alignment Scores:

Pred. No.: 1.63e-18 Length: 610
 Score: 411.00 Matches: 80
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.89% Indels: 0
 DB: 2 Gaps: 0

US-10-044-692-2 (1-1132) x BBS14188 (1-610)

QY 525 GYVAGIYGVVAlProAlaAlaGluHisArgLeuArgGluGluIleuAlaLysPhe 544
 Db 369 GGGGTGGCTGTGTTCGGCCGCGAGCACCGCTGCGGAGAGATCCTGGCAAGTTTC 428
 QY 545 LeuHISTPLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThr 564
 Db 429 CTGCACTGGCTATGATGTGTACGTCGAGCTGCTCAGAGCTTTCTTTATATGTCAG 488
 QY 565 GlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTyrPserLysLeu 584
 Db 489 GAGACACAGTTTCAAAGAACAGCGCTTTTCTACCGAGAAAGATCTCGAGCAAGTTG 548
 QY 565 GlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluAla 604
 Db 549 CAAGCATTTGATCAGACAGCACTTGAAGAGGTGCGAGCTCGGGAGCTGTGGAAGCA 608

RESULT 32

BUI39751 696 bp mRNA linear EST 25-NOV-2002
 LOCUS 60134527F1 CSEQCH24 Gallus gallus CDNA clone CHEST116f8 5', mRNA
 DEFINITION sequence.

ACCESSION BUI39751
 VERSION BUI39751.1 GI:25354188
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

1 (bases 1 to 696)

REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.,
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 2235534
 PUBMED 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)

PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source 1.696
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, HiseX"
 /db_xref="taxon:9031"
 /clone="CHEST116f8"
 /dev stage="16 day embryo"
 /lab_host="DH10B"
 /clone_1fb="CSEQCH24"
 /note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
 EORI; Site 2: NotI; Modification of pBluescript II KS(+)
 [Stratagene] vector to accommodate cDNA produced with the
 T-primed protocol (Construction of uni-directionally
 cloned cDNA libraries from messenger RNA for improved 3'
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
 ligate in double stranded adaptor containing BsgI and
 BamHI sites [5'gagcgctgacgcccgcgacgcaaaaaag]

ORIGIN

[5'aattcttttttcgagatccggggctgcagc]

Alignment Scores: 2.39e-17 Length: 696
 Pred. No.: 395.50 Matches: 85
 Score: 64.74% Conservative: 27
 Percent Similarity: 49.13% Mismatches: 58
 Best Local Similarity: 6.63% Indels: 3
 Query Match: 5 Gaps: 2

US-10-044-692-2 (1-1132) x BUI39751 (1-696)

QY 9 AlaValArgSerLeuLeuArgSerHisTyrArgGluValLeuProLeuAlaThrPheVal 28
 Db 72 GCGGTCTCGGCGCGCGCTGCGGAGCTGTACGCCAGGCCACGCCCTCGAGCCCTTCGTC 131
 QY 29 ArgArgLeu-----GlyProGlnGlyTyrArgLeuValGlnArgGlyAspProAla--- 45
 Db 132 CGCGCGCTGCAGAGAGGTGGACCGGGAGGTGCGAGTCTCGAGCGACGACCGCTCAG 191
 QY 46 AlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyrAspAlaArgProPro 65
 Db 192 TGCTACCGACCTTGCTGTGCGAGTGTGTGTCTCCCGCGGTCTCGCCGCTC 251
 QY 66 ProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAlaArgValLeu 85
 Db 252 CCGCGCCCATCTGCTTCCAGACGATTAATCAGTACAGAGCAAGTATCATCAAGATCTT 311
 QY 86 GlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAlaLeuLeuAsp 105
 Db 312 CAGAGCTGTGTGAAGAAAGAAAGAAAGAAACATCTTGCGTATGATATCTTGTGTGAT 371
 QY 106 GlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyrLeuProAsn 125
 Db 372 GAGAACAGTTGTCACTTCAGAGCTTTGCCATCTTGTGTATATACAGCTATCTGCCAAT 431
 QY 126 ThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeuLeuArgArgValGly 145
 Db 432 ACTGTACAGAAACCATTCGCTACGTAGTGCCTCTGGAGATCTCTAGTAGAGATAGG 491
 QY 146 AspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSer 165
 Db 492 GACGACGTGATGATGTACTGCTGAGGACAGTGCACCTTCTTACTGCTGCTCCCAACT 551
 QY 166 CysAlaTyrGlnValCysGlyProProLeuTyrGlnLeu 178
 Db 552 AACTGTACACAGGTCTCGCGGCACCAATTATGAATT 590

RESULT 33

BUI783093 343 bp mRNA linear EST 23-MAR-2004
 LOCUS BUI783093 RIKEN full-length enriched, 17.5 days embryo whole body
 DEFINITION Mus musculus CDNA clone l930172A03 5', mRNA sequence.

ACCESSION BUI783093
 VERSION BUI783093.1 GI:39709732
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 343)

AUTHORS Carrinci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M.,
 Aizawa, K., Arikawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
 Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watanishi, A.,
 Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,
 Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustinich, S., Beisel, K.,
 Pavani, W., Aidinis, V., Nakagawa, A., Heid, W.A., Iwata, H., Kono, T.,
 Nakachi, H., Lyons, P., Wells, C., Hume, D.A., Fasolino, M.,
 Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, O., Mombaerts, P.,
 Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
 TITLE Targeting a complex transcriptome: the construction of the mouse
 full-length cDNA encyclopedia

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Res. 13 (6B), 1273-1289 (2003)
22703353
12819125
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
further details.

FEATURES

source
1. .343
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930172A03"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_idb="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN

Alignment Scores:
Pred. No.: 3,16e-17 Length: 343
Score: 387.00 Matches: 77
Percent Similarity: 86.00% Conservative: 9
Best Local Similarity: 77.00% Mismatches: 14
Query Match: 6.49% Indels: 0
DB: 6 Gaps: 0

US-10-044-692-2 (1-1132) x BY783093 (1-343)

QY 70 SerPheArgGlnValSerCysLeuIysGluLeuValAlaArgValLeuGlnArgLeuCys 89
DB 11 TCCTTCACACAGGTGTCTCCCTGAAGAGCTGTGGCGAGGTTGGCAGAGCTCTGC 70
QY 90 GluArgGlyAlaIysAsnValLeuAlaPheGlyPheAlaLeuAspGlyAlaArgGly 109
DB 71 GAGCGCAACGAGAAAGCTGTGGCTTTGGCTTTGAGCTTTACGAGGCCAGGCC 130
QY 110 GlyProProGluAlaPheThrThrsSerValArgSerTyrLeuProAsnThrValThrAsp 129
DB 131 GGGCTCCACAGGCTTCACTAGTACGTGCTGCTGCTGCTGCCAACACTGTTATTGAG 190
QY 130 AlaLeuArgGlySerGlyAlaTyrPglyLeuLeuLeuArgValGlyAspAspValLeu 149
DB 191 ACCCTGGGTGTGAGGTGATGATGCTAGCTGTAGCCGAGTGGGCGAGACCTGCTG 250
QY 150 ValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyrGln 169
DB 251 GCTACCTGTGGCACACTGTGCTCTTATCTTGTGTCGCCCCCACTGTGCTACCGAG 310

RESULT 34
LOCUS BY784804 338 bp mRNA linear EST 23-MAR-2004
DEFINITION BY784804 RIKEN full-length enriched, 17.5 days embryo whole body
ACCESSION BY784804
VERSION BY784804.1 GI:39711443
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 338)
AUTHORS

Garnini, P., Waki, K., Shiraki, T., Komuro, H., Shibata, K., Itoh, M.,
Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
Suganara, Y., Saito, R., Oeato, N., Fukuda, S., Sato, K., Matsubara, A.,
Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,
Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustinich, S., Beisel, K.,
Pavan, W., Aldinis, V., Nakagawa, A., Held, W. A., Iwata, H., Kono, T.,
Makuchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M.,
Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,
Muramatsu, M., Okazaki, Y., Kawai, J.,
Targeting a complex transposon: the construction of the mouse
full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
further details.

FEATURES

source
1. .338
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L93018A05"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_idb="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN

Alignment Scores:
Pred. No.: 4,99e-17 Length: 338
Score: 384.00 Matches: 76
Percent Similarity: 86.00% Conservative: 10
Best Local Similarity: 76.00% Mismatches: 14
Query Match: 6.44% Indels: 0
DB: 6 Gaps: 0

US-10-044-692-2 (1-1132) x BY784804 (1-338)

QY 70 SerPheArgGlnValSerCysLeuIysGluLeuValAlaArgValLeuGlnArgLeuCys 89
DB 11 TCCTTCACACAGGTGTCTCCCTGAAGAGCTGTGGCGAGGTTGGCAGAGCTCTGC 70
QY 90 GluArgGlyAlaIysAsnValLeuAlaPheGlyPheAlaLeuAspGlyAlaArgGly 109
DB 71 GAGCGCAACGAGAAAGCTGTGGCTTTGGCTTTGAGCTTTACGAGGCCAGGCC 130
QY 110 GlyProProGluAlaPheThrThrsSerValArgSerTyrLeuProAsnThrValThrAsp 129
DB 131 GGGCTCCACAGGCTTCACTAGTACGTGCTGCTGCTGCTGCCAACACTGTTATTGAG 190
QY 130 AlaLeuArgGlySerGlyAlaTyrPglyLeuLeuLeuArgValGlyAspAspValLeu 149
DB 191 ACCCTGGGTGTGAGGTGATGATGCTAGCTGTAGCCGAGTGGGCGAGACCTGCTG 250
QY 150 ValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyrGln 169
DB 251 GCTACCTGTGGCACACTGTGCTCTTATCTTGTGTCGCCCCCACTGTGCTACCGAG 310

RESULT 35
BY775178
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BY775178 336 bp mRNA linear EST 23-MAR-2004
BY775178 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone U930091N09 5', mRNA sequence.
BY775178
BY775178.1 GI:39701816
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 336)
Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
Sugahara, Y., Saito, R., Otsu, N., Fukuda, S., Sato, K., Watanabe, A.,
Hirazane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,
Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustinich, S., Beisel, K.,
Pavan, W., Aldini, V., Nakagawa, A., Heid, W. A., Iwata, H., Kono, T.,
Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M.,
Henech, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,
Muramatsu, M., Okazaki, Y., Kawai, U. and Hayashiraki, Y.
Targeting a complex transcritpome: the construction of the mouse
full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)
22703353
12619125

Contact: Yoshinide Hayashiraki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
further details.

FEATURES
source
Location/Qualifiers
1..336
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="U930091N09"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN
Alignment Scores:
Pred. No.: 9 38e-17 Length: 336
Score: 380.00 Matches: 77
Percent Similarity: 85.00% Conservative: 8
Best Local Similarity: 77.00% Mismatches: 15
Query Match: 6 37% Indels: 0
Gaps: 0
US-10-044-692-2 (1-1132) x BY775178 (1-336)

QY 70 SerpheaTglnValSerCysLeuYsgIuLeuValAlaArgValLeuGlnArgLeuCys 89
DB 11 TCTTCCACCAAGTGTTCATCCCTGAAGAAGCTGTGGCCAGGTTGACAGAGACTTCN 70
QY 90 GUAAGGGLAAlaValLeuAlaPheGlyPheAlaLeuLeuAspGlyAlaArgGly 109
DB 71 GAGCGCAACGAGAAAGCTGCTTTGGCTTTGAGACTGCTTAACGAGCCAGAGGCG 130

QY 110 G1ProProGluAlaPheThrThrsValArgSerTyrLeuProAsnThrValThrAsp 129
DB 131 GGGCTCCCATGGCTTACTACTAGCTGGCTAGCTACTTGGCCCAACACTGTATTGAG 190
QY 130 AlaLeuArgGlySerGlyAlaTfPGLyLeuLeuAlaGValGlyAspAspValLeu 149
DB 191 ACCCTGCTGCATGCTGTCATGATGATGCTGTGGACCCAGTGGGAGACGACTGCTG 250
QY 150 ValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTfGln 169
DB 251 GCTACCTGTGGACACTGCTGTATTCTTGTGGTGGCCCCAGCTGACTTACGAG 310

RESULT 36
AW244516/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

AW244516 347 bp mRNA linear EST 25-JAN-2002
BR-END06B09 Bain Rancourt retinoic acid induced ES cell neural
differentiation subraction library Mus musculus cDNA clone 06B09
similar to gp[Af073311][Af073311 Mus musculus telomerase catalytic
subunit mRNA, complete cds, mRNA sequence.
AW244516
AW244516.1 GI:8051265
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 347)
Bain, G., Mansergh, F. C., Wide, M. A., Hane, J. E., Ito, G. A.,
Rancourt, S. L., Ray, W. J., Yoshimura, Y., Tsuzuki, T., Gottlieb, D. I.,
and Rancourt, D. E.
ES cell neural differentiation reveals a substantial number of
novel ESTs
Funct. Integr. Genomics 1 (2), 127-139 (2000)
21652683
11793228

Contact: Rancourt DE
Department of Biochemistry and Molecular Biology
University of Calgary
3330 Hospital Drive N.W., Calgary, Alberta, T2N 4N1, Canada
Tel: 403 220 2888
Fax: 403 283 8727
Email: rancourt@calgary.ca; URL: http://www.acs.ucalgary.ca/
rancourt

DNA sequencing by: University Core DNA Services, University of
Calgary. Submitted sequence has been trimmed at both ends to remove
the adaptor oligos containing the EcoRI sites, i.e. GAATTCGACATCA
(beginning) and TAGTCGCAATTC (end) removed. Therefore, reported
insert length is longer than actual EST sequence length.
Insert length: 359 Std Error: 10.00
Seq primer: T3 Or T7.

FEATURES
source
Location/Qualifiers
1..347
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129"
/db_xref="taxon:10090"
/clone="06B09"
/cell_type="embryonic stem (ES) cell"
/cell_line="D3"
/lab_host="DH5 alpha"
/clone_lib="Bain Rancourt retinoic acid induced ES cell
neural differentiation subraction library"
/note="vector: pBluescript II SK+ (Stratagene), Site_1:
EcoRI, Site_2: EcoRI, Library constructed by Dr. Gerard
Bain (present address: Hoechst-ARIAD Genomic Center,
ARIAD Pharmaceuticals Inc., 26 Landsdowne Street,
Cambridge, Massachusetts, 02139-4234, U.S.A.). To isolate
cDNAs corresponding to mRNAs which are upregulated during
the neural differentiation of ES cells in vitro, the
subtractive hybridization technique of Wang and Brown (1)
was employed. Poly(A)+ RNA was prepared from both
undifferentiated ES cells and from embryoid bodies which
had been cultured for 4 days in the absence of RA followed

Db 272 CTCAGGCCA---TTATTGAGACCAAGACATTTCTTACTCCAGGAGAGATGGCCAAAG 328
 Qy 340 GlnLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArg 359
 Db 329 CGCTTAACCCCTCATCTCTACTACTGACCAACCTCCAGACCTTAAGCTGATGGGGCCAGAGAGA 388
 Qy 360 LeuValGluThrTlePheLeuGlySerArgProTpmPheProGlyThrProArgArgLeu 379
 Db 389 CTGGTGAGATCATCTTTCTGGGCTTCAGGCTTAGACATCAGACCACTGTCAGAGACA 448
 Qy 380 ProArgLeuProGluArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsn 399
 Db 449 CACCGCTTATCGCGTGCATCTGCGAGATGCGGCCCCCTGTTCCACAGCTGCTGGTGAAC 508
 Qy 400 HisAlaGlnCysProTyrGlyValLeuLeuLeuLysThrHisCysProLeuArgAlaAla--- 418
 Db 509 CAGGAGAGTGCACCAATATGTCAGACCTCCAGGTCAATGTCAGATGGTTTGAACACCAAC 568
 Qy 419 -----ValThrProAlaAlaGlyValCysAlaArgGluLeuProGlnGlySerValAla 436
 Db 569 CAACAGGTGACAGATCCCTTG----- 589
 Qy 437 AlaProGlnGluGluSerThrArgProArgArgLeuValGlnLeuLeuArgGlnHisSer 456
 Db 590 -----AAGACACAGCCACGACGACCTCATGATTGCTCCGCTGACAGAC 634
 Qy 457 SerPro 458
 Db 635 AGTCCC 640
 RESULT 39
 CK392784 619 bp mRNA linear EST 29-DEC-2003
 LOCUS DEFINITION K0850A03-5 NIA Mouse 8.5-dpc Whole Embryo cDNA library (Long) Mus
 accession CK392784 musculus cDNA clone NIA:K0850A03 IMAGE:30083138 5', mRNA sequence.
 VERSION CK392784.1 GI:40383303
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 619)
 Pao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
 MEDLINE 21429098
 PUBMED 11544199
 COMMENT Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun-gfc.nia.nih.gov
 Plate: K0850 row: A column: 03
 Seq primer: M13 Reverse
 High quality sequence stop: 619
 POLYA=No.
 FEATURES
 source location/Qualifiers
 1..619
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:K0850A03-5"
 /clone="NIA:K0850A03 IMAGE:30083138"
 /issue_type="whole embryo including extraembryonic
 tissues at 8.5-days postcoitum"
 /dev_stage="8.5-days postcoitum"
 /lab_host="DH10B"
 /clone_11b="NIA Mouse 8.5-dpc Whole Embryo cDNA library
 (Long)"

ORIGIN

Alignment Scores:

Pred. No.:	2,24e-15	Length:	619
Score:	366.00	Matches:	97
Percent Similarity:	55.61%	Conservative:	22
Best Local Similarity:	45.33%	Mismatches:	79
Query Match:	6.14%	Indels:	16
DB:	7	Gaps:	6

/note="Vector: pSPORT1 (Invitrogen); Site.1: SalI; Site.2:
 NotI. Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (<http://igsun-gfc.nia.nih.gov/cDNA>). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
 extracted from a pool of 13 embryos at 8.5-days
 postcoitum. Double-stranded cDNAs were synthesized with an
 Oligo(dT) primer [Invitrogen:
 5'-pGACTTACTTCAGATCGGAGCGGCCCTTTTCTTTT-3'] from
 9.1 ug of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to lone-linker Lx-Sal4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.5 kb. The library was constructed
 by Yulan Pao (NIA)."

US-10-044-692-2 (1-1132) x CK392784 (1-619)

Qy 209 GlnAlaGlyValProLeuGlyLeuProAlaProGlyAlaArgArgGlySerAla 228
 Db 3 GAAAGACCGAACCCTGCGCTCCGATCTGAGATCAAGAGGACATCTGATCCAC 62
 Qy 229 SerArgSerLeuProLeuProLysArgProArgArgGlyAlaAlaProGluProGluArg 248
 Db 63 AGTACAAAGTGTCTTCAAGAGGAGCCAGATGCTACTGTCGAGAGTGAGAG 122
 Qy 249 ThrProValGlyGlnGlySerThrAlaHisProGlyArgThrArgGlyProSerAspArg 268
 Db 123 GGAACC-----CACAGGAGGTGCTACCAACCCCAATCGGCATA 161
 Qy 269 GlyPheCysValValSerProAlaArg-----ProAlaGluGluAlaThr 283
 Db 162 TCATGG--GTGCCAAGTCTGCTGCGTCCCGAGAGTCCCTACTGACAGAAAGATTGG 218
 Qy 284 SerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGlnHis 303
 Db 219 TCTTCAAGGAAGAAGGTGCTGACCTGAGTCTCT---GGGTGGGTGCTGTAAAC 275
 Qy 304 HisAlaGlyProProSerThrSerArgProProArgProTpmPheThrProCysProPro 323
 Db 276 AAGCCAGGTCCACATCTGCTGTACACCCCGCAAAATGCTTTCAGCTCAGGCCA 335
 Qy 324 ValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAsp---LysGluGlnLeuArg 342
 Db 336 ---TTATTGAGACCAAGACATTTCTTACTCCAGGGAGAGAGGCAAGAGGCTTAAC 392
 Qy 343 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 362
 Db 393 CCTCATCTTCTACTGACCAACCTCCAGCTTAAGTGGGGCAGAGACTGTGGAG 452
 Qy 363 ThrLlePheLeuGlySerArgProTpmPheProGlyThrProArgArgLeuProArgLeu 382
 Db 453 ATCATCTTCTGGGCTCAAGGCTTAGACATCAGACCACTGTCAGAGACACACCTCTTA 512
 Qy 383 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlnHisAlaGln 402
 Db 402

Db 513 TCAGCTGATGCTGAGATGCGGCCCTGTTCCACAGCTGCTGTGATGACCATGACAG 572
Qy 403 CysProTyrGlyValIleuLeuLeuYrthHisCysProLeuArg 416
Db 573 TGCCAAATGTCAGACTCTCAGGTCAATGACAGGTTTGA 614

RESULT 40
BE268183 779 bp mRNA linear EST 13-JUL-2000
LOCUS 601125261P1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345111 5',
DEFINITION mRNA sequence.
ACCESSION BE268183 GI:9141784
VERSION BE268183
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS 1 (bases 1 to 779)
TITLE NIH-MGC Consortium of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM132 row: 1 column: 16
High quality sequence step: 535.
Location/Qualifiers
1..779
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3345111"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAACAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Alignment Scores: 1.24e-14 Length: 779
Pred. No.: 357.50 Matches: 116
Score: 50.578 Consensitive: 16
Percent Similarity: 44.44% Mismatches: 50
Best Local Similarity: 6.00% Indels: 81
Query Match: 2 Gaps: 9
DB: 2

US-10-044-692-2 (1-1132) x BE268183 (1-779)

Qy 445 ProArg---ArgLeuValGlnIleuLeuArgGlnHisSerSerProTrp----- 459
Db 166 CCCCCTGTCGAAATGTCAGAGTCCAGGTGAGGTCCCGACGCTTGAGTGGCGTGAATGT 225
Qy 460 GlnValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGly 479
Db 226 GCGGTGTCGAGATGTCGAGGTCTGGCGTGAAG-----TCGCAGAGCCCTTGTC- 275
Qy 480 SerArgHisArgGlnArgArgPheLeuArgGlnThrIleValPheIleSerLeuGlyLys 499
Db 276 AGC----- 278

Qy 500 HisAlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArg----- 515
Db 279 -----TCGATGTGGCGGTCTCGGATGTGTGACAGTTC 308
Qy 516 -----AspCysAlaTrpLeuAlaArgSerPro-----Gly 525
Db 309 CCGGGGTGAGTTCACAGGCCCCCTCGGTGATCTGAGATGTCATGTCCTCTCTTAAGGG 368
Qy 526 ValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluIleLeuAlaLysPheLeu 545
Db 369 GTTGGCTGTGTCCTGGCCGACAGACCTGTGCGTGAAGAGATCTGGCCAAATCTTG 428
Qy 546 HisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGlu 565
Db 429 CACTGGCTGATGATGATGTGATAGTCTCGAGCTGCTCAGAGTCTTTTATATGTACAGAG 488
Qy 566 ThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrp-SerLysLeuG1 585
Db 489 ACCACGTTTCAAAAMAAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGACGCAAGTTCG 548
Qy 585 nSerIle-GlyIleArgGlnHisLeuLysArg-----ValGlnLeuArgGluLeuSerG 603
Db 549 AAGCATTTGGAATCAGACAGCATTTGGAAGAGGTGCTCGCTTCCGGAACTTGTTG 608
Qy 603 LuAlaGluValArg-GlnHisArgGlnLysArgProAlaLeuLeuThr-SerArgLeuArg 622
Db 609 GAAGGAGAGTCCGGCGGCTTCCGGAAGCTGCGCGCGTGTGAGAGTCCAAACTGG 668
Qy 622 gPheIleProLysProAspGlyLeuArgProIleValIleMetCysArgTyrValValGlyAl 642
Db 669 TTTCATCCCAAAAGCTGAGGCTCTG--GCCCTGTGAACCTG----- 709
Qy 642 aArgThrPheArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAlaLeuPh 662
Db 710 ----CCTAGTCTGGGGCCCAAAAGTTCGGA----- 736
Qy 662 eSerValLeuLeuTyrGlnLysArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 737 -----GAAAGGCGGGGTGCACCGGGGAGCGGGCGGGGCTC 775

RESULT 41
BU122597 875 bp mRNA linear EST 25-NOV-2002
LOCUS 60314841F1 CSEQHL18 Gallus gallus cDNA clone ChEST151a2 5', mRNA
DEFINITION sequence.
ACCESSION BU122597 GI:25332991
VERSION BU122597.1
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 875)
REFERENCE Boardman, P.E., Sanz-Ezquerro, D., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22355534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1OD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1..875
/organism="Gallus gallus"
/mol_type="mRNA"
/strains="Compton Line 151"

```

/db xref="taxon:9031"
/clone="ChEST151a12"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQC.H1.8"
/notes="Organ: small intestine; Vector: pluscript II
KS(+); Site 1: EcoRI; Site 2: NotI; Modification of
pluscript II KS(+); (Stratagene) vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pluscript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
containing BspI and BamHI sites
[5'ggcgcgtcgaagcccgatccgaataaag]
[5'aattcttttttcgagtcggtcgcacgc]"

```

ORIGIN

Alignment Scores:

```

Pred. No.: 6,26e-14 Length: 875
Score: 348.50 Matches: 105
Percent Similarity: 53.46% Conservative: 34
Best Local Similarity: 40.38% Mismatches: 90
Query Match: 5.85% Indels: 32
DB: Gaps: 9

```

US-10-044-692-2 (1-1132) x BU122597 (1-875)

```

QY 4 AlaProArgGlyAlaValArgSerLeuArgSerHis----- 17
Db 38 GCTCCGGAATGACGGGAGAGACCTTCGCGCTCGGCGCGCGCGCGCG 97
QY 18 TyrArgGluValLeuProLeuAlaThrPheValArg-----ArgLeuGlyProGlnGly 35
Db 98 TAGCCGAGGCGACGCGCTGAGAGCCTTCGCGCGCGCGCGCGAGAG-GGTGGCACCGG 156
QY 36 TrpArgLeuValGlnArgGlyAspProAla---AlaPheArgAlaLeuValAlaGlnCys 54
Db 157 GAGCTCGAGGTGCTGCGAGCGAGCGCTAGCTACGACCTTCGCTGCGCGAGTGC 216
QY 55 LeuValCysValProTyrPaspAlaArgProProProAlaAlaProSerPheArgGlnVal 74
Db 217 GTGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276
QY 75 SerCysLeuGlyLeuValAlaArgValLeuGlnArgLeuGlyGlyValArgGlyAlaVal 94
Db 277 TCCAGTCAGAGCGAGGATCATCAAGAAATCGTTCAGAGCGCTGTGTGAAGAAAGAG 336
QY 95 AsnValLeuAlaPheGlyPheAlaLeuLeuAspGlyAlaArgGlyGlyProGluAla 114
Db 337 AAGATCTCTGGGATGATGATCTCTCTGATGATGAGAAAGATGCTCACTTCAGAGTTTG 396
QY 115 PheThrThrSerValArgSerTyrLeuProAlaThrValThrAspAlaLeuArgGlySer 134
Db 397 CCATCTTGTGATATACAGCTATCTGCAATCTGTAACAGAAAGAAATTCGGATCAGT 456
QY 135 GlyAlaTrpGlyLeuLeuLeuArgArgValGlyAspAspValLeuValHisLeuLeuAl 154
Db 457 GGCCTCTGGAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 516
QY 154 AArgGlyAlaLeuPheValLeuValAlaProSerCysAlaTyrGlnValCysGlyProPr 174
Db 517 CACGCTGATCACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 576
QY 174 OleuTyrGlnLeuGlyAlaAlaThrGlnAlaArg-ProProProHisAlaSerGlyProA 194
Db 577 AATTATATGAAGTT---ATTTCGCTAACCGTAAAGGCGCATCCCA-----GGTTTGT 627
QY 194 ArgArgArgLeuGlyCysGlyArgAlaTrpAsnHisSer-----ValArg 209
Db 628 GACGACGGTACTCA-----AGGTTTAAACATATATAGCTTCTTGAATATGTCGCA 678

```

```

QY 209 lualaglyValProLeuGlyLeuProAlaProGlyAlaArgArgGlyGlySerAla 229
Db 679 AAGAGTTGTTTTCACAGGACATATCTTCCAGT-----CCCATGTGTGAAGTGCAG 732
QY 229 eArgSerLeuProLeuProLysArgProArgArgGlyAlaAlaProGluProGlu 247
Db 733 GCCGAGAA-----CGTCAGAGTCTGTCTCCAGCAGGAGG 767

```

FEATURES

```

RESULT 42
LOCUS CO014076
DEFINITION ESR802411 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone C1EC236 5' end, mRNA sequence.
ACCESSION CO014076
VERSION CO014076.1 GI:48520965
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Omygenales; mitosporic Omygenales; Coccidioides.
AUTHORS Gardner, M.J. and Cole, G.T.
TITLES Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: ESR802410
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@igir.org
Seq primer: M13 Reverse.

```

FEATURES

```

source 1..930
Location/Qualifiers
  /organism="Coccidioides posadasii"
  /mol_type="mRNA"
  /strain="C735"
  /db_xref="taxon:199306"
  /clone="C1EC236"
  /dev_stage="spherules"
  /lab_host="E. coli DH10B, TI phage resistant"
  /clone_1="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
  /note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

```

ORIGIN

Alignment Scores:

```

Pred. No.: 6.87e-14 Length: 930
Score: 348.50 Matches: 104
Percent Similarity: 50.16% Conservative: 55
Best Local Similarity: 32.81% Mismatches: 121
Query Match: 5.85% Indels: 37
DB: Gaps: 11

```

US-10-044-692-2 (1-1132) x CO014076 (1-930)

```

QY 605 GluValArgGlnHisArgGluAlaArgProAlaLeuThrSerArg----- 620
Db 4 GAGGTAGAGGAAGAAAGCGCGCGCAG-----ATCTGTGAGAGAGACCTGCGGTAC 57
QY 621 -----LeuArgPheLeuProLysProAspGlyLeuArgProAlaAsnMet----- 636
Db 58 GGCACCTTCGATGATGCTCCCAAGCGCACCGAGCTCGCCATGCTTAACCTGAGAAAG 117
QY 637 AspTyrValValGlyAlaArgThrPheArgArgGluValArgAlaGluArgLeuThrSer 656
Db 118 CGGCGCATCTCAAGTCAAGGTGAATGAAGAGATGAGCTGGGCGACAGTCCCAACAG 177
QY 657 ArgValLeuAlaLeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeu 676

```



```

Db      178 CTACTTCGACCCGTTTTCAGGTCCTTAATTGTGAAAGAGCTTCGAAAGTCGGGCTCTC 237
Qy      677 GYAlaservAlaLeuGlyLeuAspAspIleHlsArgAlaITrpArgThrPheValLeuArg 696
Db      238 GGTGGTGCATGATTCCTCGTGGGAGCATGTACGTTTCGACTGAGAGAGGTTCCGGGAGAA 297
Qy      697 -----ValArgAlaGlnAspProProGluLeuTyrPheValIysVal 711
Db      298 CTGTATCAGAGGGGAAATCAGCAGAAAGATCCG-----CTGTATTTTGTATAACTT 348
Qy      712 AspValIThrGlyAlaTyrAspThrIleProGlnAspArgLeuThrGluValIleAlaSer 731
Db      349 GACGTGCAGGCTTGTGATTCATACCTTCAGAAAGCGACTGCTGGCTTGGTTCAGCGC 408
Qy      732 IleIleLysProGlnAspThrTyrCysValArgArgTyrAlaValIle----- 747
Db      409 TTGATCTTCC--GAGATGATATACCGCGTGACAGATACGCGAGAGTGGGCTCTACAC 465
Qy      748 GlnLysAlaAlaHlsGlyHls-----ValArgLys 757
Db      466 CAGCGCGGTCTCCCGGCGCAGGAGCAAGATGAGGAGACAGCAAGCAACCCGTGAGAAAG 525
Qy      758 AlaPheLysSerHlsValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheVal 777
Db      526 ---TTTGTCCTCCAGGCGCGCTCCGCGCTGTGACTTAAAGAT---GCATACGACTTCGTC 579
Qy      778 AlaHlsLeuGlnGluThrSerProLeuArgAspAlaValIleGluIleuSerSer 797
Db      580 GTGAGCGCAGCAAGAAAGTACGAAAGAACACGCTTTGTGTCAACAGGGGAAACGAG 639
Qy      798 LeuAsnGlnAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHlsHlsAla 817
Db      640 AAACGGCAGCAGAGCGCAGACACTTTCGCGCGCTTGGAGACAGCAGCTCGGAAACAACCTG 699
Qy      818 ValArgIleArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnIleSerIleLeu 837
Db      700 GTGAAGATCGGAGAGATATTTCAGACAGAAACGGGATCCCGCAGGCGCTCGGTTGTC 759
Qy      838 SerThrLeuLeuCysSerIleuSerTyrGlyAspMetGluAsnLysLeu-----PheAla 855
Db      760 TCACATCTCTGTGCAATTTCTTACGGCGAGCAGCAAGACGAGCTTGCGCTTCTTG 819
Qy      856 GlyIleArgArgAspGlyLeuLeuLeuArgValAspAspPheLeuValThrPro 875
Db      820 GCGCGCGATGAGAAATCGCTCTGCTGCGCTCTGATGACGACTCCTGTTATCAGCAG 879
Qy      876 HlsLeuThrHlsAlaLysThrPheLeuArgThrLeuValArgGlyValPro 892
Db      880 AAGGAGAGCAGCAGCAGCGGTTTCTACCGGTGATGCTGGAAGGGGGCCA 930

RESULT 43
LOCUS      CO028055      983 bp      mRNA      linear      EST 10-JUN-2004
DEFINITION EST066439 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
ACCESSION  CO028055
KEYWORDS   Coccidioides posadasii cDNA clone CIPAO39 3' end, mRNA sequence.
SOURCE      CO028055.1 GI:46558725
ORGANISM   Coccidioides posadasii
            Coccidioides posadasii
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; Mitosporic Onygenales; Coccidioides.
REFERENCE   1 (bases 1 to 983)
AUTHORS     Gardner,M.J. and Cole,G.T.
TITLES      Analysis of gene expression in Coccidioides posadasii mycelia and
            spherules via expressed sequence tags
JOURNAL     Unpublished (2003)
COMMENT     Other ESTs: EST806440
            Contact: Gardner MJ
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208

```

```

FEATURES             Email: gardner@igr.org.
            source      Location/Qualifiers
                        1..983
                        /organism="Coccidioides posadasii"
                        /mol_type="mRNA"
                        /strain="C735"
                        /db_xref="taxon:199306"
                        /clone="CIPAO39"
                        /dev_stage="spherules"
                        /lab_host="B. coli DH10B, T1 phage resistant"
                        /clone_1lb="Coccidioides posadasii spherule cDNA library,
                        0.5 to 5.3 kb"
                        /note="Vector: pEXpress 1; Site 1: Not I; Site 2: Eco RV;
                        Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
                        kb"

ORIGIN
Alignment Scores:
Pred. No.:      1.87e-11      Length:      983
Score:          314.00      Matches:      88
Percent Similarity: 48.90%      Conservative: 45
Beet Local Similarity: 32.35%      Mismatches: 115
Query Match:    5.27%      Indels:      24
DB:              Gaps:      8

US-10-044-692-2 (1-1132) x CO028055 (1-983)
Qy      827 GlnCysGlnGlyIleProGlnIleuSerThrLeuLeuCysSerIleuSerTyr 846
Db      974 CAGAAAGAACGGGATCCCGCAGGCTCGGTGTGTGACAGATTCCTGTCAATTTCTTAC 915
Qy      847 GlyAspMetGluAsnLysLeu-----PheAlaGlyIleArgArgAspGlyLeuLeuLeu 864
Db      914 GCGCAGCAGCAAGCAGCGGAGCTTGCTTGGCGCGGATGAAAGATCGCTCTGCTG 855
Qy      865 ArgLeuValAspAspPheLeuLeuValThrProHlsLeuThrHlsAlaLysThrPheLeu 884
Db      854 CGCTGATGACGACGACTACCTGTTATCACAGAAAGAGAGCAGCAGCGGCTTCTA 795
Qy      886 ArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLysThrVal 904
Db      794 CGGTGATGCTGGAAAGGGGCGCAGAGATATGGATCTCGGTACTCCCGCAAGACGTTG 735
Qy      905 ValAsnPheProValGluAspGlnAlaLeuGlyGlyThrAlaPheValGlnMet----- 922
Db      734 GTCAACTTTGAAGTTGAC-----GTGGCGGTTACAGACATCCGGCGCTGGCGCAG 684
Qy      923 ProAlaHlsGlyLeuPheProTyrCysGlyLeuLeuAspThrArgThrLeuGluVal 942
Db      683 TCGTCGACAGACATTTCCATCTGCGGGAACCTTATCGATACAGAGCGCTGGCGATC 624
Qy      943 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAla-----SerLeuThrPhe 960
Db      623 AGCAAGATCGGACCGCGCAGCAGCAGATCTCCACGTGTGCGACTCGCTCACGCTT 564
Qy      961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db      563 GAGCTGAGAGAGACCCCGGACAGGGGTTTACCCGAAATCTGTGTATGTTTAAACTA 504
Qy      981 LysCysHlsSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db      503 CAGCGGCAACGCGATTTCTTCGACGTGAACGACATTCGCGAGGGTGTGCTGGCGGCT 444
Qy      1001 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHlsAlaCysValLeuGlnLeuPro 1020
Db      443 GTATATTCAGCGCTTCTGACTGTGCGATGAGAGATATGCTATCTGGCGTCTTCG 384
Qy      1021 PheHlsGlnGlnValITrpLysAsn-----ProThrPhePheLeuArg 1034
Db      383 CCGCGGCGAGGAGAACGCGAGAGGTGAGAGGTTCTTGATGAGACATGCTCACCCGC 324
Qy      1035 ValIleSerAspThrAlaSerLeuCysTyrSerIleLeuLysAla-----LysAsnAla 1052

```

Db 323 ACCATCGGGGCTCATGACTACGCGGTGCGCTGATCCGCTCTCGACGAAGAGCTCC 264

Qy 1053 GJymeSerLeuGlyValAlaGlyValAlaGlyProLeuProSerGluAla----- 1069

Db 263 GGGGGTACGACGCGC---GAGGCGAGAGTGGCAGACAGATTAATATGCTTTATTACA 207

Qy 1070 -----ValGlnTrpLeuGlyHisGlnAlaPhe 1078

Db 206 AGGGTGCAGATTCAGTGTGGCGGTGACGCGCTTC 171

RESULT 44

CO024489/c 1023 bp mRNA linear EST 10-JUN-2004

LOCUS EST802873 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3

DEFINITION kb Coccidioides posadasii cDNA clone CIFA132 3' end, mRNA sequence.

ACCESSION CO024489

VERSION CO024489.1 GI:48551589

KEYWORDS EST.

SOURCE Coccidioides posadasii

ORGANISM Coccidioides posadasii

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 1023)

Gardner, M.J. and Cole, G.T.

Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags

Unpublished (2003)

Other ESTs: EST802874

Contact: Gardner MJ

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 3519

Fax: 301 838 0208

Email: gardner@igmr.org.

FEATURES

source

1. 1023

location/Qualifiers

/organism="Coccidioides posadasii"

/mol_type="mRNA"

/strain="C735"

/db_xref="taxon:199306"

/clone="CIFA132"

/dev_stage="spherules"

/lab_host="E. coli DH10B, T1 phage resistant"

/clone_lib="Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb"

/note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV; Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb"

ORIGIN

Alignment Scores:

Pred. No.: 6.08e-11 Length: 1023

Score: 307.00 Matches: 92

Percent Similarity: 49.12% Conservative: 47

Best Local Similarity: 32.51% Mismatches: 120

Query Match: 5.15% Indels: 26

DB: 7 Gaps: 8

US-10-044-692-2 (1-1132) x CO024489 (1-1023)

Qy 816 HisAlaValArgIleAlaGlyLysSerTyValGlnCysGlnGlyIleProGlnGlySer 835

Db 1001 CACCTTGTGAAGATCGGAAAGAAATTTTCGA-CAGAAGAACGGGATCCCGCAGGGCTCG 943

Qy 836 IleLeuSerThrLeuLeuGlySerLeuGlyTyGlyValPheMetGluAsnLysLeu----- 853

Db 942 GTTGTGTCAAGCATCTGTGCAATTTCTTACGGCGAGCAGCAGACGACGGA-GCTGGC 884

Qy 854 PheAlaGlyIleLeuArgAspGlyLeuLeuValArgLeuValAspPheLeuLeuVal 873

Db 883 TTTCTGGGGGGCGATGAAGATTCCTCTCGCTGATGACGACTACTGCTTATTC 824

Qy 874 ThrProHisLeuThrHisAlaLysThrPheLeuArgThrPheLeuValArgGlyValProGlu 893

Db 823 ACCACAGAGAGAGACGACAGAGCGGCTTTCTACGGGTGATGCGGAGGGGCGCAGAG 764

Qy 894 TyrGlyCysValValAsnLeuArgLysThrValValAsnPheProValGlnAspGluAla 913

Db 763 TATGGGATCTCGGTGACTCCCGGCAAGACGTTGGTGAACCTTGAAATGAG----- 713

Qy 914 LeuGlyGlyThrAlaPheValGlnMet-----ProAlaHisGlyLeuPheProTrpCys 931

Db 712 GTGGGGGTTACGACATCCGCGCGCTGGGAGATCGTCGAGAGAGAAATTTCCATCTCG 653

Qy 932 GlyLeuLeuLeuAspThrArgThrLeuGlnValGlnSerAspTyrSerSerTyrAlaArg 951

Db 652 GGAAACCTTTATCGATACAGACGCTGGCGATCAGCAAGATCGACCCGCCAGCAGAC 593

Qy 952 ThrSerIleArgAla-----SerLeuThrPheAsnArgGlyPheLysAlaGlyArgAsn 969

Db 592 GACGATCTCCACGTGTCGACCTGCTCAGCTTGAGCTGAGAGAGACCCCGACAGGGG 533

Qy 970 MetArgArgLysLeuPheGlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeu 989

Db 532 TTTCACCGCAATCTCTGTCTATGTTAACTACAGCGCAGCAGCATGTTCTTCGACGTG 473

Qy 990 GlnValAsnSerLeuGlnThrValCysThrAsnLysTyrIleLysLeuLeuGlnAla 1009

Db 472 AAGCACAATTCGCGAGCGGTGCTGCGGGGTGTATATACGCGCTTCCTGACTGTGCG 413

Qy 1010 TyrArgPheHisAlaCysValLeuGlnLeuProPheHisGlnGlnValTrpLysAsn--- 1028

Db 412 ATGAGGATGTATGCGCTTATCTGCTGCGCTGCGGGGGGCGAGCAGCGAGAGGTG 353

Qy 1029 -----ProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCys 1043

Db 352 AGGAGCTCTCGATGACGACATGCTCCACCGCACATCGGGGGGCTCARTGACTACCG 293

Qy 1044 TyrSerIleLeuLysAla-----LysAsnAlaGlyMetSerLeuGlyAlaLysGlyAla 1061

Db 292 GTGCGCTGATCCGCTCTCGACGAGAGCTCCGGGGGTGACAGCGC---GAGGGCAG 236

Qy 1062 AlaGlyProLeuProSerGluAla-----ValGlnTrpLeuGlyHis 1075

Db 235 AGTGGCAGACAGATTAATATGCTTTATTACAAGGAGTGACAGATTCAGTGTGCGGTG 176

Qy 1076 GlnAlaPhe 1078

Db 175 CAGCGCTTC 167

RESULT 45

CF547484 774 bp mRNA linear EST 22-SEP-2003

LOCUS AGENCOURT_15568263 NICHD_XGC_Kid1 Xenopus laevis cDNA clone

DEFINITION IMAGE:7009014 5', mRNA sequence.

ACCESSION CF547484

VERSION CF547484.1 GI:34884316

KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Fipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 774)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP); Tumor Gene Index

Unpublished (1997)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: c9arbs-r@mail.nih.gov

Tissue Procurement: Dr. Igor Dawid

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

[illegible]

```

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST65B13"
/dev_stage="22"
/lab_host="DH10B"
/clone_1ib="CSEQCCHN23"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI, Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA constructed from 1 million independent clones. cDNA synthesized was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI

```

ORIGIN

compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9248-9252 and Bonaldo et al., Genome Research (1996) 791, except that a significantly longer reannealing hybridization was used."

Alignment Scores:	
Pred. No.:	1.57e-09
Score:	284.50
Percent Similarity:	55.03%
Best Local Similarity:	39.15%
Query Match:	4.77%
DB:	5
Length:	815
Matches:	74
Conservative:	70
Mismatches:	65
Indels:	20
Gaps:	6

US-10-044-692-2 (1-1132) X BU224024 (1-813)

Oy 73 GluValSerCysLeuIysGluLeuValAlaArgValLeuGlnIlePheGluCysGluValGly 92
 Db 1 CAGTTATCCGATCCAGACCGGAGATCATCAAGAAAGTGGTTCAGGGCTGGTGTAAAGAAA 60
 Oy 93 AlaIysAsnValLeuAlaPheGlyPheAlaLeuLeuAspGlyAlaArgIlyGlyProPro 112
 Db 61 AAGAAGAACATCCTTGGATGATGATACTCCTTGGTGAATGAGAAACAGTTCACTTCAGA 120
 Oy 113 GluAlaPheThrIleSerValIarSerTyrLeuProAsnThrValIleAspAlaLeuArg 132
 Db 121 GTTTTGGCATCTTCGTGTATATACAGCTATCTGCCAATACTGTAAACAGAAACGATTGCG 180
 Oy 133 GlySerGlyAlaIleProGlyLeuLeuLeuLeuArgValGlyAspAspValLeuAlaIleLeu 152
 Db 181 ATCATGGCCCTCTGGAGATATCTCTCTAGTACGTACGATAGGAGACGATGATGATGACTG 240
 Oy 153 LeuAlaIarGysAlaLeuPheValIleuValAlaProSerCysAlaTyrGlnValCysGly 172
 Db 241 CTGGAGCAGCTGTGGACCTCTTCATCTGGTCCCCCAAGTAACTGTATCCAGGTCTGGGG 300
 Oy 173 ProLeuTyrGlnIleuGlyAlaAlaIleThrGlnAlaArgProProPro----- 188
 Db 301 CAACCAATTTATGAACTT---ATTTCGGTAAAGTACGGCCATGCCACAGGGTTTGTTAGA 357
 Oy 189 -----HisAlaSer-----GlyProArgArgArgLeuGly 198
 Db 358 CCACGGTACTCAAGTTTAAACATATATAGCTTGGCTGACATATGTCGAAAAAGCCTTGTC 417
 Oy 199 CysGluArgAlaIlePheAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAla 218
 Db 418 TTTCACAGG-----CACTATCTTCCAAAGTACACAGTGGTGAAGTCAAGCGCG-- 465
 Oy 219 ProGlyAlaIarArgArgGlyGlySerAlaSerArg-----SerLeuProLeuPro 235
 Db 466 -----AGACGTGAGAGTGTGTCTTCACACAGAGAAACAGAAAGACCATAGAT 516
 Oy 236 LysArgProArgArgGlyAlaAlaIlePro 244
 Db 517 ACAAGCCTTAGGTCTGGTATCAAGCT 543

RESULT	48
BX882610	
LOCUS	BX882610
DEFINITION	BX882610 ccdk Oncorhynchus mykiss CDNA clone tcdbk0060c.h.01 5pbm,
ACCESSION	MRNA sequence.
VERSION	BX882610
KEYWORDS	BX882610.2 GI:42815406
SOURCE	EST.
ORGANISM	Oncorhynchus mykiss (rainbow trout)
REFERENCE	Oncorhynchus mykiss Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 946) Govoroun,M., Galguen,Y. and Le Gac,F.
AUTHORS	

TITLE
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, *Oncorhynchus mykiss*
Unpublished (2003)
JOURNAL
On Dec 18, 2003 this sequence version replaced gi:40127495.
COMMENT
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenauporte@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0060 row: h column: 1
Seq primer: M13R.
Location/Qualifiers

FEATURES

source

1.646
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcbk0060c.h.01"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/note="Vector: pT7T3D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution: AGENAE Resource centre, Francois PUMI,
Francois Pluim@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREB), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Alignment Scores:

Pred. No.: 1.4e-09 Length: 646
Score: 283.00 Matches: 61
Percent Similarity: 60.31% Conservative: 18
Best Local Similarity: 46.56% Mismatches: 52
Query Match: 4.75% Indels: 0
DB: 5 Gaps: 0

US-10-044-692-2 (1-1132) x BX882610 (1-646)

OY 1000 AenlietYrYsIlLeuLeuLeuGlnAlaTYrArGPheHsAlaCyseValLeuGlnLeu 1019
DB 3 AACATCTTAAGTTAGTGTGCTGCACGGCTTCAGGTTCCATGCTGTGCACAGAGTTTG 62
OY 1020 PropheHsGlnGlnValTrrYsAsnProThrPheLeuArGValIleSerAspThr 1039
DB 63 CCGTTTGCTCAAGAAAGTGGCGAACCACCTGTAATCTTCAATCTGGAATTG 122
OY 1040 AlaserLeuCyTYrSerIlLeuLeuYsAlaYsAsnAlaGlyMetSerLeuGlyAlaYs 1059
DB 123 GGGAGTAGTACACCAACATCTAGTACAGCTGTGCAACAAAGGTGTCTTAGCGTAAAG 182
OY 1060 GlyAlaAlaGlyProLeuProSerGlnAlaValGlnTrrPleuCyHsGlnAlaPheLeu 1079
DB 183 GCTTAAACAGGTAGCTTCAATGATAGGCGATGAACATGATATCTGTGCTTCCG 242
OY 1080 LeuYsLeuThArXrHsArGValThrTYrValProLeuLeuGlySerLeuArGThrAla 1099
DB 243 TTGGTTCTGTCCCGTATGCCCCCTTACATCTCTGCTGCTGCTAGGACACCT 302
OY 1100 GlnThrLeuLeuSerArGlyLeuProGlyThrThrLeuThrAlaLeuGlnAlaAla 1119
DB 303 AAGAGGAAGCTGAGGCGAAGCTGAGGTTTGAATTGGCCGAATCAGACAGGCTGC 362
OY 1120 AsnProAlaLeuProSerArSpheYsThrIle 1130
DB 363 ACACCCAAATGCTGAAGATTCAAGGCCATC 395
RESULT 49

BX315053
LOCUS
DEFINITION
BX315053 tccay Oncorhynchus mykiss cDNA clone tccay0029b.n.21 5prim,
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oncorhynchus mykiss (rainbow trout)
EST.
BX315053.2 GI:42620226

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
On Apr 7, 2003 this sequence version replaced gi:29595698.
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenauporte@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0029 row: n column: 21
Seq primer: M13R.
Location/Qualifiers

FEATURES

source

1.731
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tccay0029b.n.21"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, intestinal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues -
normalized + 1 subtractions (tccay); Clone distribution:
AGENAE Resource centre, Francois PUMI,
Francois Pluim@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREB), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Alignment Scores:

Pred. No.: 1.69e-09 Length: 731
Score: 283.00 Matches: 61
Percent Similarity: 60.31% Conservative: 18
Best Local Similarity: 46.56% Mismatches: 52
Query Match: 4.75% Indels: 0
DB: 5 Gaps: 0

US-10-044-692-2 (1-1132) x BX315053 (1-731)

OY 1000 AenlietYrYsIlLeuLeuLeuGlnAlaTYrArGPheHsAlaCyseValLeuGlnLeu 1019
DB 3 AACATCTTAAGTTAGTGTGCTGCACGGCTTCAGGTTCCATGCTGTGCACAGAGTTTG 62
OY 1020 PropheHsGlnGlnValTrrYsAsnProThrPheLeuArGValIleSerAspThr 1039
DB 63 CCGTTTGCTCAAGAAAGTGGCGAACCACCTGTAATCTTCAATCTGGAATTG 122
OY 1040 AlaserLeuCyTYrSerIlLeuLeuYsAlaYsAsnAlaGlyMetSerLeuGlyAlaYs 1059
DB 123 GGGAGTAGTACACCAACATCTAGTACAGCTGTGCAACAAAGGTGTCTTAGCGTAAAG 182
OY 1060 GlyAlaAlaGlyProLeuProSerGlnAlaValGlnTrrPleuCyHsGlnAlaPheLeu 1079

```

Db      183 GCTTAAACAGTAGCCTTAGATGAGGAGGAGCACTGATATACCTGCTGCTCCCTG 242
Qy      1080 LeuLysLeuThrArgHisArgValThrThrValProLeuLeuGlySerLeuArgThrAla 1099
Db      243 TTGGTCTCTCTCCGTCATGCCCCCTTACCTACCATCTCTGCTCCGCTAGCACACCT 302
Qy      1100 GlnThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAla 1119
Db      303 AAGAGGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 362
Qy      1120 AspProAlaLeuProSerAspPheLysThrIle 1130
Db      363 ACACCCAAATGCTGAAAGACTTCAAGGCCATC 395

RESULT 50
BM363763
LOCUS      BM363763 Yutaka Satou unpublished cDNA library, mature adult whole
DEFINITION animal Clona intestinalis CDNA clone cima830013 5', mRNA sequence.
ACCESSION  BM363763
VERSION     BM363763.1 GI:4775564
KEYWORDS    EST.
SOURCE      Clona intestinalis
ORGANISM    Clona intestinalis
REFERENCE   1 (bases 1 to 651)
AUTHORS     Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
TITLE       Expressed genes in Clona intestinalis (2004)
JOURNAL     Unpublished (2004)
COMMENT     Contact: Yutaka Satou
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4095
            Fax: 81-75-705-1113
            Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
            Location/Qualifiers
            source          1..651
                           /organism="Clona intestinalis"
                           /mol_type="mRNA"
                           /db_xref="taxon:7719"
                           /clone="cima830013"
                           /tissue_type="whole animal"
                           /dev_stage="mature adult"
                           /clone_lib="Yutaka Satou unpublished cDNA library, mature
                           adult whole animal"

ORIGIN

Alignment Scores:
Pred. No.:      2,48e-09      Length:      651
Score:          279.50      Matches:      75
Percent Similarity: 49.40%      Conservative: 49
Best Local Similarity: 29.88%      Mismatches: 80
Query Match:    4.69%      Indels:      47
DB:             5      Gaps:      9

US-10-044-692-2 (1-1132) x BM363763 (1-651)

Qy      455 HisSerSerPro--TyrGlnValTyrGlyPheValArgAlaCysLeuArgLysVal 473
Db      1 CATTAACACACCAACTCATCAAGTTTCTTAATGATGATGATGATGATGATGATGATGATG 60
Qy      474 ProProGlyLeu---TyrGlySerArgHisAsnGluArgArgPheLeuArgSerThrLys 492
Db      61 CCCATTCAATTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Qy      493 LysPheLeuSerLeuGlyLysHisAlaLysLeuSerLeuGlnGluLeuThrTrpLysMet 512
Db      121 AAGTTTCTTCTTCCGCGTGGTTTGACAAAGTAACGGTTGCTGACTTTACCGGGGATAG 180
Qy      513 SerValArgAspCysAlaTrpLeuArgArgSerProGlyValGlyCysValProAlaAla 532

```

```

Db      181 GTGGTGGGTGACTTACCTGAGCTC-----ATGGGGAGACAACAAGTTCT 225
Qy      533 GluHisArgLeuArgGluGlnIleLeuAlaLysPheLeuHisTrpLeuMetSerValTyr 552
Db      226 AAT-----CTATTAAATTTTCCAAATGATGATGATGATGATGATGATGATGATGATGAT 264
Qy      553 ValValGluLeuLeuArgSerPhePheTyrValThrGluThrThrPheGlnLysAsnArg 572
Db      265 ATATTGTTGTTTAAAGTGTTCCCTTATATTAACAGAAACAGCAACTTCAAAAACAGA 324
Qy      573 LeuPhePheTyrArgLysSerValTrpSerLysLeuGlnSerIleGlyTyrLeuGlnHis 592
Db      325 TTGTTCTTCTTACCAACAAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 384
Qy      593 LeuLysArgValGlnLeuArgGluLeuSerGlnIleGluValArgGlnHisArgGlnAla 612
Db      385 TTAAG-----CAAAACCGCTGGGCC 405
Qy      613 ArgProAlaLeuLeu-----ThrSerArg-----LeuArgPheIleProLys 626
Db      406 GTTCACCCCATTTGACAGATGATACCAACGTCATATTTCTCGTGAGGTTTGTCCAAA 465
Qy      627 ProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyValArgThrPheArg 646
Db      466 GTTAACGGGTTGCGACCATCATG----- 489
Qy      647 ArgGluLysArgAlaGluArgLeuThrSerArgVal-----LysAlaLeuPheSerVal 664
Db      490 AGTTTGAGGAGACCGGACAGAGTGGCTGACATGTTCCATTCGAAAGTAATTCCTTCTGTG 549
Qy      665 LeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGlyLeuAsp 684
Db      550 TTGAATATGTTGTGATGAATGAATGTCGCCAAGCCACCGGTTTGCCACACAACATGCTGT 609
Qy      685 AspIleHisArgAlaTrpArgThrPheValLeu 695
Db      610 CATATTTCATATGCGTGGAGAACAAATTTGTTCT 642

```

Search completed: October 28, 2004, 20:46:57
 Job time : 7891 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 29, 2004, 08:05:49 ; Search time 1214 Seconds

(without alignments)
4781.256 Million cell updates/sec

Title: US-10-044-692-2

Perfect score: 5961

Sequence: 1 MPRAACRAVSLRSHYRE.....TALAAANPALSPDKITLD 1132

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO/US10044692/runat_28102004_103657_1462/app.query.fasta_1.1287
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnbp -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bite -START=1 -END=1 -MATRIX=blousum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10044692@cgn2_1.1.824_@runat_28102004_103657_1462
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	3396	9 US-09-749-728B-32	Sequence 32, Appl
2	5961	100.0	3399	17 US-10-384-339C-28	Sequence 28, Appl
3	5961	100.0	4015	9 US-09-733-294A-3	Sequence 3, Appl
4	5961	100.0	4015	9 US-09-990-080-1	Sequence 1, Appl
5	5961	100.0	4015	9 US-09-843-676-224	Sequence 224, App
6	5961	100.0	4015	9 US-09-953-052-1	Sequence 1, Appl
7	5961	100.0	4015	14 US-10-053-758-224	Sequence 224, App
8	5961	100.0	4015	14 US-10-208-243-1	Sequence 1, Appl
9	5961	100.0	4015	14 US-10-054-225-224	Sequence 224, App
10	5961	100.0	4015	14 US-10-054-611-224	Sequence 224, App
11	5961	100.0	4015	14 US-10-105-603-1	Sequence 1, Appl
12	5961	100.0	4015	14 US-10-044-692-1	Sequence 1, Appl
13	5961	100.0	4015	15 US-10-335-810-1	Sequence 1, Appl
14	5961	100.0	4015	15 US-10-335-810-1	Sequence 1, Appl
15	5961	100.0	4015	15 US-10-388-578-1	Sequence 1, Appl
16	5961	100.0	4015	15 US-10-449-565-1	Sequence 1, Appl
17	5961	100.0	4015	17 US-10-602-441-1	Sequence 1, Appl
18	5961	100.0	4015	17 US-10-389-431-1	Sequence 1, Appl
19	5954	99.9	4027	15 US-10-385-882-1	Sequence 1, Appl
20	5952	99.8	3453	15 US-10-205-629-1	Sequence 1, Appl
21	5952	99.8	4027	15 US-10-325-810-343	Sequence 343, App
22	5952	99.8	1766	15 US-10-105-616-1	Sequence 1, Appl
23	5925	99.4	8742	15 US-10-105-616-6	Sequence 6, Appl
24	5593.5	93.8	3855	15 US-10-044-692-4	Sequence 4, Appl
25	5593.5	93.8	3855	15 US-10-044-539-4	Sequence 4, Appl
26	5593.5	93.8	3855	15 US-10-325-810-4	Sequence 4, Appl
27	5579	93.6	4029	9 US-09-843-676-173	Sequence 173, App
28	5579	93.6	4029	10 US-09-438-486-173	Sequence 173, App
29	5579	93.6	4029	14 US-10-053-758-173	Sequence 173, App
30	5579	93.6	4029	14 US-10-054-295-173	Sequence 173, App
31	5579	93.6	4029	14 US-10-054-611-173	Sequence 173, App
32	5579	93.6	4029	15 US-10-325-810-292	Sequence 292, App
33	3628	60.9	4170	17 US-10-602-441-5	Sequence 5, Appl
34	3505	58.8	3426	17 US-10-602-441-3	Sequence 3, Appl
35	3134	52.6	1866	14 US-10-294-778-11	Sequence 11, Appl
36	2789	46.8	51552	9 US-09-733-294A-10	Sequence 30, Appl
37	2782	46.7	4200	14 US-10-044-692-6	Sequence 6, Appl
38	2782	46.7	4200	15 US-10-044-539-6	Sequence 6, Appl
39	2782	46.7	4321	15 US-10-325-810-6	Sequence 1, Appl
40	2782	46.7	15418	9 US-09-783-203-1	Sequence 1, Appl
41	2782	46.7	15418	9 US-09-994-427A-1	Sequence 1, Appl
42	2782	46.7	15418	10 US-09-995-419A-1	Sequence 1, Appl
43	2782	46.7	15418	14 US-10-141-220-1	Sequence 1, Appl
44	2782	46.7	15418	14 US-10-023-969-1	Sequence 1, Appl
45	2782	46.7	15418	14 US-10-206-447-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-749-728B-32
; Sequence 32, Application US/09749728B
; Parent No. US20020142457A1
GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihito
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keisichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES
FILE REFERENCE: 00766.000043
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US/09/749,728B
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: PCT-JP00-01148
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT-JP00-07741

PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver.2.0
SEQ ID NO 32
LENGTH: 3396
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
OTHER INFORMATION: (1)..(3399)
US-09-749-728B-32

Alignment Scores:

Pred. No.: 0
Score: 5961.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

Length: 3396
Matches: 1132
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-044-692-2 (1-1132) x US-09-749-728B-32 (1-3396)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATCCCGGCGCTCCCGCTGCGAGCGGCTGCTCCCTGCTGCGACGACCACTACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgGluGlyProGlnGlyTyrPheArgLeuValGln 40
DB 61 GTCTGCGCTGCGACGCTGCTGCGAGCGCTGCGAGCGCTGCGAGCGCTGCGAGCGCTGCGAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CCGCGGGGACCGCGGCTTCCGCGGCTGCTGCGAGCGCTGCGAGCGCTGCGAGCGCTGCGAG 180
QY 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
DB 181 GAGCGACG 240
QY 81 ValAlaArgValLeuGlnArgLeuValArgGlyValAlaValAsnValLeuAlaPheGly 100
DB 241 GTGCGCGGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGCGCTGTGCGACGCGGCG 360
QY 121 SerTyrLeuProLeuThrValThrAspAlaLeuArgGlySerGlyAlaTyrProGlyLeuLeu 140
DB 361 AGCTACCTGCGCAACAGCGTGAACGCGACCTGCGGCGAGCGCGCGCGCGCGCGCGCGCG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGCG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyVal 180
DB 481 CTGCTGCGCTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgGlyGlyCysGlu 200
DB 541 GCCACTCAGGCG 600
QY 201 ArgAlaTyrAsnHisSerValArgGlyValAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CCGGCGCTGCAACATAGCTGAGGAGGCGCGGCTCCCTCGGCGCTGCGACGCGCGGCT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuPheArgProArgArg 240
DB 661 GCGAGAGGCG 720
QY 241 GlyValAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrPheAlaHisProGly 260
DB 721 GCGCGCTGCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780

QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGln 280
DB 781 AGGAGCGGTGACCGAGTGAACCGGTGTTCTGTGTGTGTCACTGCGACAGCCGCCGAA 840
QY 281 GlnAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAAAGCACTCTTTGGAGGGGCGCTCTGCGACGCGCGCACTCCACCACTCCGAGGCG 900
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrPheThrPro 320
DB 901 CGCCAGACCAACG 960
QY 321 CysProProValTyrAlaGlnThrValHisPheLeuTyrSerSerGlyAspGlyGln 340
DB 961 TGTCCCCGGGTGATGCGCGAGACCAAGACACTCTCTACTCTCAGCGCGACAAAGACAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1021 CTGCGCGCGCTCTCTCACTGAGCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 1080
QY 361 ValGluThrIlePheLeuGlySerArgProTyrPheProTyrThrProArgArgLeuPro 380
DB 1081 GTGAGACATCTTCTGTGTTCCAGGCGCTGAGTGCAGGAGACTCCCGCAGGTTGCGC 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlyLeuLeuGlyValHis 400
DB 1141 CGCTGCGCGCGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuValHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCGAGTGCCTCTTACGGGAGTGTCTCTCAAGACACTCCCGCTGCGAGCTGCGGTACC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGlyValProGlnGlySerValAlaAlaProGlnGlu 440
DB 1261 CCAAGACCGGTGTGTGCGCGGAGAACCCAGCGGCTGTGTGCGCGCGCGCGCGAG 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1321 GAGGACACAGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrPhe 480
DB 1381 GTGTAGGCTGTGTGTGAGGCTGTGCTGCGCGGCTGTGTGTGCTGCGCGCTGCGGCTCC 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrValHisPheLeuSerLeuGlyValHis 500
DB 1441 AGGCAACAAGAACCGCGCTCTCAAGAAACACAGAAATTCATCTCCCTGGGAGAGCAT 1500
QY 501 AlaValLeuSerLeuGlnGlnLeuThrTyrPheMetSerValArgAspCysAlaTyrLeu 520
DB 1501 GCCAAGCTCTGCTGAGAGCTGACGTGAAGATGAGGTGCGGAGCTGCGCTTGTGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlu 540
DB 1561 CGCAGAGCGCGAGGTTGTGTGTGTGCTGCGCGCGAGCAACGCTGCTGAGAGAGATC 1620
QY 541 LeuAlaValPheLeuHisTyrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
DB 1621 CTGCGCAAGTCTCTGACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 561 PheTyrValThrGlnThrThrPheGlnValAsnArgLeuPhePheTyrArgHisSerVal 580
DB 1681 TTTTATGTACGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTTACCGAAGAGTGT 1740
QY 581 TrpSerTyrLeuGlnSerIleGlyIleArgGlnHisLeuValArgValGlnLeuArgGln 600
DB 1741 TGAAGCAAGTGTGAAGCATTTGAATCAACAGCACTTGAAGAGGTGACGTGCGGAG 1800
QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
DB 1801 CTGTGGAAGACAGAGTCAAGGACATCGGGAAGCCAGGCGCGCGCTGCTGACGTTCA 1860

QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
DB 1061 CTCGGCTTCAATCCCAAGCCTGACGGGCTCGCGCGGATTTGAAATGATGACTACTGCTG 1920
QY 641 G1yAlaArgThrPheArgArgGlyIlyArgAlaGluArgLeuThrSerArgValIlyAla 660
DB 1921 GGAGCGAANAAGCTTCGCGAGAGAAAAGAGGGCGGAGCTCTCACTCAAGGATGAAAGCA 1980
QY 661 LeuPheSerValIleuAsnTyrGluArgAlaArgAspProGlyLeuLeuGlyValAsnVal 680
DB 1981 CTGTTTCAACGGCTCACTACAGCGGGCGGGCGGCGGCTCTCTGGGCGCTCTG 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
DB 2041 CTGGGCGCTGAGAGATATCCACAGGGCTGGCGCACTTCGTGCTCGGTGGGGCCAG 2100
QY 701 AspProProGlyLeuTyrPheValIlyValAspValThrGlyValaTyrAspThrIle 720
DB 2101 GACCGCGCGCTGACCTGACTTGTGTCAAGGTGATGACGGGCGGCTACGACACATC 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
DB 2161 CCCAGGACAGGCTCAGAGGTATCGCCACATCATCAACCCAGAGCACTGATGTC 2220
QY 741 ValArgArgTyrAlaValAlaGlnIlyValAlaHisGlyHisValArgIlyAlaPheLys 760
DB 2221 GTGGCTCGGTATGCGGTGTCCAGAGGCGGCCCATGGGCACTCCGAGAGCTTCAAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
DB 2281 AGCCAGCTCTCACTTGACAGACTCCAGCGGTACATCGACAGATTGCTGCTCACTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu 800
DB 2341 CAGGAGACAGCCCGCTGAGGATGCGGTGATCGAGCAAGCTCTCTTGATGATG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
DB 2401 GCCAGCAATGGCTCTTTCAGACTCTTCTCAAGCTTCATGTGCCACACCGCTGGCATC 2460
QY 821 ArgGlyIlySerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
DB 2461 AGGGGCAAGTCTCACTGACAGGCCAGGGGATCCGAGAGGCTCTCTCCACGCTG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnIlyLeuPheAlaGlyIleArgArgAsp 860
DB 2521 CTCTGACAGCTGTGCTACGGCGACATGGAACAAGCTGTGTGGGGGATTTGGGGGAGC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
DB 2581 GGGCTGCTCTGCGTTGGTGAATGATTTCTTGTGTGACACCTCACTTCAACCGCG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
DB 2641 AAAACCTTCTCAGAGACCTGTGTCGAGGTGTCCTGATATAGGCTGCGTGAACCTG 2700
QY 901 ArgIlyThrValValAsnPheProValGluAspGluAlaLeuGlyIlyThrAlaPheVal 920
DB 2701 CGGAAGACAGTGTGTAACCTTCCCTAGAAAGCGAGGCTGTGGGCGACGCGCTTTTGT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
DB 2761 CAGATGCGGGCCAGCGCTATTTCCCTGTGTGGGCTCTCTCTGATACCGGAGCCCTG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
DB 2821 GAGGTGACAGAGGACTACTCCAGCTATGCGCGAAGCTTCATAGAGCGAGTCTCACTTC 2880
QY 961 AsnArgGlyPheIlyAlaGlyArgAsnMetArgIlyLeuPheGlyValaLeuArgLeu 980
DB 2881 AACCCCGGCTTCAAGGCTGGAGGAAACATGCGCTCGCAAACTTTTGGGGCTTGTGGCGCTG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

DB 2941 AAGTGTACACCTGTTCTGATTTGGAGGTGAACAGCTTCAGACGCTGTGACACCAAC 3000
QY 1001 TLeTyrIlyIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
DB 3001 ATCTACAAGATCTTCCTGCTCAGCGGTACAGTTTCAAGATGTGTCTGAGCTCCCA 3060
QY 1021 PheHisGlnGlnValATrPlyAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
DB 3061 TTTCATACGCAAGTTTGAAGAACCACATTTTTCCTGGCGGTATCTTGACACGGCC 3120
QY 1041 SerLeuCysTyrSerIleLeuIlyAlaIlyAsnAlaGlyMetSerLeuGlyValaGly 1060
DB 3121 TCCCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 3180
QY 1061 AlaAlaGlyProLeuProSerGlyAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
DB 3181 GCGCGCGCGCTGCTGCTGCTGCGAGGCGGTGAGTGTGTGCAACAGATTTCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
DB 3241 AAGCTGACTTCACACCGGTGTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
QY 1101 ThrGlnLeuSerArgIlyLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
DB 3301 ACGAGCTGAGTGGAGACTCCCGGGAGACGAGCTGAGCTGCGCTGAGAGCGGACCAAC 3360
QY 1121 ProAlaLeuProSerAspPheIlyThrIleLeuAsp 1132
DB 3361 CCGGCACTGCGCTCACTTCAAGACATCTTGAC 3396

RESULT 2
US-10-384-339C-28
; Sequence 28, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GEN
; FILE REFERENCE: 202006/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 3399
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: telomerase reverse transcriptase
; PATENT DOCUMENT NUMBER: AF015950
US-10-384-339C-28

Alignment Scores:
Pred. No.: 0 Length: 3399
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-044-692-2 (1-1132) x US-10-384-339C-28 (1-3399)
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGln 20

Db 1 ATGCCGCGGCTCCCGCTGCCAGCCGCTGCTCCGCGGAGCCACTTACCGCAG 60
 Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
 Db 61 GTGCTGCGCTGCGCCACGTTGAGCGGCGCTGGGAGCCCGAGGCTGGCGCTGGTGAG 120
 Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 121 CGCGGGAGACCCGGCGCTTCCGCGGCTGCTGGCCAGTGCCTGCTGCTGCTGCTG 180
 Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
 Db 181 GACGACG 240
 Qy 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLeuValAlaLeuValPheGly 100
 Db 241 GTGGCCCGAGTGTGCAGAGCTGTGCGAGCGCGCGGAGAGACGTGCTGGCTTGGC 300
 Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 Db 301 TTGCGCTGTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 Qy 121 SerTyrLeuProLeuThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
 Db 361 AGCTACCTGCGCACACGAGTACCGACGACCTGCGGAGCGGAGCGGAGCGGAGCTG 420
 Qy 141 LeuArgArgValGlyAspAspValLeuValAlaLeuValAlaArgCysAlaLeuPheVal 160
 Db 421 CTGGCGCGCGTGGGCGACGAGTGTGCTTCACTGCTGGCAGCTGCGCGCTTGTG 480
 Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuValGlnLeuValAla 180
 Db 481 CTGTGTGCTCCAGCTGCGCTGACGAGTGTGCGGCGCGCGCTGACAGCTCGGCGCT 540
 Qy 181 AlaThrGlnAlaArgProProProAlaSerGlyProArgArgArgLeuGlyCysGln 200
 Db 541 GCCACTGAGCG 600
 Qy 201 ArgAlaTyrPheAlaSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CGGCGCTGGAACCATAGCTGCTGAGGAGCGCGGCTGCGCGCGCGCGCGCGCG 660
 Qy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProAlaArgProArg 240
 Db 661 GCGGAGGCGCGCGGAGTGCACGACCGAGCTTGCCTGGCCAGAGAGCCCAAGCCT 720
 Qy 241 G1ValAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
 Db 721 GCGCGTGCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
 Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 Db 781 AGGAGCGCTGACGAGTGCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 Qy 281 G1ValAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAGGCACTCTTGT 900
 Qy 301 ArgGlnHisAlaGlyProProSerThrSerArgProProAlaArgProTyrAspThrPro 320
 Db 901 CGCGGACACAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 Qy 321 CysProProValTyrAlaGlyThrTyrHisPheLeuTyrSerSerGlyAspGlyGln 340
 Db 961 TGTCCCGCGGTGACGCGAGACAGACATCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
 Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1021 CTGCGGCGCTCTTCTCTACTGAGCTCTGAGGCGCGAGCTGAGCGGCTGCGGAGCTC 1080
 Qy 361 ValGluThrTlePheLeuGlySerArgProTyrPheProGlyThrProArgArgLeuPro 380

Db 1081 GTGAGACCATCTTCTGCGGTTCAGAGCCCTGGATGCCAGGACCTCCCGAGGTTGCC 1140
 Qy 381 ArgLeuProGlnArgTyrTyrPrglMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 Db 1141 CGCTGCGCCACGAGCTACAGTGGCAAAATGCGCCCTGTTCTTGTGAGCTGCTTGGAAACAC 1200
 Qy 401 AlGlnCysProTyrGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 420
 Db 1201 GCGGAGTGCCTTACGCGGAGTGTCTCTCAAGACGACCTGCGCGGTGCGAGCTGCGTAC 1260
 Qy 421 ProAlaAlaGlyValCysAlaArgGluValProGlnGlySerValAlaAlaProGlnGlu 440
 Db 1261 CCAGCAGCGGT 1320
 Qy 441 GluAspThrAspProAspArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 Db 1321 GAGGACACAGACCCCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
 Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrPrglYser 480
 Db 1381 GTGTACGGCTTGTGCGGCGCTGCTGCTGCGCGGTGTGTGTGTGTGTGTGTGT 1440
 Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrTyrLeuPheLeuSerLeuGlyTyrHis 500
 Db 1441 AGGCACACACGACCGCTTCTTCAAGAACACCAAGATTCATCTCTCTGCGGAGCAT 1500
 Qy 501 AlaTyrLeuSerLeuGlnGluLeuThrTyrPheSerValArgAspCysAlaTyrPrgl 520
 Db 1501 GCCAAGCTCTGCTGCGAGAGCTACGCGGAGATGAGCGGCGGAGCTGCTGCTG 1560
 Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlu 540
 Db 1561 CGCAGAGCCCGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
 Qy 541 LeuAlaTyrPheLeuHisTyrPheLeuMetSerValTyrValValGluLeuArgSerPhe 560
 Db 1621 CTGCGCAAGTCTTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1680
 Qy 561 PheTyrValThrGluThrThrPheGlnLeuAsnArgLeuPhePheTyrArgGlySerVal 580
 Db 1681 TTTTATGTACGAGACACGCTTCTCAAAAGACGCTCTTTTCTACCGGAAAGATGTC 1740
 Qy 581 TrpSerTyrLeuGlnSerTyrGlyValArgGlnHisLeuValArgValGlnLeuArgGlu 600
 Db 1741 TGGAGCAAGTGTCAAAAGATGGAATGACACAGCATTTGAAAGAGGTGCACCTGCGGAG 1800
 Qy 601 LeuSerGlnAlaGlyValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGTGGAAGCAGAGGTACAGCAGCATCGGAAAGCCGCGCTGCTGACGTCACAGA 1860
 Qy 621 LeuArgPheLeuProLeuProAspGlyLeuArgProAlaLeuValAsnMetAspTyrVal 640
 Db 1861 CTCGCGTATCTCCCAAGCTTACCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
 Qy 641 GlyAlaArgThrPheArgArgGlnArgArgAlaGluArgLeuThrSerArgValAla 660
 Db 1921 GAGACGAAACGTTTCCGCAAGAAAGAGGCCGAGCGCTACCTCGAGGGTGAAGGCA 1980
 Qy 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
 Db 1981 CTGTTCAGGTGTCAACTACAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCT 2040
 Qy 681 LeuGlyLeuAspAspTyrHisArgAlaTyrPrglThrPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGCGCTGACATTCACAGGCGCTGCGGACCTTGTGTGTGTGTGTGTGTGTGT 2100
 Qy 701 AspProProGluLeuLeuTyrPheValCysValAspValThrGlyAlaTyrAspThrTle 720
 Db 2101 GACCGCGCGCTACGCTACTTGTCAAGGTGAGATGACGCGCGCGTACAGACACATC 2160
 Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLeuPrglAsnThrTyrCys 740
 Db 2161 CCCAGACAGGCTCAGGAGGTCAATCGCAGCATCATCAAAACCCAGAACAGATCTGC 2220

Db 476 CTGCGCCGCTGGGGACGACGCTGCTGCTCACTGCTGGCAAGCTGCGCGCTTTGTG 535
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyValA 180
Db 536 CTGGTGGCTCCCAAGCTGCGCTTACCAAGGTGCGGGCCGCCCTGTACAGTGTGGGCT 595
QY 181 AlAThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu 200
Db 596 GCCACTCAGGCGCGCGCCGCCCAACGCTAGTGGACCCGAAAGCGTCTGGGATGCCAA 655
QY 201 ArgAlaTTPAsnHisSerValArgGlnValProLeuGlyLeuProAlaProGly 220
Db 656 CGGCGCTGGAACATGAGCTCAGAGAGCGGGGTCCTTGAGCTGCGACGCCCGGT 715
QY 221 AlaArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
Db 716 GCGAGAGAGCGCGGGGCGAGTGCACGCCAAGTCTGCGTGGCCCAAGAGCGCCAGCGT 775
QY 241 GlyAlaAlaProGluProGluValThrProValGlyGlnGlySerThrAlaHisProGly 260
Db 776 GCGCGCTGCGCTGAGCGGAGCGGAGCGCGCTTGGGAGAGGGTCTGGGCGCCAGCGGC 835
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
Db 836 AGGACGGTGGACGAGTACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 896 GAAGCCACCTTTTGGAGGGTGGCTCTGCGACCGCGCACCTCCACCCATCCGCGGGC 955
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro 320
Db 956 CGCGAGACCAACCGGGGCGCCCATTCACATCGGGGACCAAGTCTGCGGACAGCGCT 1015
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuLysSerSerGlyAspLysGln 340
Db 1016 TGTCTCCCGGTGACGCGGAGCAACCACTTCTCTACTCTCAGGCGCAAGAGAGCAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1076 CTGGGCGCTCTCTCTCACTCACTCACTCTGAGCGCCAGCTGAGCTGCGCTGAGAGCTC 1135
QY 361 ValGlnThrLysPheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
Db 1136 GTGAGAGCATCTTCTGAGTCCAGGCGCTCGAGTGCAGAGACTCCCGCAGAGTTGCC 1195
QY 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
Db 1196 CGCGTGGCCCGCTACTGCAATGCGGCGCTGTCTTCTGAGCTGTGGAGAACACAC 1255
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db 1256 GCGAGTGCCTCTGAGGGGTCTCTCAAGAGCACTGCGCGCTGCGAGCTGCGGTACC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnLysSerValAlaAlaProGlu 440
Db 1316 CCAAGAGCGGTGTGTGTGCGCGGAGAGAGCCCAAGGCTCTGTGGGCGCGCCGAGAG 1375
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
Db 1376 GAGGACACAGACCCCGCTGCTGTGAGCTGTCTGCGCAGCAAGAGAGCCCTGAGAG 1435
QY 461 ValTyrArgLysPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
Db 1436 GTGTGCGCTTGTGCGGGCTCTGCTGCGCGGCTGTGTGCGCGCTGCGGGCTGCC 1495
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHis 500
Db 1496 AGGCAACAAGAGCGCGCTTCTCTCAGGAACACCAAGAGTTCATCTCCCTGGGAGAGCAT 1555
QY 501 AlaLysLeuSerLeuGlnLeuThrTTPLysMetSerValArgAspCysAlaThrLeu 520
Db 1556 GCCAAGCTCTGCTCAGAGAGCTGACGTGGAAGATGAGCGTGGGACTGTGGCTGGCTG 1615

QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgPheArgGlnGluLe 540
Db 1616 GCGAGAGGCCAGAGGGTGGCTGTGTGCTGCGCGGAGAGCAAGCTTGTGCTGAGAGATC 1675
QY 541 LeuAlaLysPheLeuHisThrLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1676 CTGGCCAAAGTTCCTGCACTGTGATGAGTGTATGATGATGATGATGATGATGATGATG 1735
QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1736 TTTTATGTCAACGAGACCAAGTTCAAAGAACAGGCTTTTCTTCAACGAGAGTGTCTC 1795
QY 581 ThrSerLysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db 1796 TGGAGCAAGTTGCAACATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1855
QY 601 LeuSerGluAlaGluValArgGlnHisArgGlnLysArgProAlaLeuLeuThrSerArg 620
Db 1856 CTGTGGAAGCAGAGTCAAGCAGCATCGGGAAGCGCGCGCGCTGTGACGTCCAGA 1915
QY 621 LeuArgPheLysProLysProAspGlyLeuArgProIleValAsnMetAspTyrValAla 640
Db 1916 CTGCGCTTCATCCCAAGCTGAGCGGCTGCGCGCATTTGTGAACATGATGATGATGATG 1975
QY 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGlnArgLeuThrSerArgValLysAla 660
Db 1976 GAGCGCAAGAGTTCGAGAGAAAGAGGCGAGGCTCTCACTGAGAGGTGAAAGCA 2035
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 2036 CTGTTCAAGCTGCTCAATCAAGAGCGGCGGCGCGCGCGCTCTGAGGCGCTTGTGTG 2095
QY 681 LeuGlyLeuAspAspIleHisArgAlaTTPArgThrPheValLeuArgValArgAlaGln 700
Db 2096 CTGGGCTGAGAGATATCAAGGCGCTGGCGCACTTCTGCTGCGGTGCGGGCCAG 2155
QY 701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
Db 2156 GACCGCGCGCTGAGCTGATCTTGTCAAGGTGATGTGAGCGGCGGTGAGAACCATTC 2215
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleLysProGlnAsnThrTyrCys 740
Db 2216 CCCAGAGACGGCTCAGAGAGTATGCCAGCATCATCAAAACCCAGAACATGATCGC 2275
QY 741 ValArgArgTyrAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLys 760
Db 2276 GTGCGTGGTATGCGGTGTGTGCAAGAGCGCGCATGGGCAAGTCCGCAAGGCTTCAG 2335
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2336 AGCCAGTCTTCACTTGCACACCTCAGCGGTACATGCAACAGTTCGTGCTCACTG 2395
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGlu 800
Db 2396 CAGGAGACAGCCCGCTGAGGAGATGCCGTCTCATGAGAGAGTCTCTCCATGATGAG 2455
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValAlaArgIle 820
Db 2456 GCCAGAGTGGCTTTCAGCTTTCCTTCACTTCACTTCACTTCACTTCACTTCACTT 2515
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2516 AGGGGCAAGTCTTCACTCAGTGCAGGGGATCCGCAAGGCTTCATCTCTCCAGCTG 2575
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2576 CTCTGAGCTGTGCTGACGCGCAGCAGAGGAACAAGCTGTTGCGGAGTTCGGCGGATC 2635
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GGGCTGCTCTGCGGTGTGGTGTGATTTCTTGTGTGTGACCTTCACTCAACCCAGCGG 2695

QY 861 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
DB 2696 AAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGCTGGTGGTGAACCTTTG
QY 901 ArgLysThrValValAsnProValGluAspGluValLeuGlyGlyThrAlaPheVal 920
DB 2756 CGGAAGACAGAGTGTACCTTCCTCTAGAGACGAGGGCTGGGGGAGACGGCTTTTGT
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
DB 2816 CAGATGCGGCGCCAGCGGCTATTCCTGGTGGCTGGCTGGCTGGATACCCGAGCCCTG
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
DB 2876 GAGGTGACAGAGGACTACTCCAGCATATGCCGAGCTTCATAGAGCCAGTTCACCTTC
QY 961 AsnArgGlyPheLeuValGlyValArgAsnMetArgArgGlyLeuPheGlyValLeuArgLeu 980
DB 2936 AACCGCGGCTTCAGAGCTGGAGGAGAACATGCTCCCAACTTTGGGGCTTCGGCGCTG
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
DB 2996 AAGTGTCAAGCTGTCTTCTGATTTGAGGTGAAGAGCTTCAGAGCGGTGACCAAC
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
DB 3056 ATCTACAAAGATCTCTCTGCTGACGGCGTACAGGTTTCAAGCATGTGCTGACAGCTCCA
QY 1021 PheHisGlnGlnValTyrPheAsnProThrPheLeuArgValIleSerAspThrAla 1040
DB 3116 TTTTCATCAGCAAGTTTGGAGAACCCCACTTTTTCGCGGCTCATCTGTACACAGCGCC
QY 1041 SerLeuCysTyrSerIleLeuLeuValAlaLysAsnAlaGlyMetSerLeuGlyValAlaGly 1060
DB 3176 TCCCTCTCTACTCATCTCTGAAGACCAAGACGAGGAGTCTCTGGGGGCAAGGGCC
QY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
DB 3236 GCCCGCGGCTCTCTGCTCCGAGGCGGTGCGAGTGGCTGTCACCAAGCATTCCTGCTC
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
DB 3296 AAGCTGACTGACACCGTGTCACTACGTCACCTCTGGGGTCACTCAGGACAGCCAG
QY 1101 ThrGlnLeuSerArgGlyLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
DB 3356 ACGCAGCTGAGTGGAGAGCTCCGGGGAGAGAGCTGACTGCTGAGCGCCGAGCCCAAC
QY 1121 ProAlaLeuProSerAspPheLeuThrIleLeuAsp 1132
DB 3416 CCGGCACTGCCCTCAGACTTCAAGACATCTCGAC 3451

RESULT 4

US-09-990-080-1
Sequence 1, Application US/09990080
Patent No. US2002010266A1
GENERAL INFORMATION:
APPLICANT: Morin, Gregg B.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
FILE REFERENCE: 018/258C
CURRENT APPLICATION NUMBER: US/09/990,080
PRIOR APPLICATION NUMBER: US 09/052,864
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1

Alignment Scores:
Pred. No.: 0
Score: 5961.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9
Gaps: 0

US-10-044-692-2 (1-1132) x US-09-990-080-1 (1-4015)

QY 1 MetProAlaGlyAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 56 ATGCGCGCGCTCCCGCTGCGAGACCTGGGCTCTGCTGCGAGCACTACCGCGAG 115
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
DB 116 GTGCTGCGGCTGGCCACGTTGTGCGGCGCTGGGGCCCAAGGCTGGGCTGGTGACG 175
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 176 CGCGGGAGCCCGCGGCTTTCGCGCGCTGGTGCGCCAGTGGCTGTGCGCTGG 235
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLeuGlyLeu 80
DB 236 GACGACGCGCGCGCGCGCGCGCGCGCTTCCTCCAGAGTCTGCTGTAAGAGCTG 295
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
DB 296 GTGGCGCCAGTGTCTCAGAGCTGTGCGAGCGCGCGCGGAGAACGTCTGCTCGG 355
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
DB 356 TTGCGGCTGTGAGACGGGGCGCGCGGGCGCGCGCGCTTCAACACAGCTGCGC 415
QY 121 SerTyrLeuProAlaThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeuLeu 140
DB 416 AGCTACCTGCGCAACCGGTACCGACCTGCGGGAGCGGGGCGCTGGGGCTGCTG 475
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 476 CTGGCGCGCGGTGGGAGAGAGCTGTGCTTCACTGCTGCGACGCTGGCGCTTGTG 535
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 536 CTGGGTGCTCCAGCTGCGCTTACAGGTGTGGGGCGCGCTGTACAGCTCGCGCT 595
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProAlaArgArgLeuGlyCysGlu 200
DB 596 GCCACTCAGCGCGCGCGCGCGCGCGCAACGCTAGTGACCCGAGGCGCTGGAGCGAA 655
QY 201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 656 CGGCGCTGGAACATAGCTGACGAGGAGGCGGGGCTCCCTGGGCTGCGACCGCGG 715
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 716 GCGAGAGAGCGCGGGGAGTGCAGCGGAGTGTGCGGTGCCCAAGAGCGCGCGGT 775
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 776 GCGCTGCGCTGAGCGCGAGCGAGCGCGCTTGGGAGGGGCTCTGGGCCCAACCGCGG 835
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 836 AGGAGCGCTGACCGAGGACCGTGTCTGTGTGTGTCTACCTCCAGACAGCCCGCA 895
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 896 GAAAGCACTCTTGGAGGAGTGGCTCTGTGGACGCGCCACTCCACCACTCCGTGGG 955

QY	301	ATGGINHSHIALAGIYPROBOSERTHRSARXPROPOARXPROTHPSRPHPro	320
Db	956	CGCAGACACACCGGGGGCCCCCATCCACTCGGGGCAACAGTCCCTGGACAGGCTT	1015
QY	321	CysProProValYValAGIuThrLYSHsAPheLeuTYSerSerGIYAspLYsgluGln	340
Db	1016	TGTCGCCGGTGTACGCCAGAACAGCACTTCTCTACTCCTCAGGCGACAAAGAGCAG	1075
QY	341	LeuARgProSerPheLeuLeuSerSerLeuARgProSerLeuThrLYlaARGaArgLeu	360
Db	1076	CTGGGGCCCTCTCTTCTACTCAGCTCTGAGGCCAGGCTGTAGCTGGCCCTGGAGGCTC	1135
QY	361	ValGluThrLLePheLeuGIYSerARgProTPMeCProGIYThrProARgArgLeuPro	380
Db	1136	GTGGAGACCAATCTTCTTGCGGTTCCAGGCCCTTGATGCCAGGAGACTCCCGCAGGTTGGCC	1195
QY	381	ArgLeuProGlnARgTYTPGImeLArgProLeuPheLeuGluLeuLeuGIYAsnHIS	400
Db	1196	CGCCTGCCCCAGCGCTACTGGCAAAATCGGCGCCCTGTGTTGTGAGGTGTGTTGGGAACAC	1255
QY	401	AlaGlnCysProTYArgLYValLLeuLeuLYThHIScYsProLeuARgAlaAlaValTTr	420
Db	1256	GCGCAGGCCCCCTTAAGGAGGTCTCTTAAGACGACCTGCCCGCTGGAGCTGGGCTCAC	1315
QY	421	ProAlaAlaGIYValCYsaIaArgLYuLysProGlnLYSerValAlaAProgluGln	440
Db	1316	CCACGACGGGTGTCTGTGCCCGGAGAAAGCCACAGGCTCTGTGGGGGCCCCCGAGGAG	1375
QY	441	GluAsPThrARpProARgArgLeuValGluLeuLeuARgGlnHISserSerProTPGln	460
Db	1376	GAGACACACAGCCCCCGTGGCTGTGACGTCTCGGACGACACACAGCCCTGGCAG	1435
QY	461	ValTYrgLYPheValARgAlaCYsaLeuARgArgLeuValProProGIYLeuTPGIYSer	480
Db	1436	GTGTAACGGCTTCGTGGCGGCTGTGGCGGGTGTGGTGGCCCCCAGGCTCTGGGGGCTCC	1495
QY	481	ArgHISaenGIuARgArgPheLeuARgAsnThrLYsLYsPheLISerLeuGIYsHIS	500
Db	1496	AGGCACAAACGAACCGCGCTTCTCAGAGAACACCAAGAAATTCATCTCTCGGGGAACAT	1555
QY	501	AlaLYsLeuSerLeuGlnLeuThrTYrLYsMetSerValARgAspCYsaIATProLeu	520
Db	1556	GCGAAGCTCTGCTGACAGAACTGACGTGGAAATGACGTCGGGAGCTGGGCTTGGCTG	1615
QY	521	ArgARgSerProGIYValGIYCYsValProAlaAGluHISArgLeuARgGluGluILE	540
Db	1616	CGCAGAGACCCAGGGGTTGGCTGTGTTCCGGCGCGAGACACCTGTCTGCGAGAGATC	1675
QY	541	LeuAlaLYsPheLeuHISETraLeuMetSerAlTYrValValGluLeuLeuARgSerPhe	560
Db	1676	CTGGGCAAGTTCCTGACCTGGGTGATGATGTGTAAGTCGTGTCGTGACAGTCTCAAGTCTTTC	1735
QY	561	PheTYrValThrGluThrThrPheGlnLYsaAsnArgLeuPhePheTYrArgLYSerVal	580
Db	1736	TTTATGTACACGAGAACACCGTTTCAAAAGAACAGGCTCTTCTTCTACCGGAAGAGTCTC	1795
QY	581	TPDSerLYsLeuGlnSerLIEGLYLLaArgGlnHISLeuLYsArgValGlnLeuARgGlu	600
Db	1796	TGGAGCAAGTTCACAAAGCATGGAAATCAGACGACCTTGAAGAGGGGTGCACCTGGGGAG	1855
QY	601	LeuSerGIYAlaAGIValARgGlnHISArgGluAlaARgProAlaLeuLeuThrSerARg	620
Db	1856	CTGTGCGAAGCAGAGTCAAGACATCGGGAAGCAGGCCCGGCTGCTGACGTCGAGA	1915
QY	621	LeuARgPheLISerProLYsProAspGIYLeuARgProLIEvalAsnMetAspTYrValVal	640
Db	1916	CTCCGCTTCATCCCAAGGCTCAGCGGGCTGCGCGCATTTGTGAACATGACATCACTCTGTG	1975
QY	641	GIYAlaArgThrPheARgArgGluLYsARgAlaGluARGLeuThrSerARgValLYsaIa	660
Db	1976	GAGGCGCAAGACGTTCCGACAGAAAGAGAGGCCCGACGCTTCACTCCAGGCTGAAGCA	2035

QY	661	LeuPheSerValIleuAsnTryrGlnArgAlaAaArgProGlyLeuLeuGlyAlaSerVal	680
Db	2036	CTGTTCAGCGTGTCTCACTACAGACGGGGGGGGGGCCCGCCGACCTCTCTGGGGCCCTCTGTG	2095
QY	681	LeuGlyLeuAspAspIleHisArgAlaIaTPAaGlnrPheValIleuArgValArgAlaGln	700
Db	2096	CTGGGCGTGGACGAATTCACAGAGGGCTGGCCGACCTTGCTGCTCGATGGCGGGCCGAG	2155
QY	701	AspProProGluLeuTyrPheValIysValAspValThnGlyAlaTyrAspThrIle	720
Db	2156	GACCCCGCGCTGACGCTGATCTTGTCCAGAGGGATGGACGGGGCGCGAGACACACATC	2215
QY	721	ProGlnAspArgLeuThrGluValIleAlaSerIleIleLeuAspProGlnAsnThrTyrCys	740
Db	2216	CCCCAGACAGGCTCACAGAGGTCATCCGCAAGATCATCAAAACCCAGAACAGTACTGC	2275
QY	741	ValArgArgTyrAlaValAlaGlnIyValAlaHisIleGlyHisValArgValAlaPheLys	760
Db	2276	GTGCTGCGATATGGCCGGTCCAGAAAGGCGCCCAATGGGACGTCGCAAGAGCCCTTCAAG	2335
QY	761	SerHisIaSerThrIleuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu	780
Db	2336	AGCCACGCTCTTACTTTCAGACACTCCAGCCGTACATCGACAGTTCGTGGCTACCTG	2395
QY	781	GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGln	800
Db	2396	CAGGAGACAGACCCGCTGAGGGATGCGCTGTCATGAGAGAGCTCTCCCTGAATGAG	2455
QY	801	AlaSerArgIyLeuPheAspValPheLeuArgPheMetCysHisIaValAlaArgIle	820
Db	2456	GCCAGCATGCGCTCTTCGACGCTTCTTCACGCTTCAATGTGCCACCAACCCGTCGCATC	2515
QY	821	ArgGlyIySerTyrValIleGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
Db	2516	AGGGGCAAGTCTTACGTCACAGTGGCAAGGGATCCCGAGGGCTCCATCTCTCCACGCTG	2575
QY	841	LeuCysSerLeuCysTyrGlyAspMetGlnAsnIyIleuPheAlaGlyIleArgAsp	860
Db	2576	CTCTGCACCCCTGCTCAGCGGCAATGAAACAGCTGTTCGGGGATTCCGGCGGAC	2635
QY	861	GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
Db	2636	GGGCTGCTCTCGGTTGGTGGAGATTTCTTGTGGTGCACCTCACCTCACCCGCGCG	2695
QY	881	LysThrPheLeuAlaGlnrLeuValArgIyValProGluTyrGlyCysValIlaAsnLeu	900
Db	2696	AAAACTTCTTCAGGACCCCTGTGTCGGAGTGTCCCTGAGTATGCTCGCGTGAACCTTG	2755
QY	901	ArgLysThrValIlaAsnPheProValGlnAspGlnAlaLeuGlyGlyThrAlaPheVal	920
Db	2756	CGAAAGACAGTGTGATCTTCCCTGTGAAGAACAAGGCCCTGGGGTGGCAGCGCTTTGTT	2815
QY	921	GlnMetProAlaHisIleGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu	940
Db	2816	CAGATGCGGGCCCAAGGCGCTATTCCTCCGTGGCGCGCTGCTGCTGATACCCGACCTG	2875
QY	941	GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
Db	2876	GAGGTGCAGAGGACTACTCCAGCTATTCGCCGACCTCCATCAGAGCAAGTCACTTCC	2935
QY	961	AsnArgGlyPheIyValGlyArgAsnMetArgArgIyIleuPheGlyValLeuArgLeu	980
Db	2936	AACCGGCGCTTCAAGGCTGGAGGAACAATGGCGTGGCAAACTTTGGGGATCTTGGCGGTG	2995
QY	981	IyGlyCysHisSerLeuPheLeuAspLeuGlnAlaAsnSerLeuGlnThrValCysThrAsn	1000
Db	2996	AAGTGTCAAGGCTGTCTTGTGATTTGGAGGTGAACAGCTTCCAGAGGCTGTGCACCAAC	3055
QY	1001	IleTyrGlyAlaLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
Db	3056	ATCTACAAATCTCTCTGCTGGCGAGCGTACAGGTTTACAGCATGTGTGTCAGACTCCCA	3115
QY	1021	PheHisGlnGlnValIleTyrIyAsnProThrPhePheLeuArgValIleSerAspThrAla	1040

Db 3116 TTTCATCAGCAAGTTGAGAGAACCCCATTTTCTCGCGCATCTGCAGACGCGC 3175
Qy 1041 SerLeuCyTyrSerTlleLeuYAlaYsaAenAlaGlyMetSerLeuGlyAlaYagGly 1060
Db 3176 TCCCTCTCTACTCCTCCTGTAAGCCAGAACGAGGATGTCTGCGGCGCCAAAGGAC 3235
Qy 1061 AlaAlaGlyProLeuProSerGlyAlaYalGlnTProLeuCyHieGlnAlaPheLeu 1080
Db 3226 GCGCGCGCGCTCTCTCTCTCGAGGCGCTGCGATGCTGTGCAACAGCATTCCTGCTC 3295
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACGCTGTGACCTACGTCGACCTCGGGGTCACTCAGAGACAGCCGAG 3355
Qy 1101 ThrGlnLeuSerArgYalLeuProGlyThrThrThrThrAlaLeuGlnAlaAlaAen 1120
Db 3356 ACGCAGCTGAGTGGAGACTCCCGGGGAGCAGAGCTGACTGCTGTGAGGCGCAGCCAG 3415
Qy 1121 ProAlaLeuProSerAspPheLeuThrThrThrThrThrThrThrThrThrThr 1132
Db 3416 CCGGCACTGCGCTCTCAGACTTCAGACCATCTCGAC 3451

RESULT 5
US-09-843-676-224
Sequence 224, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Langner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224
Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9 Indels: 0
DB: Gaps: 0

US-10-044-692-2 (1-1132) x US-09-843-676-224 (1-4015)
Qy 1 MetProArgAlaProArgCyArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
Db 56 ATGCGCGCGCTCCCGCGCTGCGAGCCGTGCGCTCTGTCGCGACGACCTACCGCGAG 115
Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 116 GTGCTGCGCTGCGCCACGCTTGTGTGGGCGCTGGGGCCCAAGGCTGCGCTGTGTGAG 175
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 176 CCGCGGGACCGCGCGCTTTCGCGCGCTGTGCGCCAGTGTCTGTGTGTGTGTGTGTGTGT 235
Qy 61 AspaLaArgProProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
Db 236 GACGCGAGCG 295
Qy 81 ValAlaArgValLeuGlnArgLeuGlyArgGlnArgGlyAlaYsaAenAlaLeuAlaPheGly 100
Db 296 GTGGCGCCAGAGCTGTGACAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCG 355
Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyProProGlnAlaPheThrThrSerValArg 120
Db 356 TTGCGCTGTGTGACG 415
Qy 121 SerTyrLeuProAsnThrValThrAspaLaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
Db 416 AGCTACCTGCGCCAAACAGGTGTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 475
Qy 141 LeuArgArgValGlyAspaAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 476 CTGCG 535
Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 536 CTGTGTGCTCCAGCTGTGCGCTACCGAGGTGTGCGCGCGCGCGCGCGCTGTACAGTTCG 595
Qy 181 AlaThrGlnAlaArgProProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
Db 596 GCGACTCAGGCG 655
Qy 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 656 CCGGCGCTGAAACATAGGTGTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 715
Qy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
Db 716 GCGAGAGCG 775
Qy 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260

Db 776 GAGCGTCCCTGAGCCGAGCGGACGCCCTTGGGACAGGGGTCTGGGCCCCACCCGGGC 835
Qy 261 ATGTHrArgIyProSerAspArgIyPheCyValValSerProAlaArgProAlaGlu 280
Db 836 AGGAGCGGTGGACCGAGTGACCGTGATTTCTGTGTGTGTCTGACTGCGGACGACGCCCAA 895
Qy 281 GluAlaThrSerLeuGluGluValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 896 GAAGCAGCTCTTTGGAGGGGTGGCTCTTGACAGCGGACCTCCACCCATCCCTGGGC 955
Qy 301 ArgGlnHisAlaGlyProProSerThrSerArgProArgProIleThrAspThrPro 320
Db 956 CGCCAGACCAACCGGGCCCCCATTCACATCGCGGCCACAGTCCCTGGGACAGCGCT 1015
Qy 321 CySPProValIleValGluThrIleHisPheLeuTySerSerGlyAspIleGluGln 340
Db 1016 TGTCCCCCGGTGACCGGACCAAGCACTTCTCTACTCTCTCAGGCGACAAAGAGCAG 1075
Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1076 CTGCGGCGCTCTCTTCTACTCAGCTCTGAGGCCAGCTGACTGAGCGCTCGAGGCTC 1135
Qy 361 ValGluThrIlePheLeuGlySerArgProIlePheProGlyThrProArgArgLeuPro 380
Db 1136 GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAGCTCCCGCAGATTGCC 1195
Qy 381 ArgLeuProGlnArgIleTyTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyHis 400
Db 1196 CGCTGCGCCGAGCGCTACTGGCAATGCGGCCCTCTTCTGGAGTGTGTGGAAACAGC 1255
Qy 401 AlaGlnCySPProTyArgIleValLeuLeuLeuLeuHisCySPProLeuArgAlaAlaValThr 420
Db 1256 GCGCAGTGTCCCTACGAGGGGTCTCTCAGACCGCATGCGCGCTGGAGCTGGGTCAAC 1315
Qy 421 ProAlaAlaGlyValCySPAlaArgIleValLeuProGlnGlySerValAlaAlaProGluGlu 440
Db 1316 CCAGCAGCCGATGTCTGTGCGCGGAGAACCCCGAGGGCTCTGTGGCGGCCCGCAGAGAG 1375
Qy 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1376 GAGGACAGAGCCCGCTGCTGTGTGACGTGCTCCGACAGACAGAGCCCTTGCGAG 1435
Qy 461 ValTyArgIlePheValArgAlaCySPLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db 1436 GTGTACGGCTCTCGTGGCGGCTGTCTGCGCGGCTGTGTGCGCCAGGCTCTGCGGCTCC 1495
Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrIleTySerPheIleSerLeuGlyHis 500
Db 1496 AGGCACAACGAAACCGCTTCTCAGGAACACCAAGAGTTCACTCTCTGGGAGACAT 1555
Qy 501 AlaLeuSerLeuGlnGluLeuThrTrpLeuMetSerValArgAspCySPAlaTrpLeu 520
Db 1556 GCCAAGCTCTGCGAGAGACTGACGTGGAAGATGAGCCGTGGGACTGGCTGTGCTG 1615
Qy 521 ArgArgSerProGlyValGlyCySPValProAlaAlaGluHisArgLeuArgGluGlnIle 540
Db 1616 CGCAGAGCCCAAGGGGTGTGGCTGTCTCGCCCGCAGAGCACCGTCTGCGGAGACATC 1675
Qy 541 LeuAlaTySPheLeuHisTrpLeuMetSerValTyArgValGluLeuLeuArgSerPhe 560
Db 1676 CTGGCAAGTCTCGACATGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1735
Qy 561 PheTyArgValThrGluThrThrPheGlnTySPAsnArgLeuPhePheTyArgIleSerVal 580
Db 1736 TTTTATGTACGAGACCAACGTTTCAAAGAAAGAGGCTCTTTTCTACCGGAAAGGTCTC 1795
Qy 581 TySPerIleLeuGlnSerIleGlyTleArgGlnHisLeuTySPArgValGlnLeuArgGlu 600
Db 1796 TGGACCAAGTTCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGTCACTCGGGAG 1855
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db 1856 CTGTGGAGAGCAGAGGTCAAGCATGTGGAGAGCCAGGCTCCCTCTACGTCCAGA 1915

Qy 621 LeuArgPheIleProIleProAspGlyLeuArgProIleValAlaAsnMetAspTyArgVal 640
Db 1916 CTCCGCTTATCCCAAGCTGACGGGCTGTGGCCGATTTGAAATGACATCACTGCTGTG 1975
Qy 641 GlyAlaArgThrPheArgArgGluTySPArgAlaGluArgLeuHisSerArgValIleValAla 660
Db 1976 GAGGCCAGAAAGTTCCTCCAGAGAAAGAGGGCGAGGTGTCACTTGAGGAGTGAAGGCA 2035
Qy 661 LeuPheSerValLeuAsnTyArgIleArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 2036 CTGTTACCGTGTCAACTACAGCGGGCCGGCGCGCGCTCTGCGCTGTGGCGGCTGTG 2095
Qy 681 LeuGlyLeuAspAspIleHisArgAlaTyArgThrPheValLeuArgValAlaGln 700
Db 2096 CTGGGCTGTGACATATCCACAGGGCTGTGGCACTTCTGTGCTGTGTGTGTGTGTGTGT 2155
Qy 701 AspProProProGluLeuTyTrpPheValIleAspValThrGlyAlaTyArgThrIle 720
Db 2156 GACCGCGCGCTGAGCTGTACTTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2215
Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleTySPProGlnAsnThrTyCys 740
Db 2216 CCCAGAGCAGGCTCACGAGAGTCAATGCCAGATCATCAACCCAGAACACGTACTGTC 2275
Qy 741 ValArgArgTyArgAlaValGlnTySPAlaHisGlyHisValArgGlyAlaPheLeu 760
Db 2276 GTGGCTCGGTATGCGT 2335
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyTrpMetArgGlnPheValAlaHisLeu 780
Db 2336 AGCCAGTCTTACTTGTACAGACCTCCAGCCGTACATGCAACAGTTCTGTGTGTGTGTGT 2395
Qy 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu 800
Db 2396 CAGAGAGACAGCCGCTGAGGATGCGCTGTCTGTACGAGACCTCTCTCTCAATGAG 2455
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2456 GCCACAGTGGCTTGT 2515
Qy 821 ArgGlyTySPerTyArgIleGlnCySPGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2516 AGGGGCAAGCTCTTACTGACAGTGTCCAGGGGATCCGAGGGCTCATCTCTCCACGCTG 2575
Qy 841 LeuCySPerLeuCyTyArgIleAspMetGlnAsnTySPLeuPheAlaGlyTleArgArgAsp 860
Db 2576 CTCTGAGCGCTGT 2635
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GAGCTGTCTCTGTTGT 2695
Qy 881 TySPThrPheLeuArgThrLeuValArgGlyValProGluTyArgIleCySPValAlaAsnLeu 900
Db 2696 AAAACCTTCTCAGACAGCTGTGTCCAGAGGTGTCCCTGAGTATGCTGTGTGTGAACCTG 2755
Qy 901 ArgTySPThrValAlaAsnPheProValGluAspGluAlaLeuGlyGlyThrHisAlaPheVal 920
Db 2756 CGAGAGACAGTGTGAATCTCTCTGTGAAGACAGGGCTCTGTGTGTGTGTGTGTGTGT 2815
Qy 921 GlnMetProAlaHisGlyLeuPheProTySPGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2816 CAGATCCCGCCACAGGCTTATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2875
Qy 941 GluValGlnSerAspTySPerSerTyArgIleArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGAGAGGACATCACTCAAGCTATGCCGAGACTCATAGAGCCAGTCTCACTTC 2935
Qy 961 AsnArgGlyPheTySPAlaGlyArgAsnMetArgArgGlyLeuPheGlyValLeuArgLeu 980
Db 2936 AACCGCGCTTCAAGGCTGTGAGAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2995

QY 381 LysCysHisSerLeuPheLeuAspLeuGlnValIaenSerLeuGlnThrValCysThrAsn 1000
Db 2996 AAGTGTCAAGCCCTGTTCTGGATTGTCAGGGAACAGCTTCACAGCGTGTGCAAC 3055
QY 1001 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTCAAGATCTCTCTGTCGAGCGGTACAGGTTTCAAGCTGTGTCTGCAAGCTCCCA 3115
QY 1021 PheHisGlnGlnValThrLysAsnProThrPhePheLeuArgValIleSerSerPheAla 1040
Db 3116 TTTCATCAGCAAGTTTGAAGAACCCCAATTTCCTGCGGTATCTTGACACAGGCGC 3175
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
Db 3176 TCCCTCTCTACTCATCTCTGAAGCAAGCAAGCAAGGATTCCTCTGGGGCCCAAGGCG 3235
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPleCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCGGCGGCGCTCTGCTCCGAGGCGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 3295
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTGACACCGGTGCTCCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3355
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTGGAGAGCTCCCGGGGACGAGCTGAGCTGAGCTGAGCTGAGCTGAG 3415
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGCACTGCGCTCAGACTTCAAGACATCTGAGC 3451

RESULT 6

US-09-953-052-1
Sequence 1, Application US/09953052
Patent No. US20020173476A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,052

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linearMOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454

OTHER INFORMATION: /product= "human telomerase reverse transcriptase (HTRT)"

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1

Alignment Scores:

Pred. No.:	Score:	Length:
0	5961.00	4015
100.00%	100.00%	1132
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
DB:	9	Indels: 0
		Gaps: 0

US-10-044-692-2 (1-1132) x US-09-953-052-1 (1-4015)

QY 1 MetProAlaGAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGln 20
Db 56 ATGCCGGCGGCTCCCGGTCGAGCCGTCGCTCCGTCGTCGAGCAGCACTACCGGAG 115
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 116 GTGCTGCGCGTGGCCACGCTTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 175
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProThr 60
Db 176 GCGGGGAGCCCGGCGGCTTTCGCGCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 235
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
Db 236 GACGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
QY 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyAlaLysAsnValLeuAlaPheGly 100
Db 296 GTGGCCGAGGTCTGTCAGAGGCTGTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 355
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThSerValArg 120
Db 356 TTGGCGCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 415
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140

416 AGCTACCTGCCAACAACGCTGACCGACGACCTGCGGGGAGCGGGGCGTGGCGT 475
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 476 CTGGCCGCGTGGGCGACACGACGCTGCTGCTCACTGCTGGCAACGCTGCCCTCTTTGG 535
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 536 CTGGTGGCTCCAGCTGCTGCTACAGAGTGTGGGCGCGCTGACAGCTCGGCGCT 595
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 596 GCCACTCAGGCGCGCGCGCGCGCAACGCTAGTGAACCCGGAAGGGCGCTGGGAATGCCAA 655
QY 201 ArgAlaTyrAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 656 CCGGCTTGAAACATATGCGTCAAGAGAGCGGGGTCCTCTGGGCTGCGACGCCGGGT 715
QY 221 AlaArgArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 716 GCGAGAGAGCGCGGGGCGAGTGCACGACCGAAGCTGCTGCGCAAGAGCCGAGCGCT 775
QY 241 GlyAlaAlaProGlyLeuProGlyArgThrProValGlyGlnGlySerThrAlaHisProGly 260
DB 776 GCGCTGCGCTGACCGGAGCGGACGCGCGCTGGGCGAGGGGTCTGGGCGCAACCGCGGC 835
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGly 280
DB 836 AGGACCGCTGGACCGAGTGAACGCTGCTTCTGTGTGTGTCACCTTCAGACCGCGGAA 895
QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 896 GAAGCAACCTCTTTGAGAGGTGCGCTCTGCGACCGCGCACTCCACCATTCGGGGG 955
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProThrPro 320
DB 956 CGCAGACACACCGGGGCGCGCCCATCCACATCCGCGGCAACGATCCCTGGGACAGCGCT 1015
QY 321 CysProProValTyrAlaGlnTyrHisPheLeuTyrSerSerGlyAspLysGln 340
DB 1016 TGTCCCGGTGTACCGCGAGACCAAGCACTTCTCACTCTCAAGCGCAAGAGACG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1076 CTGCGGCGCTCTTCCACTCACTCACTCTGAGGCCAGCGCTGACTGGCGCTGGAGGCTC 1135
QY 361 ValGlnThrThrPheLeuGlySerArgProTyrPheProGlyThrProArgArgLeuPro 380
DB 1136 GTGGAGACCATCTTTCTGGGTTCAGGCGCTGATGCCAGGACTCCCGCAGAGTTGCC 1195
QY 381 ArgLeuProGlnArgTyrTyrPglTyrMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1196 CGCGTCCCAAGCGCTACTGCAATGCGGCGCTGTTTCTGAGCTGCTGGGAACAC 1255
QY 401 AlaglnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1256 GCGAGAGCGCTCAAGGGGTCTCTCAAGCGACTGCCGCTGCGAGCTGCGGTACC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGly 440
DB 1316 CCAAGACCGGCTGTCTGTGCGCGGAGAGCGCCAGGCTCTGTGGGCGCGCGGAGAG 1375
QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrPgl 460
DB 1376 GAGAGACAGACCGCGCTGCTGTGTGCTGCTGCGCAAGACAGACCGCTGGCAG 1435
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrPglYser 480
DB 1436 GTGTACGGCTTCTGTCGGGCGCTGCTGCGCGCTGTGTGCGCGCGCGCTGGGCTCC 1495
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheHisSerLeuGlyLysHis 500
DB 1496 AGGCACAACGAACCGCTTCTCTCAGGAACACCAAGAAATTCTCTCTGGGGGAACAT 1555

501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
QY 1556 GCCAAGCTCTGCTGCGAGAGCTACGCTGGAAGATGAGCGTGGGGACTGGCTTGGCTG 1615
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisAsnGlnArgGlnGln 540
DB 1616 CCGAGAGACCGAGGGGTGGCTGTGTTCCGGCGCGAGCGACCGCTGCGTGAAGAGATC 1675
QY 541 LeuAlaLysPheLeuHisThrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
DB 1676 CTGGCAAGTTCCTGACTGGCTGTAGAGTGTGATGCTGTGCGAGCTCTCAAGCTTTTC 1735
QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1736 TTTTATGTCAAGAGACACACGTTTCAAAGAAAGAGCTTTTCTTCAACCGGAAGTGTCTC 1795
QY 581 TrpSerLysLeuGlnSerIleGlyTyrLeuArgHisLeuLysArgValGlnLeuArgGln 600
DB 1796 TGGACCAAGTTGCAGAAAGCATGGATGCAATCAGACGCTTGAAGAGAGTGCACCTGGGAG 1855
QY 601 LeuSerGlnAlaGlnValArgValHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
DB 1856 CTGTGGAAGCAGAGGTGAGGAGCATGGAGACCGAGCGCGCTGCTGACGCTCAG 1915
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
DB 1916 CTGCGCTTCAATCCCAACCTGACGCGGCTGCGCGCATTTGGAACATGACATACGTCGTG 1975
QY 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGlnValGlnLeuThrSerArgValLysAla 660
DB 1976 GGAGCCAGAACCTTCCGAGAGAAAGAGGCGCGAGCTTCACTCAGAGGTGAAAGCA 2035
QY 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyValaSerVal 680
DB 2036 CTGTTCAAGCTCTTAACCTACAGCGGCGCGCGCGCGCTGCTGCGGCTCTGTG 2095
QY 681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
DB 2096 CTGGGCGTGGAGATATCCAGAGGCGCTGGCGCACTTGTGCTGCTGCTGGGCGCGCAG 2155
QY 701 AspProProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
DB 2156 GACCGCGCGCTGAGCTGACTGTTGTCAAGTGTGAGTGTGAGCGGCGCTGACACACATC 2215
QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
DB 2216 CCCCAGAGACGCTCAAGAGGTCACTGCCACATCATCAACCCAGAACACGTAATGCC 2275
QY 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
DB 2276 GTGCGTGGGTATGCGGTGTCCAGAAAGCGCGCAATGGGCAAGTCCGCAAGGCTTCAAG 2335
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
DB 2336 AGCCAGGTCTTCACTTGCAGACCTTCAAGCGCTGACAGCAAGTTCGTGCTCACTG 2395
QY 781 GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
DB 2396 CAGAGACACAGCCCGCTGAGGATGCCGTGTCATGACAGCAAGGCTCCCTGATGATGAG 2455
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
DB 2456 GCCAGAGTGGCTTCTTCAAGCTTCTTCAACCTTATGTGCACACACCGCTGGCGATC 2515
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
DB 2516 AGGGGCAAGTCTTCACTTCAAGTGCAGAGGAGATCCGCAAGGCTCACTTCTCAAGCTG 2575
QY 841 LeuCysSerLeuCysTyrGlyAspMetGlnAsnLysLeuPheAlaGlyTyrLeuArgArgAsp 860
DB 2576 CTCTGACGCTGTGCTACGCGCAATGAGAACAAAGCTTTTGGCGGAGTTGGCGGAGC 2635

QY	81	ValAlaArgValLeuGlnIaArgLeuCySGIaArgGlyAlaLysAsnValLeuAlaPheGly	100
Db	296	GTGGCCCGAATGTGTGCAGAGGCTGTGTGAACGGGGCGGAGAAACATGTGGCTTCGGCC	355
QY	101	PheAlaLeuLeuLeuBspGlyAlaArgGlyGlyProProGlnAlaPheThrThrserValArg	120
Db	356	TTGGCGCTGCTGGACAGGGGCCCGGGGGGCCCCCGAAGGCTTTCACACACAGCTGGCC	415
QY	121	SerTyrLeuBProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
Db	416	AGCACTCTGCCAAACAGGTGACCGACGCACTCGGGGGAGCGGGGGTGGGGCTGGCG	475
QY	141	LeuAlaArgArgAlaGlyAspAspValLeuValHisLeuLeuLeuAlaArgCysAlaLeuPheVal	160
Db	476	CTGGCGCGCGGGCGAGAGCGTGTGTTCACCTGTGGACAGCTGCGGCTCTTTGTG	535
QY	161	LeuValAlaBProSerCysAlaTyrGlnValCysGlyProBProLeuTyrGlnLeuGlyAla	180
Db	536	CTGGTGGCTCCAGAGCTCGGCTACAGATGTGCGGGCGCGGCTGTATCCAGCTCGCGCT	595
QY	181	AlaThrGlnAlaArgProProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln	200
Db	596	GCACTACAGCGCGCGCGCGCGCACAGCTATGTGAACCCGAAAGGCTCTGGAGATGGAA	655
QY	201	ArgAlaTrpAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly	220
Db	656	CGGGCTGGAAACATACGTACAGGAGAGCGGGGCTCCCTGGGGCTGCCAGCCGGGCT	715
QY	221	AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysAlaArgProAlaArg	240
Db	716	GCGAGAGAGCGCGGGGGGACATGACAGCGCAAGTGTGCTGGCCCAAGAGGCCACAGCGT	775
QY	241	GlyValAlaLapProGluProGlnArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
Db	776	GGCGCTGCGCTTGAGCCGAGCGGACGCCCTTGTTGGCAGGGGTCTTGCGCCACCGGGC	835
QY	261	ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln	280
Db	836	AGGACGCGTGACCGAGTGAACCGTGATTTCTGTGTGGTGACCTGTGCACACCGCGCGAA	895
QY	281	GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerThrAspSerValGly	300
Db	896	GAACCCACCTTTTGGAGGGTGGCGCTCTGTGGACGGCGCACTCCACCCATCCGTGGGC	955
QY	301	ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
Db	956	CGCCAGACCAACGGGGGCCCCCATCCACATCGCGGCAACACGTCCCTGGGAACAGCTT	1015
QY	321	CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln	340
Db	1016	TGTCCCCCGGTGTACGCCGAGAACCAAGACTTCCTATCTCTAGCGAGCAACAGAACAG	1075
QY	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
Db	1076	CTGGCGGCTCTTCTTCACTCAAGCTCTCTAGGCGCCAGCTGACCTGGAGGCTCGGAGGCTC	1135
QY	361	ValGlnThrTyrLeuLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
Db	1136	GTGGAGACCAATCTTCTGGGTTCACAGCGCCGTGAATGCCAGGGAGACTCCCGGAGGTGCC	1195
QY	381	ArgLeuProGlnArgTyrTrpGlyMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis	400
Db	1196	CGCTGCGCCCAAGGCTACTGGCAAAATGGGCGCCGTCTTCTGAGAGCTGCTTGGGAACAC	1255
QY	401	AlaGlnCysProTyrGlyValLeuLeuLeuSerThrHisCysProLeuArgAlaAlaValThr	420
Db	1256	GCGAGTGCCTTACGGGGGTGTCTCTCAAGACGCACTGCGCGTGGCGAGCTCGAGTACAC	1315
QY	421	ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGln	440
Db	1316	CCAGACGCGGGGTGTGTGCCCCGGGAGAGGCCCAAGGCTCTGTGTGGGGCCCCGAGAGG	1375

OY	441	GIuAsPthrAspProAArgAgtLeuValGIInLeuLeuArgGlnhiSesSerProTPGIn	460
Db	1376	GAGGACACACACCCTCCCTCGGTGCACACTCTCCGACGACACAGCCCTCTGACAG	1435
OY	461	ValYrGcIyPheValAArgAlaCySLeuAArgArgLeuValProProGlyLeuTrpGlySer	480
Db	1436	GTCACGAGCTTCGTGCGGGCTGCTGCGGGCTGCTGCGGGCTGCTGCGGGCTCC	1495
OY	481	ArgHisAnGluAArgAArgPheLeuAArgAsnThrLysLysPheLLeSerLeuGlyVhHis	500
Db	1496	AGGCACACAGACGCCGCTTCCTCAGGAGACACCAAGAAAGTTCATCTCCCTGGGGAAGCAT	1555
OY	501	AlAlaLysLeuSerLeuGInGluLeuThrTTrpLysMetSerValAArgAspCysAlaTrpLeu	520
Db	1556	GCCACAGCTCTCCGTGCGAGAGCTGACCTGGAAGAATGAGCGTGGAGATGCGCTGTGCTG	1615
OY	521	ArgAArgSerProGluValAGlyCySValProAlaAGluhiSAArgLeuArgGluGluLe	540
Db	1616	CGCAGAGACCCAGGGAGGTGGCTGTGTTCCTCCGACGACAGACCGCTCTGCTGAGAGATC	1675
OY	541	LeuAlaLysPheLeuhiSTrPLeuMetSerValTyValValGluLeuLeuAArgSerPhe	560
Db	1676	CTGGCCAAAGTTCCTGCACTGGCTGATGATGATGATACGTCTCGAGCTGCTCAAGTCTTTC	1735
OY	561	PheTyValThrGluThrThrPheGlnLysAsnAArgLeuPheTyArgLysSerVal	580
Db	1736	TTTTATGTCACGGAGACCAAGCTTTCAAAGAACAGGCTCTTTTTCATCCGAAAGAGTCT	1795
OY	581	TrpSerLysLeuGInSerLLeGlyLeArgGlnhiSLeuLysAArgValGInLeuAArgGlu	600
Db	1796	TGGAGCAAGTTCGAAAGCATTTGGATCAGACAGCATTTGAAGAAGGGGTGCAGCTGGCGGAG	1855
OY	601	LeuSerGluAlaGluValAArgGlnhiSAArgGluAlaArgProAlaLeuLeuThrSerArg	620
Db	1856	CTGTCTCGAAGCAGAGGTCTACGAGCAGACATCGGGAAGCCAGGCGCCGCTGTGACGTCCAGA	1915
OY	621	LeuAArgPheLLeProLysProAspGlyLeuAArgProLLeValAsnMetAspTyValVal	640
Db	1916	CTCCGCTTCATCCCAAGCCCTGAGCGGGCTGGCGCATGTGGAACTATGACTATGACTGTGTG	1975
OY	641	GlyAlaAArgThrPheAArgArgGluLysAArgAlaGluAArgLeuThrSerAArgValAla	660
Db	1976	GAGCCACGAACGTTCCGACAGAAAGAGGGCCAGAGCTCTCACCTCGAGGGTGAAGCA	2035
OY	661	LeuPheSerValLeuAsnTyGluAArgAlaAArgAArgProGlyLeuLeuGlyAlaSerVal	680
Db	2036	CTGTTCAACGTCCTCACTACAGAGCGGGCGCGGCGCCGCGCTCTGGGGGCTCTGTGTG	2095
OY	681	LeuGlyLeuAspAspAspLLeHisAArgAlaTrpAArgThrPheValLeuAArgValAArgAlaGln	700
Db	2096	CTGGGCTCTGACGATATCCACAGGGGCTGGGGCACTTCGTGCTGCGGTGGGGGCCACAG	2155
OY	701	AspProProProGluLeuTyPheValLysValAspValThrGlyAlaTyAspThrLLe	720
Db	2156	GACCCGCGGCTGAGACTTACTTGTGTCAAGTGAATGTGACGGGCGGCTACGACACATC	2215
OY	721	ProGInAspAArgLeuThrGluValLLeAsSerLLeLysProGInAsnThrTyCyS	740
Db	2216	CCCCAGACAGGCTCAGCGAGGTATCGCCAGCATCAACAAACCCAGAACACACTACTGTC	2275
OY	741	ValAArgAArgTyAlaValAlaGlnLysAlaAlaHisSGLyhiSValAArgLysAlaPheLys	760
Db	2276	GTGGCTCTCGGTATGCGGTGTCCAGAAAGGCGGCCCATGGGACAGTCCGACAGGGCTTCAAG	2335
OY	761	SerHisValSerThrLeuThrAspLeuGInProTyPheAArgGInPheValAlaHisSLeu	780
Db	2336	ACCCACGCTCTACTTACAGACCTTCCAGCCGTACATGCACAGTTCGTGGCTCACTG	2395
OY	781	GInGluThrSerProLeuAArgAspAlaValLLeGluGInSerSerSerLeuAsnGlu	800
Db	2396	CAGGAGACCAAGCCGCTAGGGAGTCCGCTGTCAATCGACAGAGCTCTCCCTGAATATAG	2455
OY	801	AlAsSerGlyLeuPheAspValPheLeuAArgPheMetCysHisAlaValAArgLLe	820

Db 2456 GCCAGCAGTGGCTCTTGCAGCTCTTCTACGCTTCATGTGCACCAAGCCGTCGACATC 2515
Qy 821 ArgGlyIysSerTyrValAlaGlnCysGlnGlyLeuProGlnGlySerIleuSerThrIeu 840
Db 2516 AGGGGCAAGTCTTACGTCCAGTGCAGAGGATCCGCGAGGCTCCATCTCTCCACGCTG 2575
Qy 841 LeuCysSerLeuCysTyrGlyYAspMetGluAenlySLeuPheAlaGlyIleArgArgAsp 860
Db 2576 CTCTGCACCTCTGTGTACGCGACATGAGAACAAAGCTCTTTGCGGGGATTCGGCGGAC 2635
Qy 861 GlyLeuLeuLeuValArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GGGCTGCTCTGCGCTGTGTGTGATGATTTCTTTGTGTGACACCTCACCTCACCCACGCG 2695
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnIeu 900
Db 2696 AAAACCTTCTCCAGAACCTTGCTCGAGGTGTCTCTGATGAGCTGCTGTGTGAACCTTG 2755
Qy 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2756 CGGAAGACAGTGTGTAATCTTCTCTGAGAACAGAGCCCTGGGTGGCACGCGCTTTGTT 2815
Qy 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuAspThrArgThrIeu 940
Db 2816 CAGATGCGCGGCCACAGGCTTATTCCTGTGTGCGGCTGTGCTGTGATACCGGACCGCTG 2875
Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerIeuThrPhe 960
Db 2876 GAGGTGCAGAGGACTACTCCAGCTATGCGCGACCTCCATCAGACGCTCTCACCTTC 2935
Qy 961 AsnArgGlyPheLeuAlaGlyValArgAsnMetArgArgLysLeuPheGlyValLeuArgIeu 980
Db 2936 AACCGCGCTTCAAGGCTGGAGGAAACATGCTCGCAACTTTTGGGCTCTTGGCGCTG 2995
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2996 AAGTGTCAAGCCTGTTCTGTGATTTGACGTGAACAGCCTCCAGACGGTGTGCACCAAC 3055
Qy 1001 IleTyrIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnIeuPro 1020
Db 3056 ATCTCAAGATCTCTCTGTGACGCGTACAGGTTTCAAGCATGTGTGTGACGCTCCCA 3115
Qy 1021 PheHisGlnGlnValTyrPheAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCTACAGCAAGTTTGAAGAACCCACATTTTCTCGCGCTCATCTTACACGCGCC 3175
Qy 1041 SerLeuCysTyrSerIleLeuIlySAlaIlySAsnAlaGlyMetSerLeuGlyValIlySgly 1060
Db 3176 TCCCTCTGCTACTCATCTCGAAGACCAAGAACGACGAGATGCTCGTGGGGCCAAAGGC 3235
Qy 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrPheCysHisGlnAlaPheLeuIeu 1080
Db 3236 GCGCGCGGCTCTCTCCCTCCAGGCGCGTGCAGTGTGTGCTGCACCAAGCATTTCTGCTC 3295
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACCTCGACACGAGTGTACCTACGTCACCTCTGAGGCTCACTCGACGACGCCAG 3355
Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaIleAsn 1120
Db 3356 ACGCAGCTGAGTGGAGAGCTCCCGGGAGCAGACGCTGACCTGGAGGCGCAGCCAAAC 3415
Qy 1121 ProAlaLeuProSerAspPheIlySThrIleLeuAsp 1132
Db 3416 CCGGCACTGCTCTCAGACTTCAAGACCATCTGTGAC 3451

APPLICANT: Geron Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
FILE REFERENCE: 015389-003500PC
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/10/208,243
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/112,006
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: WO PCT/US99/06898
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1
Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-044-692-2 (1-1132) x US-10-208-243-1 (1-4015)
Qy 1 MetProAlaGlnAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
Db 56 ATGCGCGCGCTCCCGCTGTGCGAGCCGTGCGCTCTGCTGCGACACACGCGAG 115
Qy 21 ValIeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 116 GTGCTGCGCTGCGCACGTTCTGTGCGGCTTGGGAGCCCAAGGCTGGCGGCTGTGCGAG 175
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 176 CGCGGGAGCCGGCGGCTTTCCGCGCGCTGTGCGCGAGTGTGTGTGCGCTGCG 235
Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuIlySglIeu 80
Db 236 GACGACCGCGCGCCCGCGCGCTTCTCCGCGAGGTGTCTGCTGAGAGAGCTG 295
Qy 81 ValAlaArgValIleuGlnArgLeuCysGluArgGlyValIlySAsnValIleuAlaPheGly 100
Db 296 GTGGCCGAGTGTGCAAGGCTGTGCGAGCGCGCGGAGAACAGTGTGTGCTGTGCGC 355
Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyIlyProProGluAlaPheThrThrSerValArg 120
Db 356 TTGCGGCTGTGAGAGGGGCGCGGGGCGCCCGCGAGGCTTACACACGCGGTGCGC 415
Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATrpgIlyLeuLeu 140
Db 416 AGCTACCTGCGCCAAACAGGTGACGACACCTGCGGGGAGCGGGGCGTGTGGGCGCTG 475
Qy 141 LeuArgArgValGlyYAspAspValLeuValHisLeuLeuAlaArgCysAlaIleuPheVal 160
Db 476 CTGCGCGCGGTGGAGAGCGCTGTGTGCTGCTGCGACGCTGCGCGCTTTTGG 535
Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnIleuGlyAla 180
Db 536 CTGTGTGCTCCAGCTGCGCGCTTACAGGTGTGCGGGGCGCGCTTACAGCTGCGCGCT 595
Qy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 596 GCCACTCAGGCGCGCGCGCGCACACGCTAGTGACCCGGAAGCGTGTGGAGATGCGAA 655

QY 201 ArgAlaTTPaNHISerValArgGluAgiValProLeuGlyLeuProAlaProGly 220
DB 656 CCGGGCTTGAGACATGCGTCAAGGAGCGGGGCTCCCTGAGCTGCAACCCCGGCT 715
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArg 240
DB 716 GCGAGAGAGCGGGGGGCGAGTCCAGCCCAAGTCTGCTCCCAAGAGCCAGGCT 775
QY 241 GAlaAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
DB 776 GGGGCTGCGCTGAGCGGAGCGGAGCGCCGTTGGGCAAGGCTCCGAGCCCAACCGGAG 835
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 836 AGGACCGCTGGAGCCAGTACCGTGGTTCTGTGTGTGTACCTGCCAGACCCCGCGGA 895
QY 281 GAlaAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 896 GAGGCCACTCTTTGGAGGGGTGGCTCTGGCAGCGGCCACTCCACCCATCCGTGGG 955
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
DB 956 CGCCAGACACAGCGGGGCCCCCATCCACATCGCGGCCACAGTCCCTGGAGCACGGCT 1015
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuThrSerSerGlyValAspLysGln 340
DB 1016 TGTCCCGGTGTACCGCCAGACCAAGCACTTCTTACTCTCAAGGCAAGAGAGCAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1076 CTGGCGGCTCTCTTCTACTCACTCTGTGAGGCCAGCCCTGAGCGCTGGAGAGCTC 1135
QY 361 ValGluThrLysPheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
DB 1136 GTGAGAGCACTCTTCTGGGTTCAGAGCCCTGATGCCAGGACTCCCGCAGGTGGCC 1195
QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1196 CGCTGCGCCAGCGCTACTGGCAAAATCGGCGCCCTGTTCTGAGACTGCTGGGAACAC 1255
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1256 GCGCAGTGGCCCTACCGGGGTCTCTCAAGACGACTCGCGCTGGAGCTGGGTCAAC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
DB 1316 CCAGCAGCCGCTGTGTGTGCGGAGAACCCCGAGGCTCTGTGGGCGCCCGAGAGAG 1375
QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
DB 1376 GAGGACACAAACCCCGCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1435
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
DB 1436 GTGTAGCGCTTGT 1495
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheLeuLeuLeuGlyLysHis 500
DB 1496 AGGCACACAAACCCCGCTTCTCAAGAACACCAAGAAATTCATCTCCCTGGAGAACAT 1555
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
DB 1556 GCCAAGCTCTGCTGAGAGACTGACTGGAAGTGAAGTGGCGGAGCTGGCTGGCTG 1615
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluTrpLe 540
DB 1616 CGCAGAGAGCCAGGGGT 1675
QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
DB 1676 CTGGCCAAATTCGTGCACTGAGTGTATGATGTGTGTGTGTGTGTGTGTGTGTGT 1735

QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1736 TTTTATGTACAGGAGACCACTTTCAAAAGAGAGCTCTTTTCTACCGGAAAGATGTC 1795
QY 581 TrpSerLysLeuGlnSerLysGlyLysArgGlnHisLeuLysArgValGlnLeuAlaGlu 600
DB 1796 TGGAGCAAGTTGCAAGAGATTGGAATCAGACGACTTGAAGAGGTGACACTCGGAGAG 1855
QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
DB 1856 CTGTGGAGAGAGAGTTCAGAGATCGAGAGCCAGGCCCGCTCTGCTCACTCCAGA 1915
QY 621 LeuArgPheLeuProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
DB 1916 CTCCGCTTCACTCCCAAGCTGACGGGCTGGCGCGATTGTGAACATGACTACGTGCTG 1975
QY 641 GAlaAlaThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValAlaAla 660
DB 1976 GGAGCCAGAAAGTTCCGAGAGAAAGAGGCGCAGAGCTTCACTCGAGGGGTGAAGCA 2035
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
DB 2036 CTGTTCAGCGTGTCACTACAGAGCGGCGCGGCGCCCGCTCTGGGCGCTCTGTG 2095
QY 681 LeuGlyLeuAspAspLysHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
DB 2096 CTGGGCTCGAGAGATATCCAGAGGCGCTGGCGCACTTGTGTGTGTGTGTGTGTGT 2155
QY 701 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrLe 720
DB 2156 GACCCGCGCTGAGCTGTACTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2215
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerLysLysProGlnAsnThrTyrCys 740
DB 2216 CCCCAGACAGGCTACCGAGGTATCCGACAGATCATCAAAACCCAGAAACGATAGTC 2275
QY 741 ValArgArgTyrAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
DB 2276 GTGCGTGGTATGCGGTGTCCAGAGGCGCGCCCATGTGGACAGTCCGAGAGCTTCAAG 2335
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
DB 2336 AGCCAGCTCTTCACTTGAACAGCTCCAGCCGTCAATGCAAGATGTGTGTGTGTGT 2395
QY 781 GlnGluThrSerProLeuArgAspAlaValAlaIleGlnGlnSerSerSerLeuGlnGlu 800
DB 2396 CAGAGACCAAGCCCGCTGAGGAGATCCGTCGTATCGAGACAGACTCTCTCTGATGAG 2455
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLys 820
DB 2456 GCACAGAGTGGCTCTTCCACGCTTCTTCAACCTTCAATGTGCACACGCGCTGTGCATC 2515
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerLysLeuSerThrLeu 840
DB 2516 AGGAGGAGATCTTACGTCAGTGCAGAGGAGATCCGAGAGGCTCATCTCTCCAGCTG 2575
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyLysArgArgAsp 860
DB 2576 CTCTGAGGCTGTGCTAGAGGCAATGAGAACCAAGCTGTGTGGGAGTATCGCGGAGAC 2635
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
DB 2636 GGGCTGCTCTCTGT 2695
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
DB 2696 AAAACCTTCTCAGGACCTGTGTCCAGGTGTCTCTGATATAGCTGTGTGTGTGTGT 2755
QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
DB 2756 CGGAGACAGTGTGTAACTTCCCTGTAGAAAGACGAGGCGCTGGGTGGCACGCTTTGTT 2815
QY 921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940

Db 2816 CAGATGCCGCCACGCGCTATTCCTGCTGCGGCTCTGCTGATACCGGACCTG 2875
Qy 941 GJUVAGLInSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGCAGAGGACACTTCCAGCTATGCGCGACCTCCATCAGACCCAGCTCAGCTTC 2935
Qy 961 AanaRGlyPheLeuAlaGlyArgAenMetArgArgLyLeuPheGlyValLeuArgLeu 980
Db 2936 AACCGCGGCTTCAAGCGCTGGAGGAACATCGCGCAACTCTTGCGGCTCTGCGGCTG 2995
Qy 981 LysCySHISerLeuPheLeuAspLeuGlnValAenSerLeuGlnThrValCySHIAsn 1000
Db 2996 AAGTGTACAGCGCTGTTCTGATTTGACAGTGAACAGCCTCAGACGGGTGACCAAC 3055
Qy 1001 IleTyrVleIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCySHIleuGlnLeuPro 1020
Db 3056 ATCTACAGATCTCTCTGCTGAGGCGTAACGCTTCAAGCATGTGTCTGACAGCTCCA 3115
Qy 1021 PheHisGlnGlnValTyrPheAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCACTACAGCAAGTTTGGAGAAGCCCAATTTTCTCGGCTCATCTCTGACAGGCTC 3175
Qy 1041 SerLeuCySHISerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
Db 3176 TCCCTCTGCTACTCCATCTGAAAGCCAGAAAGCAGGAGATGTCGCTGGGGGCCAAGGCTC 3235
Qy 1061 AlaAlaGlyProLeuProSerGlyAlaValGlnTyrPheCySHIGlnAlaPheLeuLeu 1080
Db 3236 GCGCGCGGCTCTGCGCTCCAGAGCGCGGAGTGTGTCACCAACCATTTCTGCTC 3295
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACCGCTGTACCTHCGTGCACCTCTGCGGTCACTCGAGACGCCCTG 3355
Qy 1101 ThrGlnLeuSerArgLyLeuLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTCCGAGAGCTCCCGGGGACGACGCTGACCTCGGAGGCGCGACGAC 3415
Qy 1121 ProAlaLeuProSerAspPheLyThrIleLeuAsp 1132
Db 3416 CCGGACCTGCGCTCAGACTTCAAGACCATCTGAGC 3451

RESULT 9
US-10-054-295-224
; Sequence 224, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linguet, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054, 295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product="hTR"
/note="human telomerase reverse
transcriptase (hTR) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-295-224
Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-044-692-2 (1-1132) x US-10-054-295-224 (1-4015)

Qy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
Db 56 ATGCCGCGGCTCCCGCTGCGAGCCGTCGCTCTGCGGACCACTACCGCGAG 115
Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 116 GTGCTGCCGCTGGCCACCTTCGTGCGGCGCTGGGGGCCCAAGGCTGGCGCTGCGAG 175
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 176 CGCGGGGACCCGCGCGCTTCCGCGCGCTGGGCGCCAGGCTGGCGCTGCTGCTGCG 235
Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
Db 236 GACGACGCGCGCGCCCGCGCGCCCTCTCTCCGCAAGTGTCTGCTGAAGAGCTG 295
Qy 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyAlaLysAsnValLeuAlaPheGly 100
Db 296 GTGGCCCAAGTGTCCAGAGGCTGTGCGAGCGCGCGCGGAGAAAGTCTGCTGCGGC 355
Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyLyProProGlyAlaPheThrThSerValArg 120
Db 356 TTCGGCTGTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCTTCAACACGAGCTGCGC 415
Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATrGlyLeuLeu 140
Db 416 AGCTACCTGCGCAACACGCTACCGACGACCTGCGGGGAGCGGGGCGCTGGGGCTGCTG 475
Qy 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

D	478	CTGGCGCGCGGGGCGACGACGTCGTGTTCACTGCTGGGACGCTCGCGCTTTGTG	535
Q	161	LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
D	536	CTGTGTGCTCCACACTGAGCTTACCAAGTGTGGGGCGCGCGTGTACAGCTCGCGCT	595
Q	181	AlaThrGlnAlaAArgProProProHisAlaSerGlyProArgAArgLeuGlyCysGlu	200
D	596	GCCACTAGCGGCCGGGCCCCCGCCACACGCTAAGTGTACCCCGAAGGCGCTGTGGGTGGAA	655
Q	201	ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
D	656	CGGCGCTGGAAACATAAGCTCAGGAGAGCGCGGGTCTCCCTCGGGCTCGCACGCCGGGT	715
Q	221	AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
D	716	GCGAGAGAGCGCGGGGGGAGTGTCCACGCGGAAGTCTGCGGTGTCCAGAGAGGCCAGGCGT	775
Q	241	GlyValAlaLProGluProGlnValArgThrProValGlyGlnGlySerThrPalaHisProGly	260
D	776	GGCGCTGGCTTGTAGCGCGGACCGGACGCGCGCTGTGGAGAGGGGTCTGTGGGCCACCGGAGC	835
Q	261	ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
D	836	AGGACGCGTGAACCGAGTACCGCGGTTCGTGTGTGTGTACCTGCCACAGCCGCCGAA	895
Q	281	GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
D	896	GAACGCACCTCTTTGGAGGGTGGCGTCTGTGGACGCGGCACCTCCACCATCCGTGGGCG	955
Q	301	ArgGlnHisAlaGlyProProSerThrSerArgProAlaArgProTyrAspThrPro	320
D	956	CGCAGCAGCACACGGGGGCCCCCATCCACATCGGGCGACACACGTCCTGTGGAACCCCT	1015
Q	321	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGln	340
D	1016	TGTCCCCCGGTGTACCGGAGACCAAGCACTTCTCTACTCTTACGGCGGACAGAGACAG	1075
Q	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
D	1076	CTGGGGCCCTCTTCTCTACGACTCTGTAGGCCACAGCTGACGTGGGGCTCGGAGGCTC	1135
Q	361	ValGluThrLysPheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro	380
D	1136	GTGGAGACCACTTCTGTGGATTCCAGGCGCCGTGAATGCCAGGAGACTCCCCGAGGTGGCC	1195
Q	381	ArgLeuProGlnAsxTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
D	1196	CGCTTCCCCCAGCGCTTACTGTGGAAATGGCGGCCCTGTTTCTGGAGTCTTGGGAACAC	1255
Q	401	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
D	1256	GCGCAGTCCCTTACGGGGTGTCTCTCAAGACGACCTCCGCGTCCAGCGTGGCGGTACCC	1315
Q	421	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
D	1316	CCAGACGCGGTGTGTGTGCCCGGAGAGGCCCCAGGCGCTGTGTGGCGGCCCCGAGGAG	1375
Q	441	GluAspThrAspProArgArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln	460
D	1376	GAGGACACAGACCCCCGTGTGTGTGTGGAGCTGCTCCGACAGACAGAGCCCTTGGGAG	1435
Q	461	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer	480
D	1436	GTGTACGGCTTGTGTGGGCGCTGTGGCGCGGTGTGGCCCGGCTCTGTGGGCGTCC	1495
Q	481	ArgHisaengluArgArgPheLeuArgAsnThrLysLysPheLysSerLeuGlyLysHis	500
D	1496	AGGCAACAAGAACGCGGCTTCTCTCAGGAACACCAAGAGTTCAATCTCCCTGGGGAAGCAT	1555
Q	501	AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
D	1556	GCCAAAGCTCTGCTCTCAGAGGTGTACGTGGAAATGACGTGTGGGAGCTGTGGCTTGTGCTG	1615

QY	521	ArgArgSerProGluValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	540
Db	1616	CGCAGGAGCCCGAGGGGTGGCTGTGGTTCCCGCGCAGAGCACCGTCTGGAGGAATC	1675
QY	541	LeuAlaIysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
Db	1676	CTGGCCAAAGTTCCTGCACCTGGCTGATAGTGTGACGTCGTCAAGCTGCTCAAGTCTTTC	1735
QY	561	PheTyrValThrGluThrThrPheGluLysAsnArgLeuPhePheTyrArgLysSerVal	580
Db	1736	TTTATGTATCAGCGAGAGCACAGTTCAAAAGACAGCGCTCTTTTCTCAACCGAAGAGTCT	1795
QY	581	ThrSerLysLeuGlnSerLileGlyIleArgGluHisIleuLysArgValGluIleuArgGlu	600
Db	1796	TGGAGCAAGTTGGCAAGAGATTGGATATGACAGCACTTGAAGAGGTGTCAGCTCGGGAG	1855
QY	601	LeuSerGluAlaGluValArgGluHisArgGluAlaArgProAlaIleuLeuThrSerArg	620
Db	1856	CTGTCTGAGAGCAGAGGTCAGGCAAGCATCTGGGAAGCCAGGCCCGGCTGTGACGTCCAGA	1915
QY	621	LeuArgPheIleProLysProArgGlyLeuArgProIleValIleuMetAspTyrValVal	640
Db	1916	CTCCGCTTCATCCCAAGCCCTGACGGGCTGGCGGCGATTGTGAACATGACATCAGTGTGTG	1975
QY	641	GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
Db	1976	GGACCCAGAAAGTTCCCGACAGAAAGAAAGGGCCGAGCGTCTCACTCGAAGGTGAAGCA	2035
QY	661	LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
Db	2036	CTGTTCAGCGGTCTCACTACAGACCGGGCGGGCGCCGCGGCTCTGGGCGGCTCTGTGTG	2095
QY	681	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlu	700
Db	2096	CTGGAGCTCGAGCAATTCACAGAGGCTTGGCGCACCTTGTGTGCTGTGTGGCGGCCAG	2155
QY	701	AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
Db	2156	GACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTTACGACACATC	2215
QY	721	ProGluAspArgLeuThrGluValIleAlaSerLileLysProGluAsnThrTyrCys	740
Db	2216	CCCCAGGACAGGCTTCAGAGGTATGTGCCAGCATCTCAAAACCCAGAACAGCTACCTGC	2275
QY	741	ValArgArgTyrAlaValIleGluLysAlaAlaHisGlyHisValArgLysAlaPheLys	760
Db	2276	GTGGCTGGTATGCGGTGTCCAAAGAGCGCCCATGGGCACTGCCCAAGAGGCTTTCAG	2335
QY	761	SerHisValSerThrLeuThrAspLeuGluProTyrMetArgGlnPheValAlaHisIleu	780
Db	2336	AGCCACGCTCTTACTTTCAGACACCTCCAGCCGATACAGCAGATTCGTGTGCTCACCTG	2395
QY	781	GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu	800
Db	2396	CAGAGAGCACACCCGCTGAGGAGGATCGCGTGTCTACGAGCAGACCTCTCCCTGAATGAG	2455
QY	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
Db	2456	GGCAGCAAGTGCCTTCTCGACGTCTTCTTCAAGCTTCAATGTGCCACACAGCCGCTGCAATC	2515
QY	821	ArgGlyLysSerTyrValGlnCysGluGlyIleProGlnGlySerIleLeuSerThrLeu	840
Db	2516	AGGGGCAAGTCTTACGTTCACGTCCAGGGAGATCCCGCAGGGCTCAATCTCTCCACCTG	2575
QY	841	LeuCysSerIleuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	860
Db	2576	CTCTCAACCTGTGTGATGAGCGAATGAGAAACAAGCTGTTTGGGGGATTCGCGCGGAGC	2635
QY	861	GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisIleuThrHisAla	880
Db	2636	GGGCTGCTCTCGCGTTGTGTGAAGATTTCTGTGTGGAGACCTCACTCACCCACGCG	2695

Db 356 TTCGGGCTGCTGAGAGGGGCCCCGGGGGCCCCCGAGGCTTACACACAGCGCTGGC 415
Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgIySerGIYAlaTTrpIyLeuLeu 140
Db 416 AGCTACCTGCCCCAACAGCGGTGACCGACGCTGGGGGAGCGGGGCGGTGGGGCTGG 475
Qy 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 476 CTGGCGCGGTGGGCGACGACGCTGTGTACCTGTGACGCTGGCGGCTCTTTGTG 535
Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 536 CTGGTGGCTCCCAAGCTGCCCTTACACAGCTGTGGGGCGCGCTGTACACAGCTGGCGCT 595
Qy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
Db 596 GCACACTCAGGGCGCGCGCGCGCACAGCTAGTGAACCCCGAAGGGCGTCTGGGATGCGAA 655
Qy 201 ArgAlaTTrpAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 656 CGGGCGCTGAAACCAATAGCGTCAGAGAGGCGGGGCTCCCTGGGCTTGCACAGCGCGGT 715
Qy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProIyAspArgProArgArg 240
Db 716 GCGAGAGAGGGGGGGGGGAGTGCACCGACCGAAGTCTGCCGTTGGCCCAAGAGCGCGCT 775
Qy 241 GlyAlaAlaProGluProGluProGluProValGlyGlnGlySerTTrpAlaHisProGly 260
Db 776 GGGCGCTGCCCTGACCGGAGCGGAGCGCGGTGGGAGGGGTCTGGGGCCCAACCGGGGC 835
Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValIleSerProAlaArgProAlaGln 280
Db 836 AGAACCGGTGACCGAGTACCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
Qy 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 896 GAGGCCACCTCTTTGAGGGGTGGCTCTGTGCACCGCCACCTCCACACCATCCGGGGC 955
Qy 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
Db 956 CGGCACACACACCGGGGCCCCCATCCATCCAGCGGCGCACAGTCCCTGGAGACAGCCT 1015
Qy 321 CysProProValTyrAlaGlnThrIleHisPheLeuTyrSerSerGlyAspIyGlnGln 340
Db 1016 TGTCCCCGGTGAACCGGACGACCAAGCACTTCTTCACTCCAGGCGACAAAGAGCAG 1075
Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1076 CTGCGGCGCTCTTCTCACTCAGCTCTGTAGGCCCGCAGCTGACGTGGCGCTCGAGGGCTC 1135
Qy 361 ValGlnThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
Db 1136 GTGAGAGCCATCTTGTGGGTCCAGGCGCTGTGATGCGAGGAGACTCCCGCAGAGTTGCC 1195
Qy 381 ArgLeuProGlnArgIyTTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
Db 1196 CGCTGTGCCAGGCTACTGGCAATGCGGCCCTGTGTCTGGAGGTGCTGGGAACAC 1255
Qy 401 AlaGlnCysProTyrGlyValLeuLeuLeuYerThrHisCysProLeuArgAlaAlaValThr 420
Db 1256 GCGCAGAGGCCCTTACCGGGGTGCTCTCAGACGACGCGCGCTGCGAGGTGGGTACCC 1315
Qy 421 ProAlaIleGlyValCysAlaArgGlnLeuProGlnIySerValAlaAlaProGlnGln 440
Db 1316 CAGACACCGGTGTGTGTGCGGAGAGAGGCCCGAGGCTGTGTGGGGCGCGCGAGAG 1375
Qy 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1376 GAGGACACAGACCCCGGT 1435
Qy 461 ValTyrGlyPheValAlaGlnAlaCysLeuArgArgLeuValProProGlyLeuTTrpGlySer 480

Db 1436 GTGTACGGCTTCGTGGGGCGCTGCTGCGCGCGGTGTGCCCGGAGGCTCTTGGGGCTCC 1495
Qy 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrIleHisPheLeuSerLeuGlyLeuHis 500
Db 1496 AGGACACAGAGACCGCGCTTCTCAGAGAACCAAGAGTTCACTCTCCCTGGGGAAGCAT 1555
Qy 501 AlaIyLeuSerLeuGlnGlnLeuThrTTrpIySerSerValArgAspCysAlaTTrpLeu 520
Db 1556 GCCAAGCTCTGCTGACGAGACCTGACGTCGAGAGATGAGCGTGGGAGACTGCGCTGGCTG 1615
Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnIle 540
Db 1616 CCGAGAGACCCAGGGGT 1675
Qy 541 LeuAlaIyPheLeuHisTTrpLeuMetSerValTyrValIleGlnLeuLeuArgSerPhe 560
Db 1676 CTGGCCAAAGTTCTGTCACTGTGCTGTATGATGTGTATCGTCTGAGCTGTCTCAGCTTTTC 1735
Qy 561 PheTyrValIleThrGlnThrPheGlnIyAsnArgLeuPhePheTyrArgIySerVal 580
Db 1736 TTTTATGTACAGAGACACAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCT 1795
Qy 581 TrpSerIyLeuGlnSerIleGlyTTrpLeuGlnHisLeuIyAspArgValGlnLeuArgGln 600
Db 1796 TGGACCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCACTGGGGAG 1855
Qy 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db 1856 CTGTGGAAGACAGAGTCAAGCAGCATGGGAAGCCAGCGCGCTGCTGACGTCAGCA 1915
Qy 621 LeuArgPheIleProIyAspArgGlyLeuArgProIleValAsnMetAspTyrValIle 640
Db 1916 CTCCCTTCATCCCAACCTGTACCGGGCGCGCGCGATTTGGACATGAACTACGTCGTG 1975
Qy 641 GlyAlaArgThrPheArgArgGlnIyAspArgAlaGlnArgLeuThrSerArgValIyAsp 660
Db 1976 GAGGCGAGAGCTTCCGAGAGAAAGAGGCGGAGCTTCACTCCAGGGTGAAGCA 2035
Qy 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 2036 CTGTTCAAGGTCTCACTACGACAGGGGGCGCGCGCTGCTGGGCGCTCTGTG 2095
Qy 681 LeuGlyLeuAspAspIleHisArgAlaTTrpArgThrPheValLeuArgValArgAlaGln 700
Db 2096 CTGGGCTGTGAGATATCCAGGCGCTGGCGCACCTTGTGTGTGTGTGTGTGTGTGTGT 2155
Qy 701 AspProProProGlnLeuTyrPheValIyAspValIleArgValAlaTyrAspThrIle 720
Db 2156 GACCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCATC 2215
Qy 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleIyAspProGlnAsnThrTyrCys 740
Db 2216 CCGCAGAGACAGCTCAGAGGTCACTGCCACATCATCAACCCAGAAACAGTATGCTGC 2275
Qy 741 ValArgArgTyrAlaValAlaGlnIyAspAlaHisLeuGlnValArgIyAspIlePheIy 760
Db 2276 GTGCGTGGTATGCGGTGTGTGAGAGGCGCGCATGGAGCATGCGCAAGGCTTCAAG 2335
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2336 AGCCAGCTCTTCACTTGCACAGACTCCAGCGGTACATCCAGACAGTGTGTGCTACCTG 2395
Qy 781 GlnIleThrSerProLeuArgAspAlaValIleIleGlnIleSerSerSerLeuLeuGln 800
Db 2396 CAGAGAACAGCCCGGTGAGGATGCGCTGTCAATCGAACAAGTCTCTCTGAATGAG 2455
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
Db 2456 GCCAGAGTGGCTCTTCAAGCTTTCACCTTCATGTATGTGCACACAGCGCTGGCATTC 2515
Qy 821 ArgGlyIySerSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2516 AGGGGCAAGTCTCACTCAAGTGCAGAGGAGATCCCGAGGGGTCTCATCTCTCCAGCGT 2575

```

OY 841 LeuCySerLeuCyTyrGlyAspMetGluAenlyLeuPheAlaGlyIleArgArgAsp 860
Db 2576 CTCTGCAAGCTGTGCTTACGGCACAATGAGAAACAGCTTTGGCGGGATTCGGGGAGC 2635
OY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GGGCTGCTCTCGTGGTGGATGATTTCTTGGTGAACCTCACCTCACCCACCGCG 2695
OY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAenLeu 900
Db 2696 AAAACCTTCTCAGAGACCTGATGCGAGGTGTCCTGAGTAAGCTGCGCTGATGAGATTG 2755
OY 901 ArgLysThrValValAspPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2756 CGAAGACAGTGTAACTTCTCTGTAGAAAGAGAGCCCTGGTGGCAGCGCTTTGTT 2815
OY 921 GlnMetProAlaHisGlyLeuPheProTyrGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2816 CAGATGCGCGCCACGAGCTTATTCCTGCTGCGGCTGCTGCTGATACCGGACCTG 2875
OY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGCAAGAGGACTACTCCAGCTATGCCGAGCCTCATCAGAGCCAGTCTCACTTC 2935
OY 961 AsnArgGlyPheLeuValAlaGlyAspMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2936 AACCCGCGCTTCAAGGCTGGAGAAATGCTGCGAACTTTGGGGTCTTTCGCGCTG 2995
OY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2996 AAGTGTACAGGCTGTTCTGGATTGGACGTGAACAGCCTCAAGCGGTGGTGGACCAAC 3055
OY 1001 IleTyrValLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ACTCTCAAGATCTCTCTGTGAGGCTACAGGCTTCAAGCATGTGTGTGAGCTCCCA 3115
OY 1021 PheHisGlnGlnValTyrPheAspProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCATCAGCAAGTTTGGAGAAACCCCAATTTTCTCGCGCTCATCTCAACAGCGCC 3175
OY 1041 SerLeuCyTyrSerIleLeuValAspAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
Db 3176 TCCCTCTGTACTCATCTGAAAGCAAGCAAGGATGCGTGGGGGCAAGGCGC 3235
OY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnThrPheCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCCGCGCGCTCTGCTCCGAGGCGCTGAGTGTGCTGCGCACCAACATTTCTGCTC 3295
OY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTGCAACCGTGTACCTAGCGCACTCTGGGGTCACTCGAGCAAGCGCCAG 3355
OY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3356 ACGGAGCTGAGTCGGAAGCTCCCGGGAGAGAGCTGACCTCGAGAGGCCCGCAGCAAC 3415
OY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGCACTGCGCTCAGACTTCAAGACCAATCTGAGC 3451

```

RESULT 11 US-10-105-963-1

```

; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Genon Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; TITLE OF INVENTION: Recombination

```

```

; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-044-692-2 (1-1132) x US-10-105-963-1 (1-4015)

OY 1 MetProAlaGlnAlaProAlaArgCysArgAlaValArgSerLeuLeuArgSerHisIleTyrArgGlu 20
Db 56 ARGCGCGCGCTTCCCGCTGCGAGCCGTGCGCTCTCGTGGAGCACTACCGCGAG 115
OY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheArgLeuValGln 40
Db 116 GTGCTGCCCTGCGCAAGTTCGTGCGCGCTGCGGCGCCCGAGGCTGCGCGCTGCGAG 175
OY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 176 CGCGGGAGACCGCGCGCTTTCGCGCGCTGCGCGCCAGTGCCTGCTGCTGCTGCTG 235
OY 61 AspAlaArgProProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80
Db 236 GACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 295
OY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
Db 236 GTGCGCGCGCTGCTCAAGGCTGTGCGAGCGCGCGCGAGAACTGCTGCTGCTGCGC 355
OY 101 PheAlaLeuLeuAspGlyAlaArgGlyLysProProGluAlaPheThrThrSerValArg 120
Db 356 TTGCGGCTGCTGAGAGGGGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
OY 121 SerTyrLeuProAlaThrValThrAspAlaLeuArgLysSerGlyValAlaTyrGlyLeuLeu 140
Db 416 AGCTACCTGCGCCCAACAGCTGACCACTGCGCGGGAGCGGGGCGCGCGCGCGCTG 475
OY 141 LeuArgArgValAlaAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 476 CTGCGCGCGGGGAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 535
OY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 536 CTGCTGCTGCGCAAGTGTGCGCTACCAAGGTGTGCGGCGCGCTGACCAAGTGTG 595
OY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProPheArgArgLeuGlyCysGlu 200
Db 596 GCCACTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
OY 201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 656 CGGCGCTGAGACCAAGCTCAGGAGCGCGGGGCTCCCTGCGCTGCGAGCGCGCGGT 715
OY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240

```

Db 716 GCGAGAGCGCGGGGGCAGTCCAGCCCAAGCTCTGCCCTTCCCAAGAGGCCAGGGCT 775
Qy 241 G1yAlaAlaPProGluPProGluThrProValGlyGlnGlySerTyrPalaHisProGly 260
Db 776 GGGGGCTGCCCTGAGCGGAGCGAGCGCCGTTGGGCGAGGGGCTCTGGGCGCCAGCCGGGCG 835
Qy 261 ArgThrArgGlyPProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
Db 836 AGAGACCGGTGACCGAGTACCGGTGTTCTGTGTGTCTGAGTGTCTGACCTGACAGACCCCGCGCA 895
Qy 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 896 GAAGCAACCTCTTTGGAGGGGTGGCTCTGTGGAGCGGCGACCTCCACCCATCCGTGGGCG 955
Qy 301 ArgGlnHisHisAlaGlyPProProSerThrSerArgPProArgPProThrAspThrPro 320
Db 956 CGCCACACACACCGGGGGCCCCCATCCACATCCGGCGCACAGTCCCTGGAGACAGCGCT 1015
Qy 321 CysPProValThrValGluThrLysHisAspLeuTyrSerSerGlyAspLysGln 340
Db 1016 TGTCCCTCCGTGACCGCGAGACCAAGCACTTCTCTACTCTCAGGCGCAAGAGACAG 1075
Qy 341 LeuArgPProSerPheLeuLeuSerSerLeuArgPProSerLeuThrGlyAlaArgArgLeu 360
Db 1076 CTGGGGCCCTCTTCTCACTCACTCTGAGGCGCCAGGCTGACTGGCGCTCGAGAGGCTC 1135
Qy 361 ValGluThrLysPheLeuGlySerArgPProTyrMetPProGlyThrProArgArgLeuPro 380
Db 1136 GTGAGAGCAATCTTTCTGGGTTCAGAGCCCTGGATGCCAGAGACTCCCGCGAGTTGGCC 1195
Qy 381 ArgLeuPProGlnArgTyrTyrPProGlnMetArgPProLeuPheLeuGlnLeuLeuGlnHis 400
Db 1196 CGCTGCCCCAGAGGCTACTGGAATGGGCCCCCTGTTCTGGAGCTGTGGGAACCAAC 1255
Qy 401 AlaGlnCysPProTyrGlyValLeuLeuLysThrHisCysPProLeuArgAlaAlaValThr 420
Db 1256 GCGGAGTGCCTTAACGGGGTGTCTCTCAAGACGACACTGCCGCTGGAGCTGGGCTACCC 1315
Qy 421 ProAlaAlaGlyValCysAlaArgGluLysPProGlnGlySerValAlaAlaPProGlnGlu 440
Db 1316 CCGAGACCGGTGTCTGTGCCCCGAGAGACCCCCAGGCTCTGTGGGAGCCCCCGAGAG 1375
Qy 441 GluAspThrAspPProArgArgLeuValGlnLeuLeuArgGlnHisSerSerPProTyrGln 460
Db 1376 GAGGACACAGACCCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1435
Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValPProPProGlyLeuTyrGlySer 480
Db 1436 GTGTACGGCTTCGTGCGGGCTGTGCTGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGT 1495
Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheLysSerLeuGlyLysHis 500
Db 1496 AGGGACAAACGAGCCCGCTTCTCAGAAACACCAAGATTCATCTCTCCCTGGGGAAGCAT 1555
Qy 501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysSerSerValArgAspCysAlaTyrLeu 520
Db 1556 GCCAAGCTCTGTCGACGAGACTGACGTGGAATGACGTCGCGGACTCGCTTGCGCTG 1615
Qy 521 ArgArgSerPProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlu 540
Db 1616 CGCAGAGGCCCGAGGGGT 1675
Qy 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1676 CTGGCCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1735
Qy 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerVal 580
Db 1736 TTTTATGTACGAGAGACCAAGCTTCAAAAAGAACAGGCTCTTTTCTACCGGAAAGAGTGC 1795
Qy 581 TrpSerLysLeuGlnSerLysGlyLysLeuArgGlnHisSerLeuLysArgValGlnLeuArgGlu 600
Db 1796 TGGAGCAAGTTCGAAAGATTGGAATCAGACGACTTGGAAGGGGTGCACCTCGGGAG 1855

Qy 601 LeuSerGlnAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1856 CTGTCCAGACAGAGGCTCAGGACAGATCGGGAAAGCCAGGCCCGCCCTGCTGAGCTCAGA 1915
Qy 621 LeuArgPheLysPProLysPProAspGlyLeuArgPProLysValAsnMetAspTyrValVal 640
Db 1916 CTCCGCTTCACTCCCAAGCTGACGGGCTCGGGCGGATTTGTGAACATGACATGCTGCTGT 1975
Qy 641 G1yAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1976 GAGCCCAAGAGCTTCCGAGAGAAAGAGGCGGAGCTCTACCTCGAAGGTGAGAGCA 2035
Qy 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgPProGlyLeuLeuGlyAlaSerVal 680
Db 2036 CTGTTACGCTGCTCAACTACAGAGCGGGCGGGCGCCCGGCTCTGGGCGCTCTGTG 2095
Qy 681 LeuGlyLeuAspAspLysHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
Db 2096 CTGGGCTGAGACGATTCACAGGGGCTGGGCGACCTTCTGTGTGTGTGTGTGTGTGTGTGT 2155
Qy 701 AspPProPProGluLeuThrPheValLysValAspValThrGlyAlaTyrAspThrLys 720
Db 2156 GACCCGCGCTGAGCTGTACTTGTCAAGGTGATGAGGGCGGCTACGACCATC 2215
Qy 721 ProGlnAspArgLeuThrGluValLysAsnSerLysLeuLysPProGlnAsnThrTyrCys 740
Db 2216 CCGGACGACAGGCTCAGGAGGTATCGCCAGCATCAACACCCGAAACACCTACTGTC 2275
Qy 741 ValArgArgTyrAlaValAlaGlnLysAlaHisGlyHisValArgLysAlaPheLys 760
Db 2276 GTGCGTCCGTATGCGGTGTCCAGAGGCGCCCATGGGACAGTCGCGAGAGGCTTCAAG 2335
Qy 761 SerHisValSerThrLeuThrAspLeuGlnPProTyrMetArgGlnPheValAlaHisLeu 780
Db 2336 AGCCAGCTCTCACTTACAGACCTCCAGCGTACAGGCAAGTTGTGTGTGTGTGTGTGTGT 2395
Qy 781 GlnGluThrSerPProLeuArgAspAlaValAlaLysGlnGlnSerSerSerLeuAsnGlu 800
Db 2396 CAGGAGACAGCCCGCTAGGAGATGCCCTGCTCATCGAGAGAGCTCTCTCTGAATAG 2455
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLys 820
Db 2456 GCGAGAGTGGCTCTTGGAGCTTCTTCAAGCTTCACTGTGACACGCGCTGTGAGTTC 2515
Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyLysPProGlnGlySerLysLeuSerThrLeu 840
Db 2516 AGGGGCAAGTCTTACGTCAAGTCCAGGGGATCCCGAGGGCTCATCTCTCCACGCTG 2575
Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyLysArgArgAsp 860
Db 2576 CTCTGAGCTGTGTGTACCGGACATGAGAAACAAGCTGTGTGGGAGATTCGGGAGAC 2635
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GGGCTGTCTCGGCTGT 2695
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValPProGlyTyrGlyCysValValAsnLeu 900
Db 2696 AAAACCTTCTCAGAGCCTTGTGCGAGGTGTCCCTGAGTATGCTGTGTGTGTGTGTGT 2755
Qy 901 ArgLysThrValAlaAsnPhePProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2756 CGGAAACAGTGTGAATCTCTCTGTGAAGACAGAGGCTTGTGGTGGACAGGCTTTTGT 2815
Qy 921 GlnMetProAlaHisGlyLeuPhePProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2816 CAGATCCCGGCCACGCGCTATTCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2875
Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerLysArgAlaSerLeuThrPhe 960
Db 2876 GAGTGCAGAGGACTACTACAGTATGCTGCGGAGCTTCATCAGAGCCAGTCTCACCTTTC 2935

QY 961 AsnArgIlyPheIyAlaIyArgAsnMeCArgAllyLeuPheGlyValLeuArgLeu 980
Db 2936 AACCGCGGCTTCAAGGCTGGAGGAACATGCTCCAAACTTTGGGGTCTTGGGGCTG 2995
QY 961 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2996 AAGTGTCAAGCTCTTTCTGATTTGGCAGGTGAACAGCTCCAGACGGGTGTCACCAAC 3055
QY 1001 IleTyrIlyIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTCAAGATCTCTGCTGAGCGGTACAGGTTCACGCAATGTGTGCTGCAAGCTCCCA 3115
QY 1021 PheHisGlnGlnValTyrIlyAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTGATCAGCAAGTTTGGAGAACCACATTTTCTCGGGTCTATCTCTACACGGGC 3175
QY 1041 SerLeuCysTyrSerIleLeuIlyAlaIyAsnAlaIyMetSerLeuGlnValIyGly 1060
Db 3176 TCCCTCTGCTACTCATCTGAAAGCCAAAGACGAGGATGTGCTGGGGGCCCAAGGCGC 3235
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrLeuCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCGGCGGCGCTCTGCTCCCTCCAGGCGGTGAGCTGTGTGCTGACCACCAATTCCTGCTC 3295
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACCGTGTCTACCTACGCGCACTCTGGGGTCACTACGACGCCACG 3355
QY 1101 ThrGlnLeuSerArgIlyLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTCGGAAGCTCCGGGAGACGACGTGACTGCTGGAAGGCCGACAGCAAC 3415
QY 1121 ProAlaLeuProSerAspPheIySerThrIleLeuAsp 1132
Db 3416 CCGGCACTGCTCTCAGACTTCAAGACCACTCTGGAC 3451

RESULT 12

US-10-044-692-1

Sequence 1, Application US/10044692

Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse transcriptase (hTERT) catalytic protein component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-044-692-2 (1-1132) x US-10-044-692-1 (1-4015)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
Db 56 ATGCCGGCGGCTCCCGCTGCGAGCCGAGCGGCTCTCGTCTGCGACCACTACCGCGAG 115
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 116 GTGCTGCGCTGGCCACGTTCTGTGGGCGGCTGGGGGCCCAAGGCTGCGCTGTGCAG 175
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 176 CCGGGAGACCGGCGGCTTTTCCGCGCGCTGTGGCCGCTGCTGTGCTGTGCTGCTG 235
QY 61 AspAlaArgProProProAlaAlaPheSerPheArgGlnValSerCysLeuIyGlnLeu 80
Db 226 GACGCAAGCGGCGGCGGCGGCGGCTCTCCGCGCAGGTGTCTGCTGAAGAGCTG 295
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaIyAsnValLeuAlaPheGly 100
Db 236 GTGGCGCCAGTGTCTCAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGTGCTGTGCGC 355
QY 101 PheAlaLeuLeuAspGlyAlaAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
Db 356 TTGGCGCTGTGAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 415
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATrpgIyLeuLeu 140
Db 416 AGCTACCTGCGCCCAACAGGTGACGACCGACCTGCGGGGAGGCGGCGGCGGCGGCGGCTG 475
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 476 CTGGCGCGCGTGGCGAGACGACTGTGTTCACCTGTCTGCGACGCTGCGCGCTCTTTGTG 535

161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
536 CTGGTGGCTCCAGCTGCGCTACCAAGGAGTGGCGGCGCGCTGTACAGCTCGGCGCT 595
181 AlaThrGlnAlaArgProProProHisAlaSerGlyProProArgArgArgLeuGlyCysGln 200
596 GCCACTCAGGCG 655
201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
656 CCGGCTTGAACCATGAGCTCAGGAGGCGCGGCGCTCCCTGCGCTGCGCGCGCGCGCT 715
221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
716 GCGAGAGGCGCGCGGCGCGAGTGCACCGCAAGCTGCGCTGCGCGCGCGCGCGCGCGCT 775
241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerThrAlaHisProGly 260
776 GCGGCTGCGCTTACCGCGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 835
261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGln 280
836 AGGACCGGTGACCGAGTGAACGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
896 GAGGCCACCTCTTGGAGGGGTGCTCTGCGCAGCGCGCACCTCCACCCATTCGTGGCT 955
301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProThrArgProThrPro 320
956 CCGCAGACACCGCT 1015
321 CysProProValTyrAlaGlnThrLysPheLeuTyrSerSerGlyLysGlnGln 340
1016 TGTCTCCCGGTGTACCGCGAGACCAAGCACTTCTCTCACTCTCAAGCGCAAGAGGAG 1075
341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgGlnLeu 360
1076 CTGGGCGCT 1135
361 ValGlnThrLysPheLeuGlySerArgProThrMetProGlyThrProArgArgLeuPro 380
1136 GTGGAGACCATCTTCTGGGCTTCAAGCGCTGATGCGCAGGAGCTCCCGCGAGCTGGCC 1195
381 ArgLeuProGlnArgTyrThrGlnMetArgProLeuPheLeuGlnLeuLeuGlnLysAsnHis 400
1196 CGCTGCGCGAGCGCTACTGCAATGCGCGCGCTGTCTGTGTGTGTGTGTGTGTGTGTGT 1255
401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
1256 GCGGAGTGGCGCTTACGGGGTCTCTCAAGCGCATGCGCGCTGCGAGCTGCGGTACG 1315
421 ProAlaAlaGlyValCysAlaArgGlnLysProGlnLysSerValAlaAlaProGlnGln 440
1316 CCACAGCGCGGT 1375
441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProThrGln 460
1376 GAGGACAGACCGCGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1435
461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrGlySer 480
1436 GTGTACGGCTTGT 1495
481 ArgHisAlaGlnLysArgPheLeuArgAsnThrLysLysPheLysSerLeuGlyLysHis 500
1496 AGGCAACAAGACCGCGCTTCTCAAGAAACCAAGAACTTCACTCCCTGGGGAGAGAT 1555
501 AlaLysLeuSerLeuGlnLysLeuThrTyrLysMetSerValArgAspCysAlaThrLeu 520
1556 GCCAAGCTCTGCTGT 1615
521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnLeu 540

1616 CGCAGAGCCAGGGGTGGCTGTCTTCCGCGCGAGAGACCGCTGTGCTGAGAGATC 1675
541 LeuAlaLysPheLeuHisThrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
1676 CTGGCAAGGTCTCTGCACTGGCTGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1735
561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPheThrArgLysSerVal 580
1736 TTTATGTGCGAGACAGCGTTTCATTAAGAAACAGGCTCTTTTCTTACCGGAAGAGTGTCT 1795
581 TrpSerLysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGln 600
1796 TGAAGCAAGTTGCAAGAGATTGAAATCAGACAGCACTTGAAGAGGGTGCAGCTCGCGGAG 1855
601 LeuSerGlnAlaGlnValAlaArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
1856 CTGTGGAAGCAGAGGTGACGAGCAGATCGGAGACCGCGCGCGCGCGCGCGCGCGCGCT 1915
621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
1916 CTCCGCTTCACTCCCAAGCTGAGCGGCTGCGCGCATTTGTGAACATGACTAGCTGCTGT 1975
641 GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValAlaAla 660
1976 GAGGCCAAGAGTTCCGCGAGAAAGAGGCGCGAGGCTCTCACTCGAGGGGTGAAGCA 2035
661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
2036 CTGTTCACCGGTCTCACTACAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTG 2095
681 LeuGlyLeuAspAspIleHisArgAlaThrArgThrPheValLeuArgValAlaGln 700
2096 CTGGGCTCGAGAGATATCACAGGGCGTGGCGCACTTGTGTGTGTGTGTGTGTGTGTGTGT 2155
701 AspProProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
2156 GACCGCGCGCTGAGCTGTCTGT 2215
721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
2216 CCCAGAGACAGCTACCGAGAGTATCCCGAGCATCATCAACCCCGAGAACAGCATCTGC 2275
741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgValAlaPheLys 760
2276 GTGCGTGGGTATCGGT 2335
761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisSerLeu 780
2336 AGCCAGCTCTTACCTTGAACAACCTCAAGCCGTATCGACAGTGTGTGTGTGTGTGTGTGT 2395
781 GlnGlnThrSerProLeuArgAspAlaValAlaIleGlnGlnSerSerSerLeuAsnGln 800
2396 CAGAGACACAGCCCGT 2455
801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValAlaArgIle 820
2456 GCCAGAGTGGCGCTTTCGACGCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2515
821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
2516 AGGGGCAAGTCTTACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2575
841 LeuCysSerLeuCysTyrGlyAspMetGlnAsnLysLeuPheAlaGlyIleArgArgAsp 860
2576 CTGTGACGCTGT 2635
861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
2636 GGGCTGTCTCTGT 2695
881 LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrGlyCysValValAsnLeu 900

Db 2696 AAAACCTTCTCAGAGACCCCTGGTCCGAGGTGTCTCCGTAGTATGCTCGCTGTGACTTG 2755
Qy ArglyThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2756 CGGAGACAGTGTGTAACTTCCCTGTAGAGAGAGCCCTGSGTGGCAGCGGCTTTGTT 2815
Qy GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2816 CAGATGCCGCGCCACGGCCTATTCCTCGTGTGCGGCTGTGCTGTGATACCGGAGCCCTG 2875
Qy GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGACAGAGGACTTCTCCAGCTATGCCCCGACCTCCATCAGACCGCAGTCTCACCTTC 2935
Qy AsnArgGlyPheValAlaGlyValArgAsnMetArgGlyValLeuPheGlyValLeuArgLeu 980
Db 2936 AACCGGGCTTCAGAGCTGGAGAGACATGCGTCCGAACTCTTTGGGGCTCTGGGGCTG 2995
Qy LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2996 AAGTGTACAGCTGTCTTCTGGATTGTGACGTTGACAGCTCCAGACGGTGTGACCAAC 3055
Qy 11eTyrValLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTACAAGATCTCTCTGCTGACGCGTACAGGTTTCAAGCTGTGTGCTGACGCTCCCA 3115
Qy PheHisGlnGlnValTTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCATCAGCAAGTTTGGAGAACCCCAATTTCCTGCGGTATCTCTGACACGGGC 3175
Qy SerLeuCysTyrSerIleLeuValAlaLysAsnAlaGlyMetSerLeuGlyValAlaGly 1060
Db 3176 TCCCTCTCTACTCATCTCTGAAAGCAAGAACGAGGATCTCCCTGGGGGCCCAAGGC 3235
Qy 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTTrpLeuCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCGCGCGGCGCTCTCCCTCCAGGCGCGTACAGTGTGTGCTGCCACCAAGCATTTCTGCTC 3295
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACGCTGTCCCTACGCGCCACTCTGGGGTCACTCAGGACACCGCG 3355
Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGAGCCCTGAGAGCGCAGCCAC 3415
Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGCACTGCCTCAGACTTCAAGACCATCTGAGC 3451

RESULT 13
US-10-044-539-1
Sequence 1, Application US/10044539
Publication No. US2003010093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTrr"
/note= "human telomerase reverse
transcriptase (hTrr) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1
Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-044-692-2 (1-1132) x US-10-044-539-1 (1-4015)
Qy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
Db 56 ATGCCGCGGCTCCCGCTGCGAGCCGTCGCTCTCTGCGGACGACCACTACCGCGAG 115
Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTrpArgLeuValGln 40
Db 116 GTGCTGCGGCTGCGCAGCTGTGTGGCGGCTGCGGCGCCGAGGCTGGCGGCTGTGAG 175
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysValAlaCysValProTTrp 60
Db 176 CGCGGGGACCGCGCGCTTTCGCGCGCTGTGTGGCCAGTGTGTGTGTGTGTGTGTGTG 235
Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
Db 236 GAGCGAGCGCGCGCGCGCGCGCGCGCTTCTTCCGCGAGGTCTCTGCTGAAGAGCTG 295
Qy 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyAlaLysAsnValLeuAlaPheGly 100

Db 296 GTGGCCGAGTGTCTGAGAGAGCTGTGCGAGCGCGCGAGAGACGTGTGCTTCGCG 355
QY PheAlaLeuLeuAspGlyAlaArgGlyProProGluAlaPheThrThrSerValArg 120
Db 101 PheAlaLeuLeuAspGlyAlaArgGlyProProGluAlaPheThrThrSerValArg 120
Db 356 TTGCGGCTGTCTGAGAGAGCGCGCGGAGCGCGCGCGAGGCTTCCACACGCGTGGCC 415
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaIleProGlyLeuLeu 140
Db 416 ACTACCTGCTCCCAACACGCGTGAACGACGACCTGCGGGGAGCGGGGCGTGGGGGCTGTG 475
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 476 CTGCGCGCGGTGGGAGCACACGTGTGTTCACCTGCTGACACGCTGCGCTCTTTGGG 535
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 536 CTGCTGTGCTCCCAAGCTGCTGCTACAGGTGTGCGGGCGCGCGCTGTACACGCTGGCGCT 595
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 596 GCGACTCAGCGCGCGCGCGCGCGCACGCTAGTGAACCCCGAAGGCGTCTGGGATTCGAA 655
QY 201 ArgAlaIleProAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 656 CCGGCTGTGAGACCATAGCTGTACAGGAGCGCGGGGTCTCCCTGGGCTGTGACCGCGGT 715
QY 221 AlaArgArgArgGlyValSerAlaSerArgSerSerLeuProLeuProAlaArgProArgArg 240
Db 716 GCGAGAGAGCGCGGGGCGAGTGTCCAGCCAGACCTGCTGCTCCCAAGAGCGCGCGCT 775
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
Db 776 GCGGCTGCTGTGAGCGGAGCGAGCGCGCGTGTGGCGAGGGGCTGTGGCGCACCGCGGCG 835
QY 261 ArgThrArgGlyProSerArgArgGlyPheCysValValSerProAlaProAlaGlu 280
Db 836 AGGACCGGTGTGACCGGT 895
QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 896 GAAAGCACTCTTTGAGAGGT 955
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
Db 956 CCGCAGACACACGCGCGCGCGCGCGCATCATCGCGCGCACAGTCCCTGTGGAGCAGCGCT 1015
QY 321 CysProProValTyrAlaGluThrHisPheLeuTyrSerSerGlyValAspGlyGln 340
Db 1016 TGTCCCGCGGTGTACCGCGAGACCACTTCTCTACTCTCTCAGCGAGCAAGAGGCGAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1076 CTGCGGCGCTCTCTTACTTACTGAGCTCTGTAGGCGCGAGCTGTGCGCTGTGAGAGCTC 1135
QY 361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
Db 1136 GTGAGACACATCTTCTGAGGTTCAGAGCCTGTGATCCAGAGGACTCCCGCAGGTGTGCC 1195
QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyValAsnHis 400
Db 1196 CCGCTTCCCGAGCGCTACTGTGCAATGCGCGCTCTTTCTGTGAGGTGTGTGGAAACAC 1255
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db 1256 GCGCAGTGTCCCTTACGCGGTGTCTCTACAGACGACCTGCGCGGTGTGAGCTGTGAGTACC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
Db 1316 CCGAGCAGCGGT 1375
QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1376 GAGGACACAGACCCCGT 1435

QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db 1436 GTGTACGCGCTGTGTGCGGCGCTGTGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1495
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
Db 1496 AGGCACAAACGAGCGCGCTCTCTCAGGAACACCAAGAAATTCATCTCTCTGGGGAAGCAT 1555
QY 501 AlaLysLeuSerLeuGlnGlyLeuThrTrpLysMetSerValArgAspCysAlaIleProLeu 520
Db 1556 GCGAAGCTCTGTGTCTCAGAGCTGTACGTGTGAGAGAGTACGTGTGCGGACTGTGCGCTGTG 1615
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluIle 540
Db 1616 CCGACAGACCCAGGGGT 1675
QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1676 CTGCGCAAGTTCCTTGTACGT 1735
QY 561 PheTyrValIleThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1736 TTTTATGTACGAGAGACACGTTTCAAAAGAACAGGCTCTTTTCTTACCGAAGGTGTTC 1795
QY 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db 1796 TCGACCAAGTTGCAAAAGCATTTGATGATCAGACACTTGAAGAGGTGTGTGTGTGTGTGTGT 1855
QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlyAlaArgProAlaLeuLeuThrSerArg 620
Db 1856 CTGTGTGAGAGCAGAGT 1915
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db 1916 CTCCGCTTCACTCCCAAGCTGTACGCGGCTGTGCGCGCATTTGTGAACATGTACTGTGTG 1975
QY 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGlnArgLeuThrSerArgValLysAla 660
Db 1976 GGAGCAGAAAGCTTCCGCGAGAAAGAGGCGAGCGCTGTCTACCTCAGAGGTGTGAAGGCA 2035
QY 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 2036 CTGTTTCAAGGTGTCTAACAACAGCGCGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGT 2095
QY 681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
Db 2096 CTGGGCTGTGAGATATTCACAGGGCTGTGGCACCTTGTGTGTGTGTGTGTGTGTGTGTGT 2155
QY 701 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
Db 2156 GACCGCGCGCTGAGCTGTACTTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2215
QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db 2216 CCCACAGACAGCTACCGAGGTGTATCGCACATCATCTAAACCCCAAGAACAGTATGTC 2275
QY 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2276 GTGCTGT 2335
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
Db 2336 AGCCAGCTTCTTACCTTGTACAGACCTCCAGCGGTACATGTGACAGATGTGTGTGTGTGTGT 2395
QY 781 GlnGluThrSerProLeuArgAspAlaValValIleGlnGlnSerSerSerLeuLeuGln 800
Db 2396 CAGGAGACCAAGCGCGT 2455
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2456 GCGACAGTGTGCTTGT 2515

```

821 ArgGlySerThrValGlnCysGlnGlyLeuProGlnGlySerIleuSerThrIleu 840
2516 AGGGGCAAGTCTTACTGACAGTCCAGGGGATCCCGAGGGCTCATCTCCAGCGCTG
841 LeuCysSerThrCysTyrGlyAspMetGluAsnGlyLeuPheAlaGlyIleArgArgAsp 860
2576 CTCTGCACCTCTGTCTACGCGCAGTGGAGAACAGCTGTTGGCGGGGATTCGGGGGCG
861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHileuThrHila 880
2636 GGGCTGCTCTGCGTGTGGATGATTTCTGTGGTACACCTTCACCTCCACCGCGG
881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
2696 AAAACCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGGTGTGAAGTGG
901 ArgGlyThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
2756 CGGAAGACAGTGGTAACTTCCCTGAGAACAGAGGCGCTGGGTGGCAGCGCTTTTGT
921 GlnMetProAlaHileGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrIleu 940
2816 CAGATGCCGGCCCGACGGCTATTTCCCTGTGTGGCGCTGCTCTGAGTATCCCGAGCGCTG
941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
2876 GAGGTGCGAGAGGAGTACTCCAGCTATGCCGAGCTCCATCAGAGCCAGTCTCACTTC
961 AsnArgGlyPheLeuAlaGlyArgAsnMetArgArgGlyLeuPheGlyValLeuArgLeu 980
2936 AACCCGGGCTTCAGAGCTGGAGAACATGCGTCCGAACTCTTGGGGTCTTGGCGGCTG
981 LysCysHileSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
2996 AAGTGTCAAGCTGTGTTCTGAGTGTGACGGTGAACAGCTCCAGAGCGGTGTGACCAAC
1001 IleTyrIleLeuLeuLeuGlnAlaTyrArgPheHilaCysValLeuGlnIleuPro 1020
3056 ATCTCAAGATCTCTCTGTGTGACGGGTACAGGTTTCAAGCATGTGTGTGACAGCTCCA
1021 PheHileGlnIleValTrrPylAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
3116 TTTCATCAGCAAGTTTGGAAAGCAACCCCATTTTCTCGCGTCATCTCTACACAGCGCC
1041 SerLeuCysTyrSerIleLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 1060
3176 TCCCTCTGTACTCTCATCTCTGAAGCAAGCAAGCAAGGATGTGCTGGGGGCGCAAGGCGC
1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTrrPleuCysHileGlnAlaPheLeuLeu 1080
3236 GCGGCGGCGCTCTGCGCTCCAGGGCGGTGCGAGTGTGCTGCCACCAAGCATTTCTGCTC
1081 LysLeuThrArgHileArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
3296 AAGTGACTCGACACGCTGTACCTACGTACGTCATCTCTGGGCTCACTCAGGACAGCGCCG
1101 ThrGlnLeuSerArgIleuProGlyTrrThrLeuThrAlaLeuGlnAlaAlaAlaAla 1120
3356 ACGCAGCTGAGTGGAGAGTCCCGGGGAGAGAGCTGAGTACCTGGAGGCGCAGCGCAAC
1121 ProAlaLeuProSerAspPheIleThrIleuAsp 1132
3416 CCGGCACTGCGCTTCAGACTTCAAGACATCTCGAC 3451

```

RESULT 14
US-10-325-810-1

/ Sequence 1, Application US/10325810
/ Publication No. US20030204069A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.

```

Mortin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product="hTTR"
/note="human telomerase reverse
transcriptase (hTTR) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-325-810-1

```

Alignment Scores:

```

Prid. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

```



```

QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLeuProGlnAsnThrTyrCys 740
Db 2216 CCCAGAGACAGGCTCAGGAGGTCATCGCAGCATCATTAACCCAGAACACGTAATCTCC 2275
QY 741 ValArgArgTyrAlaValAlaGlnIleValAlaIleGlyHisValArgIleValPheIleYs 760
Db 2276 GTGCTCTGGTATGCGGTGTCAGAAAGGCGCCCATGGGCACTGCGCAAGGCTTCAAG 2335
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
Db 2336 AGCCACGCTCTACCTTGACACACCTCCAGCGTACATGACGACAGTTCGTGGCTCACTCG 2395
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGln 800
Db 2396 CAGAGACACAGCCCGCTGAGGAGATCCGCTCATTCAGACAGCTCTCTCTGAAATGAG 2455
QY 801 AlaSerSergIleuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2456 GCCACAGAGTGGCTCTTGCACGCTTCTTCACTGATGTCACACCGCGTGGCATC 2515
QY 821 ArgGlyIleSerSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrIleu 840
Db 2516 AGGGGCAAGTCTTACGTCAGAGCCAGGGGATCCGCAAGGCTCCATCTCTCCACGCTG 2575
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnIleuPheAlaGlyIleArgArgAsp 860
Db 2576 CTCGCAAGCTGTGTCATGCGGACATGAGAACAAAGCTTTGGCGGATTTGGCGGGAGC 2635
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GGGCTGCTCTCGTGGTGGATGATTTCTTGGTGGTACACCTCACTCCACCCACGCG 2695
QY 881 LysThrPheLeuArgThrIleuValArgGlyValProGluTyrGlyCysValValAsnIleu 900
Db 2696 AAAACCTTCTCAGAGACCTGGTCCGAGGTGTCCTGATAGCTGCTGCTGTGAACCTTG 2755
QY 901 ArgIleThrValIleAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2756 CGGAAGACAGTGTGTAATCTTCCCTGTAAGACAGAGCCCTGGTGGCAGCGCTTTGTT 2815
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrIleu 940
Db 2816 CAGATGCGGCGCCACGAGCTATTTCCCTGTGCGGCTGCTGCTGATGATCCGAGACCTG 2875
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGACAGAGACTACTCCAGCTATGCCGAGACCTCCATCAGAGCCAGTCTCACTTC 2935
QY 961 AsnArgGlyPheIleValAlaGlyAsnMetArgArgIleuPheGlyValLeuArgIleu 980
Db 2936 AACCGCGGCTTCAAGGCTGGAGAACATGCTCGCAACTTTGGGGGTCTTGGCGGCTG 2995
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2996 AAGTGTCAAGCTGTTCTGATTTGACGTGAACAGCTCCAGCGGTGGTGGCAAC 3055
QY 1001 IleTyrIleIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTCAAGATCTCTCTGTGACAGGCTACAGGTTTCAAGCATGTGTGTGAGCTCCCA 3115
QY 1021 PheHisGlnGlnValITrpIleAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCTATCAGCAAGTTTGGAGAACCCCACTTTTCTGCGGCTCATCTCTCAACGGGCT 3175
QY 1041 SerLeuCysTyrSerIleLeuIleValAlaIleAsnAlaGlyMetSerLeuGlyValAlaIle 1060
Db 3176 TCCCTCTGCTACTCATCTGAAAGCAAGACGAGGATGCTCTGGGGGCGCAAGGCTG 3235
QY 1061 AlaAlaGlyProLeuProSergIleuAlaValGlnITrpLeuCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCGCGCGGCGCTCTGCTCCAGGCGGTGAGGCTGTGTGTCACCAAGCATTTCTGCTC 3295

```

```

QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCCAGACCGGTGTACACCTGACCACTCGGGGTCACTCAGAGACACCCAG 3355
QY 1101 ThrGlnLeuSerArgIleuPheProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTCGGAAGCTCCCGGGAGCAGACGTGACTGCTGCTGGAGCGCAGCAAC 3415
QY 1121 ProAlaLeuProSerAspPheIleThrIleLeuAsp 1132
Db 3416 CCGGCACTGCCCTCAGACTTCAAGCACTCTGAGC 3451

RESULT 15
US-10-388-578-1
; Sequence 1, Application US/10388578
; Publication No. US20030224411A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; APPLICANT: Shelton, Dawne
; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Hum
; FILE REFERENCE: 135/001
; CURRENT APPLICATION NUMBER: US/10/388, 578
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Custom
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-388-578-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-044-692-2 (1-1132) x US-10-388-578-1 (1-4015)
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
Db 56 ATGCCGCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCGCAGCACTACCGCGAG 115
QY 21 ValLeuProIleuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 116 GTGCTGCCGTGGCCACGCTGTGTGGGGGCTGGGGGCCCAAGGGCTGGCGGTGGAG 175
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProITrp 60
Db 176 CCGCGGGACCGGCGGCTTTCCGCGCGCTGTGGCCGAGTGTGCTGTGCTGCTGCTGG 235
QY 61 AspAlaArgProProProProAlaAlaProSerPheArgGlnValSerCysLeuIleuGluLeu 80
Db 236 GACGACCGCGCGCCCGCGCGCCCTCTTCCGCGAGGTGTCTGCTGAAAGAGCTG 295
QY 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyAlaIleAsnValLeuAlaPheIle 100
Db 296 GTGGCCGAGGTGTGCAAGGCTGTGCGAGCGCGCGGGAAGAGTGTGCTGCTTGGC 355
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyIleProProGluAlaPheThrThrSerValArg 120

```

DB 356 TTTCGGCTGTGTACAGCGGCCCCCGAGGCTTACCAACAGCTGGCC 415
QY 121 SerTyrLeuProAsnThrValThraSpAlaLeuArgIleSerGlyValATrpIleLeu 140
DB 416 AGCTACCTGCCAACAACGGTGAACGACGCTGCGGGGAGCGGGCGGTGGCTGCTG 475
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 476 CTGCGCGCGGTGGGCGACACGCTGCTTCACTGCTGGACGCTGCGCGCTTTTGG 535
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 536 CTGGTGGCTTCCAGCTGCGCTTACACAGTGTGCGGCGCGCTGTACCAAGCTCGCGCT 595
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 596 GCCACTCAAGCGCGCGCGCGCACAGCTAGTGAAGCCCGAAGCGCTGGGATGCGAA 655
QY 201 ArgAlaATrPAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 656 CGGCGCTGGAACCATAGCGCTCAGAGGCGCGGGTCCCTGGGCTTGCAGCCCGGCT 715
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 716 GCGAGAGAGCGCGGGGCGAGCTGCCACCGAAGCTGCGCTGCCAAGAGCGCGCGCT 775
QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
DB 776 GGGCGTGGCCCTGAGCGGAGCGAGCGCGCGTGGGCGAGGGGTCTGGGCGCACCGGCGC 835
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValIleSerProAlaArgProAlaGln 280
DB 836 AGAAGCGGTGACCGAGTGAACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
QY 281 GlnAlaATrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 896 GAGGCAACCTCTTGGAGGGTGGCTCTGAGCAGCGGCACCTCCACCATCCGCTGGGCG 955
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
DB 956 CGCGAGACACACCGGGGCGGCGGCTCCATCCATCGGGGCGACAGTCCCTGGGAGCGCT 1015
QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 1016 TGTCTCCCGGTGTACGCGGAGACCAAGCACTTCTCTCACTCTCAAGCGCAAGAGCGAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaATrGArgLeu 360
DB 1076 CTGGCGGCTCTCTCTCACTCAAGCTCTGAGGCGCAGCTGACTGGCGCTCGAGGCTC 1135
QY 361 ValGlnThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
DB 1136 GTGAGAGCAATCTTCTGGTTCAGAGCCCTGAGTGCAGAGGAGACTCCCGCAGAGTTGCC 1195
QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1196 CGCTGCGCCCAAGCGCTACCTGCAATGCGGCGCTGTCTTCTGAGAGCTTGGGAAACAC 1255
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuAlaAlaValThr 420
DB 1256 GCGCAGTGCCTCTAGGGGTGCTCTCAAGACGACAGTCCCGCTGCGAGCTGGCTACC 1315
QY 421 ProAlaIleGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
DB 1316 CCAGAGCGGCTGTGTGTGCGCGAGAGAGCCCAAGGCTTGTGGGCGCGCCGAGAGAG 1375
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
DB 1376 GAGGACACAGACCCCGCTGCTGGTGTGAGCTGCTCCGCGACAGACAGAGCCCTGGCAG 1435
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
DB 1436 GTGTACGCTTTCGTCGGGCGCTGCTGCGCGGCTGTGTGCGCGCGCGCGCGCTTCC 1495
QY 481 ArgHisGlnGlnArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
DB 1496 AGGCAACAACAGACCGCTTCTCAGGAAACCAAGAAATTCACTTCTCCCTGGGAAACAT 1555
QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaATrPLeu 520
DB 1556 GCCAAGCTCTCGCTGAGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTGGCTG 1615
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluIle 540
DB 1616 CGCAGAGCCCGAGGGGTGTGGCTGTGTTCGCGCGCAGAGACCGCTGCTGCGTGAAGAAATC 1675
QY 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValGlnLeuLeuArgSerPhe 560
DB 1676 CTGGCCAGTTCTGTGCACTGGCTGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1735
QY 561 PheTyrValThrGlnThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1736 TTTTATGTCAAGAGACCAAGCTTCAAAAGAACAGGCTTTTCTACCGGAAAGTGTCT 1795
QY 581 TrpSerLysLeuGlnSerIleGlyTyrAlaArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB 1796 TGGAGCAAGTTGCAAGAGCATTTGAAATGACAGCACTTGAAGAGGTGTGACCTCGGAG 1855
QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
DB 1856 CTGTGGAAGACAGAGTCAAGCATCGGAGCGAGCGCGCGCTGCTGACCTCCAGAG 1915
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValIleAsnMetAspTyrValVal 640
DB 1916 CTCCGCTTCACTCCCAACCTGACCGGCTGCGCGGATTTGGAACTGTGACTGACTGTG 1975
QY 641 GlyAlaATrPThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
DB 1976 GAGGCAAGACCTTCCAGAGAAAGAGGCGCAGGCTCTCACTGAGGGTGAAGCA 2035
QY 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
DB 2036 CTGTTCAAGGTGCTCACTCAAGAGCGGCGCGCGCGCTCTGCGGCGCTCTGTG 2095
QY 681 LeuGlyLeuAspAspIleHisAlaArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
DB 2096 CTGGGCTGAGAGATTCACAGGCGCTGGCGACCTTGTGTGTGTGTGTGTGTGTGTGT 2155
QY 701 AspProProGlnGlyLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
DB 2156 GACCGCGCGCTGAGCTGTACTTGTCAAGTGTGATGTGAGCGGCGGTACGACACCATC 2215
QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
DB 2216 CCCAGAGACGCTCAAGAGGTGATCGCGCAGCATCATCAACCCCAAGAACCGATCTGC 2275
QY 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
DB 2276 GTGCGTGGTATGCGGTGTTCAGAGGCGCGCATTTGGGACGTCCGCAAGGCTTTCAG 2335
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
DB 2336 AGCCAGCTCTCAACCTTGACAGACCTCCAGCGCTACATCGACAGATTGCTGACTCACTG 2395
QY 781 GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
DB 2396 CAGAGACACAGCCCGCTGAGGAGTGTGCTGTCACTGACAGACAGTCTCTCTGATATGG 2455
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
DB 2456 GCCAGAGTGGCTCTTCAAGCTTCTTCAAGCTTCAATGTGCAACACCGCTGGCGAATC 2515
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
DB 2516 AGGGGCAAGTCTCACTCAAGTGCAGGGAGATCCCGCAGAGGCTCCATCTCTTCCAGCTG 2575


```
Oy 841 LeuCySerLeuCySTYRGIYAAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2576 CTCTGCACCCCTGTGTCTACGGGACATGAGAAACAAGCTGTTGGCGGATTCGGCGGAGC 2635
Oy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GGGCTGCTCTGTGGTGTGGATGATTTCTGTGTGTGACACTCACCCTCACCCACGGG 2695
Oy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTYRGIYCyValValAsnLeu 900
Db 2696 AAAACCTTCTCAGAGACCTGTGTCCAGAGTGTCCCTGAGTATGCTGCGTGTGAACCTTG 2755
Oy 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2756 CGGAGACAGTGTGTAACTTCCCTGTAGAAAGAGGCCCTGTGGTGGACGGCTTTGT 2815
Oy 921 GlnMetProAlaHisGlyLeuPheProTYRGIYLeuLeuLeuAspThrArgThrLeu 940
Db 2816 CAGATGCCGGCCCAAGGCTATTCCTGTGTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2875
Oy 941 GluValGlnSerAspTYRGIYSerSerTYRAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGCAGAGGACTACTCCAGCTATGTCCGACCTCCATCAGACCAAGTCTCACTTC 2935
Oy 961 AsnArgGlyPheLeuAlaGlyValArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2936 AACCCGGCTTCAAGGCTGTGGAGAAACATGCGGAAACCTTTGGGGCTTGGCGGCTG 2995
Oy 981 LysCysHisSerLeuPheLeuAspLeuGluValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2996 AAGTGTCAAGCTGTGTTCTGTGATTGTGACAGTGAAACAGCTCCAGCGGTGTGACCAAC 3055
Oy 1001 IleTYRGIYLeuLeuLeuGlnAlaTYRArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTACAAGATCTCTCTGTGTGAGGCGTACAGATTTCACGCAATGTGTGTGTGTGTGTGTGT 3115
Oy 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCATCAGCAAGTTTGGAGAAACCCACATTTTCTGTGGCTCATCTGTGACAGGCC 3175
Oy 1041 SerLeuCySTYRGIYSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
Db 3176 TCCCTCTGTCTACTCATCTCTGAAAGCAAGCAAGAGGATTCGCTGGGGGCCCAAGGCC 3235
Oy 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCCGCCGGCCCTCTGTGCTCCAGGCGCGTGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3295
Oy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACCGTGTCACTACGCGCACTCTGGGGTCACTCAGGACAGCCCAAG 3355
Oy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTGGAGAGTCCCGGGGAGAGACGCTGACCTGCGGAGGCCGAGCCCAAC 3415
Oy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGCACTGCTCAGACTTCAAGACCATCTGGAC 3451
```

Search completed: October 29, 2004, 16:24:57
Job time : 1435 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 09:37:01 ; Search time 1193 Seconds
(without alignments)
4981.010 Million cell updates/sec

Title: US-10-044-692-2
Perfect score: 5961
Sequence: 1 MPRAPRCAVMSLRSHYRE.....TALSAANPALPSDEKTLTD 1132

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh
-O=/cgn2.1/USPTO_epool/US10044692/runat_28102004_103654_1349/app_query.fasta_1.1287
-DB=N Geneseq_23Sep04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMF=pmo -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044692_@CGN_1_1.683_@runat_28102004_103654_1349 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	3396	4	AAH48235
2	5961	100.0	3396	4	AAH49601
3	5961	100.0	3396	4	AAH44366
4	5961	100.0	3396	12	ADG70113
5	5961	100.0	3399	6	ABV78144
6	5961	100.0	3399	6	ABZ35720

7	5961	100.0	3399	6	ABX09963	Abx09963 Human tel
8	5961	100.0	3399	6	ABL91685	Ab191685 Human pol
9	5961	100.0	3399	12	ADG90598	Adg90598 Human TER
10	5961	100.0	3798	2	AAV27876	Aav27876 Human tel
11	5961	100.0	3955	2	AAV22379	Aav22379 Human tel
12	5961	100.0	4015	2	AAZ00724	Aaz00724 Human tel
13	5961	100.0	4015	2	AAZ20279	Aaz20279 Human tel
14	5961	100.0	4015	2	AAZ30154	Aaz30154 CDNA enco
15	5961	100.0	4015	4	AAH45901	Aah45901 Human hte
16	5961	100.0	4015	6	AAH46821	Aah46821 Human tel
17	5961	100.0	4015	6	ABH97534	Abh97534 Cancer ce
18	5961	100.0	4015	8	ACC57552	Acc57552 Human tel
19	5961	100.0	4015	8	ABZ22474	Abz22474 Human tel
20	5961	100.0	4015	8	ACC44482	Acc44482 Human tel
21	5961	100.0	4015	8	ABJ18391	Abj18391 Group III
22	5961	100.0	4015	10	ACC58039	Acc58039 Human tel
23	5961	100.0	4015	12	ADG85223	Adg85223 Human tel
24	5961	100.0	4015	12	ADH82171	Adh82171 Human cat
25	5961	100.0	4042	2	AAV72117	Aav72117 Human cat
26	5961	100.0	4070	6	ABL53711	Ab153711 Human tel
27	5956	99.9	4015	2	AAZ08150	Aaz08150 Human tel
28	5954	99.9	3396	2	AAH18266	Aah18266 Telomeras
29	5954	99.9	3964	2	AAH18254	Aah18254 Human tel
30	5954	99.9	4023	2	AAV60320	Aav60320 Human tel
31	5954	99.9	4027	2	AAH89424	Aah89424 Human EST
32	5954	99.9	4027	3	AAZ29388	Aaz29388 hEST2, a
33	5954	99.9	4027	10	ADH47060	Adh47060 Human TER
34	5954	99.9	4027	20	ADH40481	Adh40481 Human tel
35	5952	99.8	3457	8	ABZ76217	Abz76217 Human TER
36	5952	99.8	4037	2	AAV22428	Aav22428 Human tel
37	5952	99.8	3766	6	AAH46790	Aah46790 PGRN145 p
38	5925	99.4	8742	6	AAH46793	Aah46793 PWB5A p1
39	5903	98.7	3500	2	AAH18275	Aah18275 Telomeras
40	5882	98.7	3918	2	AAH18269	Aah18269 Telomeras
41	5882	98.7	3918	2	AAH18278	Aah18278 Telomeras
42	5874	98.5	3543	8	ABZ69628	Abz69628 Plasmid c
43	5871	94.5	3203	2	AAH18268	Aah18268 Altered C
44	5601	94.0	3323	2	AAH18277	Aah18277 Altered C
45	5593.5	93.8	3855	2	AAV22382	Aav22382 Human tel

ALIGNMENTS

RESULT 1	AAH48235
ID	AAH48235 standard; DNA; 3396 BP.
XX	
AC	AAH48235;
XX	
DT	21-SEP-2001 (first entry)
XX	
DE	Heart muscle cell differentiation related DNA SEQ ID NO: 32.
XX	
KW	Heart muscle cell; human; cell differentiation; heart disease; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200148151-A1.
XX	
PD	05-JUL-2001.
XX	
PF	27-DEC-2000; 2000MO-JP009323.
XX	
PR	28-DEC-1999; 99JP-00372826.
XX	
PR	28-FEB-2000; 2000MO-JP001148.
XX	
PR	02-NOV-2000; 2000MO-JP007741.
XX	
PA	(KYOM) KYOMA HAKKO KOGYO KK.
XX	
PI	Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
XX	Yamada Y;
DR	WPI; 2001-425656/45.


```

QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 CTGTGGAGACAGAGAGCTACGGCAGCATCGGAGACAGGCCCCCTGCTGACGTCACCA 1860
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db 1861 CTCCGCTTCATCTCCCAAGCGCTACGGGCTGCGCGCATGTGAACATGGAACATCACTCGTG 1920
QY 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1921 GGAGCGCAACACCTTCCGACAGAAAAGAGGCGGAGCGCTCACCTCGAGGCTGAGAGGA 1980
QY 661 LeuPheSerValLeuAsnTyrGlyLysArgAlaArgArgProGlyLeuLeuGlyValAsnSerVal 680
Db 1981 CTGTTCAAGCTCTCAACTACAGAGCGGCGCGGCCCCGCTCTGAGGCCCTCTGTG 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGCTCGAGAGATATCCACAGGGCGCTGGCGCACCTTGCTGCTGCTGCTGCGGCGCCAG 2100
QY 701 AspProProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
Db 2101 GACCCGCGCGCTGAGACTGTTGTCAAGGTGATGTGACGGGCGCGCTACGACACACATC 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db 2161 CCCCGAGACAGGCTACAGGAGGATCCGCGACACATCATTAACCCCAAGACCGATATCTC 2220
QY 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2221 GTGGCTCGGTATGCGGTGTCCAGAAAGCGCGCATGGGCACTGCGCAAGCGCTTTCAAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2281 AGCCACGCTCTACCTTGAACAGACCTCCAGCGCTACATGCAAGTTCCTGCTCAACCTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
Db 2341 CAGGAGACAGGCGCGCTGAGGAGTGGCTGCTGATCGACAGACAGCTCTCTCTGAAATGAG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
Db 2401 GCCACGACGTGGCTCTTGAGACTCTTCCATAGCTTCAATGTGCACACGCGCGGCATC 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGGGGCAAGTCTCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2521 CTCTGACGCTGTGCTACGGGCAATGAGAAACAGCTTTTGCGGGATTCGCGCGGAGC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGGCGTCTCTCTGCTTGTGATGATTTCTTGTTGTGATCAACCTCACTCAACCGAG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2641 AAAACCTTCTCAGGAGCCTGTGTCGAGGTGTCCCTGAGTATGCTGCTGTGAACTTG 2700
QY 901 ArgLysThrValValAspPheProValGluAspGluAlaLeuGlyGlyLysThrLysPheVal 920
Db 2701 CGGAAGACAGGTGTAACTTCCCTGTAGAGAGAGAGGCGCTGGGTGGCAAGGCTTTTGT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCGCGCCACAGGCTTATCCCTGTGTGCGGCTCTGTGTGATACCGGAGACCTG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2821 GAGGTGACAGAGGACTACTCCAGCTATGCGCGGACCTCATGAGACGAGCTCAACCTTC 2880

```

```

QY 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGCGCTTCAAGGCTGGGAGGAACAGCGTCCAAACTCTTTGGGGTCTTGGCGCTG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2941 AAGTGTCAAGCTGTCTTGTGATTTGCAAGTGAACACCTTCCACAGCGGTGTGCACCAAC 3000
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATTTCAGATCTCTCTCTGCTGAGCGGTACAGTTCACGATGTGTCTGACGCTCCCA 3060
QY 1021 PheHisGlnGlnValTyrLysAspProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3061 TTTCATCAGCAAGTGTGGAAGAACCCACATTTTCTGCGCGGTATCTCTACACAGGCGC 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaGly 1060
Db 3121 TCCCTCTCTACTCTCATCTGTAAGCCAAAGACGAGGAGTGTCTGTGGGGCCAAAGGC 3180
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrLeuCysHisGlnAlaPheLeuLeu 1080
Db 3181 GCGCGCGGCTCTGCTCTCCAGGCGGTGAGTGTGTGTGCTGCTGACCAAGCATCTCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3241 AAGCTGACTCGACACAGGTGTACCTACGTGCCACTCTGGGGTCACTCAGACAGCCGACG 3300
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3301 ACGCAGCTGAGTCGGAACCTCCGGGAGACGACGTGACTGCTGCTGAGGCGCGACAGCA 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3361 CCGGCACTGCTCTCAGACTTCAAGACATCTCGAGC 3396

RESULT 2
ID AAH49601 strand; DNA; 3396 BP.
XX AAH49601;
AC AAH49601;
XX 24-SEP-2001 (first entry)
DT
XX
XX Human coding sequence #2.
DE
XX Angiogenesis; cardiant; cell differentiating agent; bone marrow;
XX heart muscle cell; heart disease; human; ds.
XX
OS Homo sapiens.
XX
XX W0200148149-A1.
XX
XX
XX 05-JUL-2001.
XX
XX 28-FEB-2000; 2000MO-JP001148.
XX
XX 28-DEC-1999; 99JP-00372826.
XX
XX (KYOM ) KYOMA HAKKO KOGYO KK.
XX
XX
XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
XX
XX WPI; 2001-418252/44.
XX
XX P-PSDB; AAG64329.
XX
XX New adult bone marrow-originated cells capable of differentiating into
XX heart muscle cells, applicable as remedies for various heart diseases
XX particularly with damaged heart muscle accompanying degeneration.
XX
XX Disclosure; Page 134-142; 158pp; Japanese.
XX
XX The present invention relates to cells isolated from bone marrow, which
XX

```

CC are capable of at least differentiating into heart muscle cells. The
CC cells are applicable as remedies for various heart diseases particularly
CC with damaged heart muscle accompanying degeneration. The present sequence
CC was used to illustrate the present invention

XX Sequence 3396 BP; 549 A; 1157 C; 1088 G; 602 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3396
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-044-692-2 (1-1132) x AAH49601 (1-3396)

```
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisArgArgGlu 20
DB 1 ATGCGCGCGCTCCCGCTCCGAGCGTCCGCTCCCTGTCGCGAGCCACTACCGCGGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
DB 61 GTGCTGCGCGCTGCGACGTTCTGTCGCGCGCTGCGCGCGCTGCGCGCTGCGCGAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTTP 60
DB 121 CGCGGGGAGCCGGCGGCTTTCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGlnLeu 80
DB 181 GAGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 ValAlaArgValLeuGlnArgLeuGlyGlnArgGlyValAlaValSerValLeuAlaPheGly 100
DB 241 GTGCGCGCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 101 PheAlaLeuLeuArgGlnValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGCGCGCTGTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATTPGlyLeuLeu 140
DB 361 AGCTACTGCGCGCAACAGCGTGACGACGACTGCGGGGAGAGCGGGGCGTGGGGCTG 420
QY 141 LeuArgArgValGlyAspArgValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGCGCGCGCGCGCGAGAGCTGTGCTGCTCACTGTGCGACGCTGCGCGCTTGTG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGCTGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 541 GCCACTCAGGCGCGCGCGCGCGCACAGCTAGTGACCCCGAGAGGCTGTGGGTGGAA 600
QY 201 ArgAlaThrPheAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGGCGCTGGAACCAATGAGTCAAGGAGCGCGGGATCCCGCTGAGGCTGCGAGCCGGGT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCGAGAGAGCGCGGGGGAGTGCACAGCGAGAGTCTGCGCTTGGCCCAAGAGCCAGCGT 720
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
DB 721 GGGCGCTGCGCTGAGCGCGAGCGCGCGCGCTTGGGCGAGGGGTCTTGGCGCCACCGG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 AGGAGCGCTGAGCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
```

```
QY 281 GluAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAGGACACCTTTTGGAGGGGGCGCTCTGTGCGACGCGCACTCCACCCATCGGTGGGC 900
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro 320
DB 901 CGCCAGCACCAAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 960
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGln 340
DB 961 TGTCCCGCGGTGAGCGCGAGACCAAGCACTTCTCTACTCTCAAGCGAGCAAGAGAGAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1021 CTGCGCGCGCTCTCTACTCACTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1080
QY 361 ValGluThrTlePheLeuGlySerArgProProPheTProGlyTTPProArgArgLeuPro 380
DB 1081 GTGGAGACCATCTTCTGAGTTCAGCGCGCTGAGTGCAGGGAGACTCCCGGAGGTTGCC 1140
QY 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuGlyAsnHis 400
DB 1141 CGCTGCGCGCGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCGCAGTCCCGCTTACGGGGGTGCTCTCAAGACGCACTCCCGCTGCGAGCTGCGGCTCAC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
DB 1261 CCAGAGCGCGGTGTGTGCGCGGGAGAGCCCGAGGCTCTGTGGCGGCGCGCGCGAG 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
DB 1321 GAGGACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer 480
DB 1381 GTGTACGGCTTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
DB 1441 AGGCAACAGAGCGCGCTTCTCAAGAACACCAAGAACTTCTCTGCGGAGAGCAT 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTTPLysMetSerValArgAspCysAlaTTPLeu 520
DB 1501 GCCAAGCTTCTGCTGAGAGCTGACGTGAGAGTGAAGTGGGACTGCGCTTGGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlu 540
DB 1561 CGCAGAGAGCCAGGGGTGTGGCTGTGTGCGCGCGAGACCGCTGTGCTGAGAGATC 1620
QY 541 LeuAlaLysPheLeuHisTTPLeuMetSerValTyrValAlaGluLeuLeuArgSerPhe 560
DB 1621 CTGGCCAACTTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTTC 1680
QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1681 TTTTATGTACGAGAGACAGTTTCAAAAGAACAGGCTCTTTTTCACCGGAGAGTGTTC 1740
QY 581 TTPSerLysLeuGlnSerTleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB 1741 TGGAGCAAGTGTGAAGCATTTGAATCAACACAGCATTAAGAGGGTGAAGCTGCGGAG 1800
QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
DB 1801 CTGTCCGAAGCAGAGTTCAGGAGCATTCGGGAAGCCAGGCGCGCGCTGTGACGTCCAGA 1860
QY 621 LeuArgPheLleProLysProAspGlyLeuArgProLleValAsnMetAspTyrValVal 640
DB 1861 CTCGCTTATCCCGCAAGCCTGACGGGCTGCGCGCGCATTTGTGAACATTCACGTCGTG 1920
QY 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValAla 660
```



```

Db      1921 GGAGCCAAACGCTCCGAGAGAAAGAGGCGCGACCTCCTCAGCTCGAGGGTGAAGCA 1980
Qy      661  LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db      1981 CTGTTACAGCGTCTCAACTACAGAGCGGGCGCGCCCGGCTCTTGCGGCCCTCTG 2040
Qy      681  LeuGlyLeuAspAspIleHisArgAlaTyrPheValLeuArgValArgAlaGln 700
Db      2041 CTGGGCTCTGAGAGATTCACAGGGGCTGGCGCCTTCTGCTGCTGCTGCGGCCAG 2100
Qy      701  AspProProGlyLeuLeuTyrPheValIysValAspValThrGlyAlaTyrAspThrIle 720
Db      2101 GACCGCGCGCTGAGCTGACTTTGTCAAGGTGTGATGTGACGGGCGCGTACACACATC 2160
Qy      721  ProGlnAspArgLeuThrGluValIleAlaSerIleIleLeuProGlnAsnThrTyrGly 740
Db      2161 CCCGAGAGACGGCTCAGCGAGGTCACTCCGACATCATCAACCCCAAGAACAGTATGC 2220
Qy      741  ValArgArgTyrAlaValAlaGlnIysAlaAlaHisGlyHisValArgIysAlaPheIys 760
Db      2221 GTGCTCGGTATGCGGTGCTCAGAGAGCGCCCATGGCAGCTCCGCAAGGCTTCAG 2280
Qy      761  SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db      2281 AGCCAGCTCTCACTTGAACAACCTCCAGCCGTACATGCAAGTGTGGGTCACTG 2340
Qy      781  GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuGlnGlu 800
Db      2341 CAGGAGACCAAGCCCGCTGAGGATGCGTCTCATCGACAAGAGCTCCCTCTGATGAG 2400
Qy      801  AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValAlaArgIle 820
Db      2401 GCCAGAGTGGCTCTTCAAGCTTCTCAAGCTTCATGTGCCACCAAGCCGTGGCATT 2460
Qy      821  ArgGlyIysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db      2461 AGGGGCAAGTCTCACTGCTCAGTGCAGAGGAGATCCGCAAGGCTCATCTCTCCACGCT 2520
Qy      841  LeuCysSerLeuCysTyrGlyAspMetGluAsnIysLeuPheAlaGlyIleArgArgAsp 860
Db      2521 CTCTGACGCTGTGCTACGCGCAATGAGAAACAAGCTTTTGGCGGGGATTCGCGCGGAC 2580
Qy      861  GlyLeuLeuLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db      2581 GGGCTGCTCTCTGCTGATGATGATTTCTTGTGTGACACTCACCCTCACCGCAGCG 2640
Qy      881  LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db      2641 AAAACCTTCTCAGACCTGATCCGAGGTGTCTGAGTATGGCTGCTGGTGAACCTTG 2700
Qy      901  ArgIysThrValValAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheVal 920
Db      2701 CGGAAGACAGTGTGAACTTCTCTGTAGAAGACAGAGCCCTGGGTGGCAGCGCTTTGTT 2760
Qy      921  GlnMetProAlaHisGlyLeuPheProTyrPheGlyLeuLeuLeuAspThrArgThrLeu 940
Db      2761 CAGATGCCGCGCCACGCGCTATTCCTCTGTGGGCTCTGCTGTGATACCGGAGCCCTG 2820
Qy      941  GluValAlaGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db      2821 GAGGTGACAGAGCACTACTCCAGCTATGCCCGGACCTCCATCAGACCGAGCTCACCTTC 2880
Qy      961  AsnArgGlyPheIysAlaGlyArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu 980
Db      2881 AACCGCGGCTTCAAGGCTGGAGAGAACATGCGTCCGAACTTTTGGGGCTTGGCGGCTG 2940
Qy      981  LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db      2941 AAGTGCACAGCGCTTTCTGTGATTGTGACAGGTAAACAGCTCCACAGCGGTGTCCACAA 3000
Qy      1001  IleTyrIysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020

```

```

Db      3001 ATCTAACAAGATCTCTGCTGAGCGGTACAGGTTTCAAGCATGTGTGCTCAGCTCCA 3060
Qy      1021  PheHisGlnGlnValIleThrIysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db      3061 TTTCTATCAGCAGATTGGAGAGAACCCCACTTTTCTCTGCGGTGATCTCTCAACGGGC 3120
Qy      1041  SerLeuCysTyrSerIleLeuIysAlaIysAsnAlaGlyMetSerLeuGlyValIysGly 1060
Db      3121 TCCCTCTGCTACTCATCTGTAAGAACCAAGAACGAGGATGTCTGCTGGGGGCGCAAGGCG 3180
Qy      1061  AlaIaGlyProLeuProSerGluAlaValGlnTyrPheCysHisGlyAlaPheLeuLeu 1080
Db      3181  GCCGCGCGCTCTCTCCCTCCAGGCGGTGACAGTGTGTGTGACCAAGCATTTCTGTCTC 3240
Qy      1081  LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db      3241 AAGCTGACTCGACACCGGTCTCACTTACGTGCCACTCTGAGGTCACTCAGGACAGCCCG 3300
Qy      1101  ThrGlnLeuSerArgIysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db      3301 AGCAGCTGAGTGGAGAGCTCCGAGGAGCAGACGCTGACTGCTGGAGGCGCAGCAAC 3360
Qy      1121  ProAlaLeuProSerAspPheIysThrIleLeuAsp 1132
Db      3361 CCGGCACTGCCCTCAGACTTCAAGACCAATCTTGAC 3396

RESULT 3
AAH44366
ID   AAH44366 standard; cDNA, 3396 BP.
XX
AC   AAH44366;
XX
DT   26-SEP-2001 (first entry)
XX
DE   Human telomerase nucleotide sequence SEQ ID NO:32.
XX
KW   Differentiation; heart muscle cell; cytokine; transcription factor;
KW   proliferation; surface antigen; heart disease; cardiomyocyte;
KW   bone marrow; umbilical blood cell; heart muscle degeneration;
KW   myocardial infarction; ss.
XX
OS   Homo sapiens.
XX
PN   M0200148150-A1.
XX
PD   05-JUL-2001.
XX
PF   02-NOV-2000; 2000MO-JP007741.
XX
PR   28-DEC-1999; 99JP-00372826.
XX
PR   28-FEB-2000; 2000MO-JP001148.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI   Yamada Y;
XX
DR   MPI; 2001-425655/45.
XX
DR   P-PSDB; AAB999930.
XX
PT   Cells capable of differentiating into cardiomyocytes and originating in
PT   bone marrow or umbilical blood cells for study of cardiomyocyte
PT   differentiation and treatment of heart disease.
XX
PS   Disclosure; Page 141-147; 187p; Japanese.
XX
CC   The present invention describes cells originating in bone marrow or
CC   umbilical blood cells which are capable of differentiating into
CC   cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
CC   differentiation of the cells; (2) a method for carrying out the
CC   differentiation into cardiomyocytes, regulated by a promotional and/or
CC   inhibitory factor; (3) a method for the differentiation of the cells into
CC   cell types other than cardiomyocytes; (4) drug compositions promoting the

```

CC Formation of heart muscle and regeneration of heart tissue which contain
 CC the cells; (5) a method for the production of antibodies which recognise
 CC the cells; especially antibodies which recognise a surface antigen on the
 CC cells; (6) a method for screening factors which promote the proliferation
 CC of the cells; (7) a method for immortalising the cells by expressing
 CC telomerase in them; (8) drug compositions for the treatment of heart
 CC disease which contain the immortalised cells; and (9) cell-free
 CC supernatant from the culture of the cells and its use in promoting their
 CC differentiation into cardiomyocytes. The cells are used in the treatment
 CC of diseases involving heart muscle degeneration, such as myocardial
 CC infarction and in the study of cardiomyocyte differentiation. AAH44351 to
 CC AAH44409 and AAB99915 to AAB99935 represent sequences used in the
 CC exemplification of the present invention

XX Sequence 3396 BP; 549 A; 1157 C; 1088 G; 602 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3396
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-044-692-2 (1-1132) x AAH44366 (1-3396)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTrpArgGlu 20
 DB 1 ATGGCCGCGCTCCCGCTGCGAGCCGTCGCTCCCTGCGCAGCCATCCCGCAG 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
 DB 61 GTGCTGCGCCCTGCGCAGCTTCGTCGCGCCGCTGCGCGCCAGGGCTGCGCTGCGCAG 120
 QY 41 ArgGlyAspProAlaIlePheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
 DB 121 CGGGGGGACCCGCGGCTTCGCGCGCTGCGGCGCAGGCTGCGTGGCGCTTGG 180
 QY 61 AspAlaArgProProProAlaIleProSerPheArgGlnValSerCysLeuArgGluLeu 80
 DB 181 GAGCGACGCGCGCCCGCGCCCTCTTCGCGCAGGTGCTGCTGAGAGAGCTG 240
 QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyValAlaValAsnValLeuAlaPheGly 100
 DB 241 GTGGCCCGAGTGTGCGAGGCTGTGCGAGCGCGCGCAGAACCTGCTGCGCTTGGC 300
 QY 101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGluAlaPheThrThrSerValArg 120
 DB 301 TTGGCTGCTGAGCGGGGCGCGGGGGCCCGCCGAGGCTTTCACACAGCGTGGC 360
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrpGlyLeuLeu 140
 DB 361 AGCTACCTCCCAACAGCGGTGACCGACGCGCTGCGGGGAGCGGGGCGTGGGGCTGCTG 420
 QY 141 LeuAlaArgValAlaGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 DB 421 CTGCGCGCGGTGGCGACGACGCTGCTGCTTCACTCTGACGCTGCGCGCTCTTTGG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuThrGlnLeuGlyAla 180
 DB 481 CTGGTGCTCCAGCTGCGCTACAGGAGTGGGGCGCGCTGTACACAGCTGGCGCT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 DB 541 GCCACCTCAGGCGCGCGCCCGCAGCGTACGAGACCCCGAAGGGCTCTGGGATCCGA 600
 QY 201 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB 601 CGGGCTTGAGACCATGCTCAGGAGGCGCGGGGTCCCTCGGCGCTGCGACGCCCGGT 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB 661 GGAGAGGCGCGGGGCGAGTGCAGCCGAGTCTCCCTTGGCCCAAGAGGCCCAAGCGGT 720

QY 241 GlyAlaAlaProGluProGluThrProValGlyGlnGlySerTrpAlaHisProGly 260
 DB 721 GGCGCTGCCCTGAGCGGAGCGAGCGCCGTTGGGCAAGGGTCTCTGGGCCACCGCGGC 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 DB 781 AGAGCGCGGTGACCGAGTGAACCGTGGTTCCTGTGTGTCTCACTTCCGAGACCGCGGA 840
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 DB 841 GAAGCAGCTCTTTGGAGGGTCCGCTCTTGGCAGCGCCATCCACCCATCCGTGGC 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
 DB 901 CGCAGACACACGCGGGCCCCCATCCACATCGCGGCCACACGTCCTGGGACAGCCT 960
 QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
 DB 961 TGTCCCCCGGTGTACGCGCAGACCAAGCATTCTCTACTCTCAGGCGCACAAGAGAGCAG 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 DB 1021 CTGGGCTCTCTCTCTACTCACTCTCTGAGGCCAGCTTACCTGCGCGTGGAGGCTTC 1080
 QY 361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
 DB 1081 GTGAGAGACCATCTTTCTGGGTTCCAGGCCCTGATGCGCAGGAGTCCCGCGAGTTGCC 1140
 QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuGlyLysHis 400
 DB 1141 CCGCTGCGCCAGCGCTACCGGAAATGCGCGCCGTTCTGGAACCTGCTGGGAACCA 1200
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrLysCysProLeuArgAlaAlaValThr 420
 DB 1201 GCGCAGTGCCTTACGGGGTCTCTCAAGACGACCTGCGCGCTGCGACTCGGTAC 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGln 440
 DB 1261 CCAGCAGCGGTGTGTGTCGCCGGAGAGCCCGAGGCTGTGGCGGCCCCCGAGAG 1320
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
 DB 1321 GAGGACACAGACCCCGTGTGCTGTCAGCTGCTCCGACACAGCAGCCCTGGCGCAG 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
 DB 1381 GTGTACGCTTGTGTGCGGCTCTGCGCGCGCTGCGCGCTGCGCGCTCTGGGGCTTC 1440
 QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
 DB 1441 AGGCAACAAGACCGCGCTTCTCAGAGAACCAAGAACTCATCTCCCTGGGGAAGCAT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
 DB 1501 GCCAAGCTTCTGCTCAGAGGTGACGTGAGAGAGGTGCGGAGCTGCGCTTGGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGluIle 540
 DB 1561 CGCAGAGCCCGAGGGGTGTGTGTGTCGCGCGCGCAGACACGCTGTGCTGAGAGATC 1620
 QY 541 LeuAlaLysPheLeuHisIleTrpLeuMetSerValTyrValAlaGlnLeuLeuArgSerPhe 560
 DB 1621 CTGGCCAACTTCTCAGCTGCTGATGATGTGATGCTGTGAGACTGCTGAGCTTTC 1680
 QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
 DB 1681 TTTTATGTCAACGAGACCACTTTCAAAAGAACAGCTTTTCTTACCGAAGAGTGTG 1740
 QY 581 TrpSerLysLeuGlnSerIleGlyTyrLeuArgGlnHisLeuLysArgValGlnLeuArgGlu 600
 DB 1741 TGAAGCACTTCAAAAGATTGGATTCAGACAGCACTTGAAGAGGCTGACCTTGGCGAG 1800

QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGTGGAGAGAGAGAGTCAAGGAGCATCGGAGAGCCAGGCCCTGTGTGACGTCCAA 1860
 QY 621 LeuArgPheIleProIleProIleProIleLeuArgProIleValAsnMetAspTyrValVal 640
 Db 1861 CCCCCCTTCATCCCAAGAGCTTCAAGGGCTGCGGCGCCATTGTGAACATGTGACATCACTGCTG 1920
 QY 641 G1ValAaGTrhPheArgArgGluLysAsaGlaGluArgLeuThrSerArgValLysAla 660
 Db 1921 GGAGCCAGAGACGTTCCGAGAGAAAAGAGGCGGAGCGTCTCACTTCGAGGGTGAAGGCA 1980
 QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
 Db 1981 CTGTTCAAGGTGCTCAACTACAGAGGGGCGGCGCCCGGCTCTCTGGGCGGCTCTG 2040
 QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrPargTrhPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGGCGCTGGAGCATTCACAGAGGCGGCTGCGCACCTTGCTGCTGCTGCGGCGCCAG 2100
 QY 701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
 Db 2101 GACCCGCGCGTGAAGTGTACTTGTCAAGGTGATGTACGGGCGCGTACACACCATC 2160
 QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLeuProGlnAsnThrTyrCys 740
 Db 2161 CCCCAGAGACAGGCTCACGAGGTCATCGCAGATCATCAACCCAGAACAGATCTCTC 2220
 QY 741 ValAaGTrhArgAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
 Db 2221 GTGGCGTGGTATGCCGTGTCCAGAGGCGCGCCCAAGGCGCACCTCGCAAGGCGTTCAAG 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 Db 2281 ACCCAGCTCTCACTTGAACAAGCTTCAAGCGTACATGACAGTTCGTGCTGCTCCG 2340
 QY 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
 Db 2341 CAGAGAGACAGCCCGCTGAGGATGCGCGTGTATGACAGACAGCTCTCCCTGAAATGAG 2400
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValAlaArgIle 820
 Db 2401 GCACAGAGTGGCTCTTGCACGCTTCTCAACGCTTATGTGACACACCGCGCGCATC 2460
 QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db 2461 AGGGGCAAGTCTTCACTCCAGAGTCCAGGGGATCCCGCAGGCGCTCCATCTCTCCAGCTG 2520
 QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
 Db 2521 CTCTGCAAGCTGTGCTACGCGCAATGAGAGACAGCTGTTGCGGGGATTCGCGCGGAGC 2580
 QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHisAla 880
 Db 2581 GGGCTGCTCTCTGCTGTGGATGATTTCTTGTTGTGACACCTCACTCACCCACGCGG 2640
 QY 881 LysThrPheLeuArgTrhLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
 Db 2641 AAAACCTTCTCTAGAGACCTGTGCTCGAGGTGTCCTCGATATGCGCGGTGGAACTTG 2700
 QY 901 ArgLysThrValAlaAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
 Db 2701 CGGAAGACAGTGTGAATCTCTGTAGAGAGAGAGCCCTGGGTGGACAGGCTTTTGT 2760
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgTrhLeu 940
 Db 2761 CAGATCCCGGCCCAAGCGCTATATCCCTGTGTGGGCGCTCTGCTGATACCCGAGACCTG 2820
 QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgTrhSerIleArgAlaSerLeuThrPhe 960
 Db 2821 GAGGTGCACAGGACACTTCCAGCTATGCGCGGACCTTCATCGAGCCAGCTTCACACTTC 2880
 QY 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980

Db 2881 AACCCGCGCTTCAAGCTGGAGAGAAATGCTCCCAACTCTTGGGCTCTTGGCGGCTG 2940
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 Db 2941 AAGGTCAACAGGCTGTCTTCTGTGATTTGACAGTGAACAAGCTTCCAGACGGTGTGCACCAAC 3000
 QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db 3001 ATCTACAGATCTCTCTCTGTGAGGCGTACAGTTTCAAGCATGTGTGTGACAGTCCCA 3060
 QY 1021 PheHisGlnGlnValTyrLysAsnProThrPheLeuArgValIleSerAspThrAla 1040
 Db 3061 TTTCATCAGCAAGTTTGGAGAAACCCACATTTTCTCGGCGGTCACTTCACACGCGCC 3120
 QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
 Db 3121 TCCCTCTGCTACTCATCTGAAAGCCAAAGAGGAGATGTGCTGGGGGCGCAAGGCGC 3180
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
 Db 3181 GCCGCGGCGCTCTGCTGCTCCAGAGCGGTGACGTGCTGTGCACACCATTCCTGCTC 3240
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3241 AAGCTGACTGCACACCGTGTCACTACGTGCCACTCTCGGGGTCACTCAGACAGCCAG 3300
 QY 1101 ThrGlnLeuSerArgLysLeuProGlyLysThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 Db 3301 ACGCAGCTGAGTGGAGAGCTCCGGGGAGAGAGCTGACGTGACCTGTGAGGCGCGCAAC 3360
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 Db 3361 CCGGCACTGCTCTCACTTCAAGACATCTTGAC 3396

RESULT 4
 ADG70113
 ID ADG70113 standard; DNA; 3396 BP.
 AC ADG70113;
 AC 11-MAR-2004 (first entry)
 DT 11-MAR-2004 (first entry)
 DE hTERT coding sequence.
 DE ds; gene; cytosolic; gene therapy; reverse transcriptase-inhibitor;
 KW HIV-1; reverse transcriptase; human telomerase reverse transcriptase;
 KW hTERT; chimeric; catalytic site; unregulated cellular growth; cancer;
 KW tumor.
 OS Homo sapiens.
 OS WO2003095605-A2.
 OS 20-NOV-2003.
 PF 14-APR-2003; 2003WO-EP003874.
 PR 08-MAY-2002; 2002US-0378820P.
 PR (PHMA) PHARMACIA ITAL SPA.
 PA Moll J, Schumacher A, Stouren P;
 PI Moll J, Schumacher A, Stouren P;
 XX MPI; 2004-012095/01.
 DR P-PSDB; ADG70114.
 XX New HIV-1 Reverse Transcriptase and human Telomerase Reverse
 PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
 PT treating or preventing unregulated cellular growth, e.g. cancer cell or
 PT tumor growth.
 PS Example 1; SEQ ID NO 3; 141bp; English.

XX The invention relates to the isolation of compounds that bind and inhibit
 CC the activity of HIV-1 reverse transcriptase (RT) or human telomerase
 CC reverse transcriptase (hTERT). The method involves determining these
 CC compounds using a HIV-1 RT/hTERT chimeric construct containing the
 CC catalytic sites of each enzyme. The nucleic acid is useful for treating
 CC or preventing unregulated cellular growth, including cancer cell and
 CC tumor growth. It is also useful in gene therapy. Compounds that inhibit
 CC telomerase activity can be used to treat cancer. The vectors of the
 CC invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
 CC express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
 CC coding sequence for the human TERT protein.

XX Sequence 3396 BP; 549 A; 1157 C; 1088 G; 602 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3396
Score:	5951.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-044-692-2 (1-1132) x ADG70113 (1-3396)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 DB 1 ATGCCCGCGCTCCCGCTGCCAGCCGTCGCTCCCTGCTGCAGCCACTACCGCGAG 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPhrArgLeuValGln 40
 DB 61 GTCCTCCGCTGGCCAGTTCGTCGCGCGCTGCGGCCCCAGGGGCTGGCGGCTGTGACG 120
 QY 41 ArgGlyASPProAlaIaIaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 DB 121 CGCGGGGACCCCGCGCTTCCGCGCGCTGTGTGCCAGTGGTGTGCGCTGCGCTG 180
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
 DB 181 GAGCGACCG 240
 QY 81 ValAlaArgValLeuGlnArgLeuCysGlyArgGlyAlaIaLysAsnValLeuAlaPheGly 100
 DB 241 GTGGCCGAGTGTGAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 QY 101 PheAlaLeuLeuAspGlyValIaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 DB 301 TTCGCGCTGTGGACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTTPGlyLeuLeu 140
 DB 361 AGCTACCTGCCAACAACGGGTGACCGACCTGCGGGGAGCGGGGCTGTGGGCGCTG 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 DB 421 CTGCCCGCGGTGGCGACACAGTCTGTCACTGTGTGCAAGCTGCGCGCTCTTTG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 DB 481 CTGGGTGGCTCCAGAGCTGCGCTACAGGTGTGGCGGGCGCGCTGTACAGCTCG 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 DB 541 GGCACACAGCG 600
 QY 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB 601 CGGGCTGGAACATAGCTTCAAGGAGCGCGGGGTCTCCCTGTGGCTGTCAAGCCCG 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB 661 GCGAGGAGCGCGCGGGGCGAGTCCAGCGCAAGTCTGCGCTGCCAAGAGCGCGGG 720

QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
 DB 721 GGGCGTCCCTGAGCCGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 DB 781 AGAGCCGCTGACCGAGTACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 281 GlnAlaThrSerLeuGlnGlyValLeuSerGlyTTPhrArgHisSerHisProSerValGly 300
 DB 841 GAAGCCACTCTTTGGAGGGTGGCTCTGTGGCAGCGCCACTCCACCATCCGTGGGC 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
 DB 901 CGCGAGCACAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGln 340
 DB 961 TGTCCCGCTGTACCGCGAGACCAAGCACTTCTCTACTCTTCAAGCGACCAAGAGCAG 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 DB 1021 CTGGGCGCT 1080
 QY 361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
 DB 1081 GTGAGACCATCTTTCTGGGTTCCAGGCCCTGTGATGCCAGGAGACTCCCGCAGGTG 1140
 QY 381 ArgLeuProGlnArgTyrTTPGlnMetLysProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 DB 1141 CGCCTGCCAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
 DB 1201 GCGAGTGCCTTACGGGGTGTCTCTCAAGAGCACTGCGCGCTGCGAGCTGCGTCA 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGlu 440
 DB 1261 CCAGCAGCGCGGTGTGTGTGCGCGGAGAACCCAGAGGCTGTGTGGCGCGCG 1320
 QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 DB 1321 GAGGACACAGACCCCGTGTGCTGTGTGAGCTGTCTCCAGCAACAGACGCGCG 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
 DB 1381 GTGTACGGCTTGTGTGGGCTGTGTGCGCTGTGCGCGCGCGCGCGCGCGCGCG 1440
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
 DB 1441 AGGCACAACGAACCGCGCTTCTCTCAGAAACCAAGAGTTCATCTCCTGGGGAAGCAT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
 DB 1501 GCGAAGCTCTGTGACAGACTGACGTGGAAGTGAACGTGGGAGACTGGGCTTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlyGlnIle 540
 DB 1561 CGCAGAGACCCAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
 QY 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 DB 1621 CTGGCCAAGTTCCTGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
 QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerVal 580
 DB 1681 TTTTATGTCAAGAGACCAACGTTTCAAAAGAACAGGCTTTTTCACCGGAAGATGTC 1740
 QY 581 TyrSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGln 600
 DB 1741 TGGAGCAAGTTCGAAAGATGGAATCAGACAGCACTTGAAGAGGTGTGAGCTGCGGAG 1800
 QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620

```
DB 1801 CTGTGGGAAGCAGAGTCAGGAGCATCGGAAGCCGCGCTGTGACGTCCAGA 1860
QY 621 LeuAArgPheIleProIyPProAspGlyLeuAArgProIleValAsnMetLysPyrValVal 640
DB 1861 CTCCCTTCATCCCAAGCCTGACGGCTGCGCGCATTTGTGAACATGGACATCACTGCGTG 1920
QY 641 GlyAlaArgThrPheArgArgGlnIlybAArgAlaGluArgLeuThrSerArgValIlybAla 660
DB 1921 GGAGCCAGAACCTTCGCGAGAAAGAGGCGCGAGCTCTCACTTCGAGGGTGAAGGCA 1980
QY 661 LeuPheSerValIleuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyValAsnVal 680
DB 1981 CTGTTCAAGCTGCTCAACTACAGAGCGGCGCGCGCTCTGCTGCGCGCTCTG 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTTPArgThrPheValLeuArgValArgAlaGln 700
DB 2041 CTGGGCTCGAGAGATATCCACAGGGCGCTGGCCGACCTTGCTGCTGCGCGCGCCAG 2100
QY 701 AspProProProGluLeuTyrPheValIlybValAspValThrGlyValAspThrIle 720
DB 2101 GACCCGCGCGCTGAGCTGACTTTGTTCAGAGTGAATGTACGGGCGCGTACACACCATC 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
DB 2161 CCCACGAGCAGGCTCACGGAGGTCACTCCGACATCATCAACCCAGAACAGTATCTGC 2220
QY 741 ValAArgArgTyrAlaValAlaGlnIlybAlaHisArgIlybValArgIlybValAspIlyb 760
DB 2221 GTGCTCGGTATGCGGTGTCCAGAGGCGCGCCCATGGGCACTCCGCAAGGCTTCAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGluPheValAlaHisLeu 780
DB 2281 AGCCAGCTCTTCACTTGAACAAGCTCCAGCCGTACATGACAGTTCGTTGCTCACTTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGln 800
DB 2341 CAGGAGACCAAGCCGCTGAGGGATGCGTGCATGACAGACAGCTCCCTCGATGAG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
DB 2401 GCCACAGAGGCGCTCTTCACAGCTTCCTCAAGCTTCATGTGCCACACCCGCGCCATC 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
DB 2461 AAGGGGCAATCTTACCTCCAGAGGCGGAGATCCCGCAGGCGCTCCATCTCTCCAGCTG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnIlybLeuPheAlaGlyIleArgArgAsp 860
DB 2521 CTCTGAGGCTGTGCTACCGGCACTGAGAACAGCAAGCTTTTGGGGGATTCGGCGGAGC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
DB 2581 GGGCTGCTCTCTCGTTGGTGAATTTCTTGTGGTGAACCTCACTCACTCCACGCGG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
DB 2641 AAAACCTTCTCAAGGACCTTGCTCGAGGTGTCCCTGAGATGAGCTGCGGTGGAACTTG 2700
QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
DB 2701 CGGAAGACAGCTGTGAATTCCTCTGTAGAAAGAGAGCCCTGGGTGGCAACGGCTTTGTT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
DB 2761 CAGATGCCCGGCCACCGCTATATCCCTGTGTGGCGCTCTGTGTGATACCGGAGACCTG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
DB 2821 GAGGTGCAAGCAGACTACCTCAGCTATGCGGAGCTTCATCAAGACAGTCTCAACCTTC 2880
QY 961 AsnArgGlyPheIlybAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuAlaGlu 980
```

```
DB 2881 AACCGCGCTTCAGGCTGGAGAGAACATGCGTCCGAACTCTTGGGGTCTTGGCGGCTG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
DB 2941 AAGTGTCAAGCTGTCTTCTTGATTTGGATTTGGAGTGAACAGCTTCACAGCGGTGACCAAC 3000
QY 1001 IleTyrIlybIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValIleuGlnLeuPro 1020
DB 3001 ACTACAAAGATCTCTCTGTGAGCGGTACAGGTTTCAACGATGTGTGTGACGCTCCCA 3060
QY 1021 PheHisGlnGlnValITrPylAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
DB 3061 TTTTCATCGCAGATTTGGAGAACCCCACTTTTCTCGCGGTCTATCTTCAACGGCC 3120
QY 1041 SerLeuCysTyrSerIleLeuIlybAlaIlybAsnAlaGlyMetSerLeuGlyValIlybGly 1060
DB 3121 TCCCTGTCTACTCCATCTGAAAGCAGAACGAGGATTCGCTGGGGGCGCAAGGCC 3180
QY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
DB 3181 GCGCGCGGCGCTGTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
DB 3241 AAGCTGACTCGACACCGTGTCACTTACGTGCCACTCTGGGGGTCACTCAGGACAGCCCA 3300
QY 1101 ThrGlnLeuSerArgIlybLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
DB 3301 ACGCAGCTGAGTGGAGAGCTCCGGGAGACGACGTGACTGCTCGTGGAGGCCGACGCAAC 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
DB 3361 CCGGCACTGCCCTCAGACTTCAAGACATCTCGAC 3396

RESULT 5
ABV78144
ID ABV78144 strand; DNA; 3399 BP.
XX
AC ABV78144;
XX
XX 15-NOV-2002 (first entry)
XX
DE Human telomerase reverse transcriptase DNA SEQ ID NO 28.
XX
XX RNA inhibition; dRNA1; gene expression inhibitor; oncogene; cytostatic;
XX
XX viricide; protozoicide; gene; ds.
XX
OS Homo sapiens.
XX
XX
XX MO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Roost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 129-130; 203pp; German.
XX
XX The invention relates to inhibiting expression of a target gene (I) in a
```

cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA is complementary to (i) and at least one end of dsRNA has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. In humans, also genes in plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a gene related to the invention

XX Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) x ABV78144 (1-3399)

```
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATGCCGCGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGAGCCACTACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
DB 61 GTCGTGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 ArgGlyAspProAlaIlePheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CCGCGGGAGCCCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80
DB 181 GAGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyArgGlyAlaIleAsnValLeuAlaPheGly 100
DB 241 GTGGCGCGAGGTGTGAGAGGCTGTGCGAGCGCGCGCGAGAACGTCGTGCGCTTCG 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTCGCGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeuLeu 140
DB 361 ACCTACCTCCCAACACGCGTGAACGCGAGCGCGGAGCGCGGCGTGTGGGCGTGTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisIleLeuAlaArgCysAlaIleuPheVal 160
DB 421 CTGGCGCGGTGGGCGACGACGCTGTGCTTCACCTGTGCGACGCTGCGCTCTTTTG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGGTGGCTCCAGCTGCGCGCTACGAGGTGTGGGGCGCGCGCTGTACACAGCTCG 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 541 GCCACCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 201 ArgAlaTyrAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGGGCGCTGAGACCAATGCGTCAAGAGGCGCGGGGTCCCTGTGGCGCTGCGACCG 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
```

```
DB 721 GCGCTGCGCTGAGCGGAGCGGAGCGCGCGCTTGGGACAGGGGTCTCGGGCCACCGGG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValIleSerProAlaArgProAlaGlu 280
DB 781 AGAGCGCGTGAACGAGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAGGCACTCTTTGGAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 301 ArgGlnHisIleAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
DB 901 CCGCAGACACAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 321 CysProProValTyrAlaGlyThrIleHisPheLeuTyrSerSerGlyAspIleGln 340
DB 961 TGTTCCTCCGTGTAGCGCGAGCAAGCACTTCTCTACTCTCTCAAGCGCACAAAGAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyValaArgArgLeu 360
DB 1021 CTGGCGCGCTCTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 361 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
DB 1081 GTGAGAACCATCTTCTGGGTTCCAGCGCTGATGCCAGGAGACTCCCGCAGTTGCC 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1141 CGCTGTCCCGAGCGGTACTCGGAAATGCGCGCGCTGTGTGTGTGTGTGTGTGTGT 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaIleValThr 420
DB 1201 GCGAGTGCCTTACGCGGGTGTCTCTCAAGAGCATGCGCGCTCGAGCTCGGGTAC 1260
QY 421 ProAlaIleGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
DB 1261 CCAGAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1321 GAGAGACAGACCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB 1381 GTGTAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrIleLysPheIleSerLeuGlyLysHis 500
DB 1441 AGGCACAAAGAAACGCGCTTCTCTCAAGAAACAAAGAAATTCATCTCTCTGGG 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaIleuLeu 520
DB 1501 GCCAAGCTCTCGCTCAGAGGTGACGTGAGAGAGGTGAGAGGTGAGAGGTGAGAG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlu 540
DB 1561 CGCAGAGGCGCGAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 541 LeuAlaLysPheLeuHisTyrLeuLeuSerValIleValGlnLeuLeuArgSerPhe 560
DB 1621 CTGGCGCAAGTCTCTCACTGAGGTGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 561 PheTyrValIleThrGluThrThrPheGlnLysAsnArgLeuPheThrArgLysSerVal 580
DB 1681 TTTTATGTACGAGAACCAAGTTTCAAAAGAACAGGCTTTTGTACCGGAAGAGTGT 1740
QY 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLysLysArgValGlnLeuArgGlu 600
DB 1741 TCGAGCAAGTTCAGAAAGCATTTGATCAGACGACTTGAAGAGGTGTGAGTGTGG 1800
QY 601 LeuSerGluAlaGluValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
```


Db 1801 CTGTCGAGACGAGGTCAGGAGCATCGGAGAACGAGCCGCTGCTGACGTCACAA 1860
 QY 621 LeuArgPheIleProIlyProIlyLeuArgProIleValAsnMetAspTyrValVal 640
 Db 1861 CTCGGCTTATCCCAAGGCTGACGGGCTGCGGCTGATGTGAACATGACCTACGTCG 1920
 QY 641 G1yAlaArgThrPheArgArgGluIyAsnValAG1yArgLeuThrSerArgValIyAsn 660
 Db 1921 GGAAGCAGAACGTTCCGAGAGAAAGAGAGGCGGAGCGCTCACCTCGAGGGTGAAGCA 1980
 QY 661 LeuPheSerValIleuAsnTyrG1yValArgAlaArgArgProG1yLeuLeuG1yAlaSerVal 680
 Db 1981 CTGTTACAGGCTGCTCAACTACGAGCGGCGGCGGCGCTGCTGAGGCGCTGCTG 2040
 QY 681 LeuG1yLeuAspAspIleHisArgAlaATPArgThrPheValIleuArgValArgAlaGln 700
 Db 2041 CTGGGGCTGAGCATATCCAGAGGCTGCGGACCTTGCTGTGTGTGTGTGTGTGTGTGT 2100
 QY 701 AspProProProG1yLeuTyrPheValIyAsnValIyAsnValIyAsnValIyAsnValIy 720
 Db 2101 GACCCGCGCGCTGAGCTGACTTGTCAAGGTGATGTACGGGCGCGCTACACACCATC 2160
 QY 721 ProG1nAspArgLeuThrG1yValIleAlaSerIleIleIyProG1nAsnThrTyrCys 740
 Db 2161 CCCAGAGACAGGCTCACGAGGTCATCGCAGCATCATCAACCCAGAACAGTACTCG 2220
 QY 741 ValArgArgTyrAlaValValG1yAsnValIleAlaHisG1yHisValArgIyAsnValIy 760
 Db 2221 GTGGCTGGGTATGCCGTGTGTCCAGAGGCGCGCCAGAGGCGACGTCCGAGAGGCTTCAAG 2280
 QY 761 SerHisValSerThrLeuThrAspLeuG1nProTyrMetArgG1nAsnValIleHisLeu 780
 Db 2281 ACCCAGCTCTTCACTTGAACAACCTCCAGCGCTACATGCAAGTTCGTGGCTCACTCG 2340
 QY 781 G1nG1yThrSerProIleuArgAspAlaValIleG1yG1nSerSerSerLeuG1nG1n 800
 Db 2341 CAGGAGACAGGCGCGCTGAGGATGCCGTGCATGACAGAGCTCTCCCTGATGAG 2400
 QY 801 AlaSerSerG1yLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 Db 2401 GCCAGAGTGGCTCTTTCAGAGCTTCTTCAAGCTTATGTCACACACCGCGGCCATC 2460
 QY 821 ArgG1yIySerSerTyrValG1nG1yG1nG1yIleProG1nG1ySerIleLeuSerThrLeu 840
 Db 2461 AGGGGCAAGTCTTACCTCCAGTGCACGGGATCCCGCAGGGCTCATCTCTCCAGCTG 2520
 QY 841 LeuCysSerLeuCysTyrG1yAspMetG1yAsnIyLeuPheAlaG1yIleArgArgAsp 860
 Db 2521 CTCTGACGCTGTGCTACGGCGCATGAGAACAGCTGTTGCGGGGATTCGGCGGAGC 2580
 QY 861 G1yLeuLeuLeuValIleuValIleuValIleuValIleuValIleuValIleuValIleu 880
 Db 2581 GGGCTGCTCTCGT 2640
 QY 881 IySerThrPheLeuArgThrLeuValArgG1yValIleProG1yTyrCysValValIleuLeu 900
 Db 2641 AAAACCTTCTTCAAGACCTGCTCGAGGTGTCTCGATGATGCTGCTGCTGTGAACCTTG 2700
 QY 901 ArgIySerThrValIleuAsnPheProValG1yAspG1yValIleuG1yG1yThrAlaPheVal 920
 Db 2701 CGGAAGACAGTGTGAATTCCTCTGTGAAGAGAGAGGCTGCTGCTGCTGCTGCTGCTG 2760
 QY 921 G1nMetProAlaHisG1yLeuPheProTyrG1yG1yLeuLeuLeuAspThrArgThrLeu 940
 Db 2761 CAGATGCCGCGCCACGCTATTCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820
 QY 941 G1yValG1nSerAspTyrSerSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db 2821 GAGGTGACAGAGGACCTACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTT 2880
 QY 961 AsnArgG1yPheIyAsnValIyArgAsnMetArgArgIyLeuPheG1yValIleuArgLeu 980
 Db 2881 AACCGGCGGCTTCAAGGCTGAGAGAACATGCGTCCGAAACTCTTGGGGTCTTGGCGGCTG 2940

QY 981 IyCysHisSerLeuPheLeuAspLeuG1nValIleAsnSerLeuG1nThrValCysThrAsn 1000
 Db 2941 AAGTTCACAGGCTGCTTGTGATTTTGCAGTGAACAGCTTCAAGAGCTGTGACACCAAC 3000
 QY 1001 IleTyrIyIleLeuLeuLeuG1nAlaTyrArgPheHisAlaCysValIleuG1nLeuPro 1020
 Db 3001 ACTTCACAGATCTCTCTGTGTGACAGGCGTACAGTTCACAGATGTGTGTGTGTGTGTGT 3060
 QY 1021 PheHisG1nG1nValITripIyAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db 3061 TTTTCATCAGCAAGTGTGAAGAACCCCATTTTCTGCGGTGATCTTCAACAGCGGC 3120
 QY 1041 SerLeuCysTyrSerIleLeuIyAsnAlaIyAsnAlaG1yMetSerLeuG1yAlaIyG1y 1060
 Db 3121 TCCCTGTGCTACTCCATCTGAAGCCAGAACGAGGAGATGCTGTGGGGCCAGAGGCG 3180
 QY 1061 AlaAlaG1yProLeuProSerG1nAlaValG1nTyrPheCysHisG1nAlaPheLeuLeu 1080
 Db 3181 GCGGCGGCGCTCTGCGCTCGAGGCGGTGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
 QY 1081 IyLeuThrArgHisArgValIyThrTyrValProLeuLeuG1ySerLeuArgThrAlaGln 1100
 Db 3241 AAGCTGACTCGACACCGTGTCACTTACGTGCCACTCTGGGGTCACTCAGAGACAGCCAG 3300
 QY 1101 ThrG1nLeuSerArgIyLeuProG1yIyThrThrLeuThrAlaLeuG1nAlaIleAsn 1120
 Db 3301 AGCAGCTGAGTGGAGAGCTCCGGGAGACAGAGCTGAGTGTGCTGTGAAGCCCGACCAAC 3360
 QY 1121 ProAlaLeuProSerAspPheIySerThrIleLeuAsp 1132
 Db 3361 CCGGCACTGCCCTCAGACTTCAAGACATCTCGGAC 3396
 Db
 RESULT 6
 ABZ35720
 ID ABZ35720 standard; DNA; 3399 BP.
 XX
 AC ABZ35720;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Human elomerase reverse transcriptase polynucleotide SEQ ID NO 28.
 XX
 KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytosolic; virotoxin;
 KW protozoan; gene expression; antisense; tumour; infection; plasmidum;
 KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
 KW Hepatitis C virus; human papilloma virus; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10100588-A1.
 XX
 PD 18-JUL-2002.
 XX
 PF 09-JAN-2001; 2001DE-01000588.
 XX
 PR 09-JAN-2001; 2001DE-01000588.
 XX
 PA (RIBO-) RIBOPHARMA AG.
 XX
 PI Kreutzler R, Limmer S, Roost S, Hadwiger P;
 XX
 DR WPI; 2002-683450/74.
 XX
 PT Inhibiting expression of target genes, useful e.g. for treating tumors,
 PT by introducing into cells two double-stranded RNAs that are complementary
 PT to the target.
 XX
 PS Claim 13; Page 25-26; 100pp; German.
 XX
 CC The invention relates to inhibiting expression of a target gene in a cell
 CC by introducing at least two oligonucleotides (dsRNAi and II), both
 CC with a double-stranded (ds) structure of at most 49 sequential nucleotide

CC pairs. At least part of one strand (S1, S2) of the ds structures in each
 CC of dsRNA1 and II are complementary to regions in the target gene. The
 CC method uses antisense inhibition of gene expression using double stranded
 CC RNA inhibition (RNAi). The method is particularly used to treat tumors
 CC or infections, especially by Plasmidum or viruses/viroids (pathogenic on
 CC humans, animals or plants). The method provides more effective inhibition
 CC of expression than known methods using a single dsRNA, even at very low
 CC concentrations. When dsRNA has at least one unpaired nucleotide at the
 CC end, stability (and thus effective concentration in the cell) is improved
 CC and efficiency can be increased further by pretreating the cells with
 CC interferon. The present sequence is that of a target DNA of the invention
 CC
 XX Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

pred. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) x AB235720 (1-3399)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
 Db 1 ATCCCGCGGCTCCCGCTGCGAGCGGTGCTCCCTGCTGCGAGCCACTACCGCGAG 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 Db 61 GTCTGCGCGCTGCGACGTTCTGCGCGCGCTGCGGCGCCAGGCGCTGCGCGTGGCAG 120
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 121 CGCGGGAGCCCGGCGGCTTCCGCGCGCTGCTGCGCCAGTGGCTGCTGCGCGCTGCG 180
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
 Db 181 GAGCGACGCGCGCGCGCGCGCGCGCGCTTCCGCGAGGTGCTGCGTGAAGAGCTG 240
 QY 81 ValAlaArgValLeuGlnArgLeuGlyGlnArgGlyValAlaValSerValLeuAlaPheGly 100
 Db 241 GTGGCCCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGAGAACTGTGCTGCGCTTGGC 300
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnValaPheThrThrSerValArg 120
 Db 301 TTGGCGCTGTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCTTCCAGACCACTGCGCGC 360
 QY 121 SerTyrLeuProAlaThrValThrAspAlaLeuArgGlySerGlyAlaTTPGlyLeuLeu 140
 Db 361 AGCTACCTGCGCAACAGGTGAGCGGACCTGCGGGGAGCGGGGCGTGGGGCTGCTG 420
 QY 141 LeuArgArgValGlyArgAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 421 CTGGCGCGGTGGCGAGCGAGCTGTGCTTCACTGTGCGACGCTGCGGCTTGTG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 481 CTGTGCTCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCGCTTACAGCTGCGGCT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
 Db 541 GCGCACTCAGGCG 600
 QY 201 ArgAlaThrPheHisSerValArgGlyValAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CGGGCGCTGGAACCACTACGTCAGGAGCGCGGGTCCCTGCGCGCTGCGAGCGCGCGGT 660
 QY 221 AlaArgArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db 661 GCGAGAGCGGT 720
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260

Db 721 GCGCTGCG 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 Db 781 AGGAGCGGTGAGCCAGAGGACCGTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 281 GlnAlaThrSerLeuGlnGlyValaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAGGCACTCTTGTGAGGGTGTGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProArgProTTPAspThrPro 320
 Db 901 CGCGAGACCAACG 960
 QY 321 CysProProValTyrAlaGlnThrArgHisPheLeuTyrSerSerGlyAspLysGlnGln 340
 Db 961 TGTCCCGGTGTAGCGGAGACCAAGCACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyValaArgArgLeu 360
 Db 1021 CTGGCGCGCT 1080
 QY 361 ValGlnThrTTPPheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
 Db 1081 GTGAGACCACTTCTGT 1140
 QY 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuGlyValaHis 400
 Db 1141 CGCTGTCCCG 1200
 QY 401 AlaGlnCysProTyrGlyValaLeuLeuTyrHisCysProLeuArgAlaAlaValThr 420
 Db 1201 GCGAGTGTCCCTTCT 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGln 440
 Db 1261 CCAGCAGCGGT 1320
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
 Db 1321 GAGGACACAGACCCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer 480
 Db 1381 GTGTAGCGCTTGT 1440
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysValPheTTPSerLeuGlyLysHis 500
 Db 1441 AGGCAACAGAACCGCGCTTCT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTTPLysMetSerValArgAspCysAlaTTPLeu 520
 Db 1501 GCCAGCTCTCGCTGAGAGCTGAGCTGAGAGTGAAGTGTGCGGGACCTGCGTGAAGAGT 1560
 QY 521 ArgArgSerProGlyValaGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluTie 540
 Db 1561 CGGAGGAGCCAGGGGT 1620
 QY 541 LeuAlaLysPheLeuHisTTPLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 Db 1621 CTGGCCAAAGTCTCTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
 QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
 Db 1681 TTTTATGTCAAGAGACACAGTTTCAAAAGAACAGGCTTTTCTTCTACCGAAGAGTGC 1740
 QY 581 TTPSerLysLeuGlnSerTTPGlyLysArgGlnHisLeuLysArgValGlnLeuArgGln 600
 Db 1741 TGGAGCAAGTTCGAAGCAATTGGAATCAGACAGCACTTGAAAGAGGAGTGTGCGGGAG 1800
 QY 601 LeuSerGlnAlaGlyValaArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620

```

Db 1801 CTGTGGAGCAGAGGCTCAGCGACATCGGAGAACCGCCCTGCTGACGTCACGA 1860
QY LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrVal 640
Db 1861 CTCCTGCTTCATCCCAAGGCTTACCGGCTGCGGCTGATGTGACATGACATGACGTCG 1920
QY 641 G1yAlaArgThrPheArgArgGlyLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1921 GGAGGCAGAAAGCTTCGCGAGAGAAAGAGGCGGACGCTCACCTCGAGGGGAGAAAGCA 1980
QY LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1981 CTGTTACAGGCTGCTCAACATACAGCGGCGCGCGCCGCTCTGAGGCGCTCTG 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTProArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGCTGAGAGATACACAGAGGCTGCGACCTTGCTGTGCTGTGCGGCGCCAG 2100
QY AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
Db 2101 GACCGCGCGCTGAGCTGACTTTGTCAAGGTGGATGTACGGGCGCGTACGACACATC 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyr 740
Db 2161 CCCGAGGACAGGCTCAGGAGGTCAATCGCAGCATCATCAACCCGAGAAACGTACTGC 2220
QY 741 ValArgArgTyrAlaValAlaGlnLysAlaIleHisGlyHisValArgLysAlaPheLys 760
Db 2221 GTGCGCTGGATAGCCCTGCTCCAGAAAGCGCCCAATGGGACGTCGCAAGGCTTCAAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2281 ACCCAAGTCTTCACTTACACAGACCTCCAGCGCTACATGACAGATTCGTGGCTCACCTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGlu 800
Db 2341 CAGGAGACCGGCGCGCTGAGGAGTGCCTGTCATGACAGAGCTCTCCCTGAAATGAG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisIleAlaValArgIle 820
Db 2401 GCCAGAGTGGGCTCTTCAACGCTTTCACGCTTATGTGCCACCAACCGCGGCCATC 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGGGGCAATCTCTACCTCAGTCCAGTCCAGGGATCCCGAGGGCTCTCTCCAGCTG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2521 CTCTGAGCTGTGTGCTACCGGCGACATGAGAAACAACCTGTTGCGGGGATTGCGCGGAC 2580
QY 861 GlyLeuLeuLeuValArgLeuValAspAspPheLeuValThrProHisLeuThrHisAla 880
Db 2581 GGGCTGCTCTCTGGTGTGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGGG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2641 AAAAAGCTTCTCAGACACCTGTGTCGAGGTGTCCTGAGATATGCTGCGTGGTGAACCTTG 2700
QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheVal 920
Db 2701 CGGAAGACAGTGTGAATCTTCCCTGTAGAAGACAGAGGCTCGGTGGCAAGGCTTTGTT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTProCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCGCGCCACAGCGCTAATCCCTGAGTGGGCTCTGCTGTGATACCCGAGACCTCG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2821 GAGGTGCAAGACGACATCTCCAGCTATGCCCGGACCTCATCAGACCGACGTCACTTC 2880
QY 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGCGGCTTCAAGGCTGAGAGAACATGCGTGCAGAAACTTTTGGGGTCTTGGCGGCTG 2940

```

```

QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2941 AAGTGTCAAGGCTGTCTTGTGATTTTGACAGTGGAACAGGCTCAGAGCGTGTGACCAAC 3000
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTACAAAGATCTCTCTGCTGAGCGGTACAGTTCATCAGCATGTGTGCTGACGCTCCA 3060
QY 1021 PheHisGlnGlnValTTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3061 TTTTCATCAGCAAGTTTGAAGAACCCCAATTTCCTGCGGTATCTTGAACAGGCGC 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGly 1060
Db 3121 TCCCTCTGCTACTCCATCTGTAAGCCAGAAACGAGGATGCTGCGGGGCGCAAGGCG 3180
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTProLeuCysHisGlnAlaPheLeuLeu 1080
Db 3181 GCCGCGGCGCTCTGCGCTCCAGAGCGGTGACAGTGGCTGTGCCAACACATTCCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3241 AAGCTGACTGACACCGTGTACCTACCTGCTGAGGCTGAGGCTGAGGCGGCGGAGGCG 3300
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3301 ACCGAGCTGAGTGGAGAGCTCCCGGGAGCAGACGTGACTGCTGAGAGGCCGAGCAAC 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3361 CCGGACCTGCTCTCAGACTTCAAGACATCTCGAC 3396
RESULT 7
ABX09963
ID ABX09963 standard; DNA; 3399 BP.
AC ABX09963;
XX
XX 23-JAN-2003 (first entry)
DT
XX
XX Human telomerase reverse transcriptase DNA fragment SEQ ID 28.
DE
XX
XX Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
KW prion; inhibition; human; de.
XX
XX Homo sapiens.
OS
XX
XX DE10100587-C1.
PN
XX
XX 21-NOV-2002.
PD
XX
XX 09-JAN-2001; 2001DE-01000587.
PF
XX
XX 09-JAN-2001; 2001DE-01000587.
PR
XX
XX (RIBO-) RIBOPHARMA AG.
PA
XX
XX Kreutzler R, Limmer S, Rost S, Hadwiger P;
PI
XX
XX WPI; 2002-742209/81.
PT
XX
XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.
PS
XX
XX Disclosure; Page 30-31; 98p; German.
CC This invention describes a novel method for inhibiting expression of a
CC target gene by introducing into the cell that contains the targeted gene at
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
CC structure of not more than 49 consecutive nucleotides (nt), where at
CC least a segment of one strand of the ds structure is complementary with

```

CC the target gene and the cells are treated with interferon before
 CC introduction of dsRNA. The method is used to inhibit expression of
 CC target genes, particularly oncogenes, cytokine genes, Id (not defined)
 CC protein genes, developmental or prion genes, or genes expressed in
 CC pathogenic organisms (particularly plasmoidal) or in viruses or viroids
 CC (pathogenic in humans, animals or plants). Treating the cells with
 CC interferon greatly increases the extent to which dsRNA can inhibit
 CC expression of the target genes, and the effect is even greater when dsRNA
 CC are modified to increase their stability. ABX0936-ABX10075 represent
 CC gene fragments used to illustrate the method of the invention
 CC
 XX
 SQ Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) X ABX09363 (1-3399)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 Db 1 ATGCCGGCGGCTCCCGCTGCCAGCGGTGCGCTCCCTGCTGCCAGCCACTACCGCGAG 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTThrArgLeuValGln 40
 Db 61 GTCTCGCCCTGCGCACGTTCGTGCGCGCTGCGCGCTCCAGCGCGCTGCGCTGCGCGAG 120
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 121 CCGGGGAGCCCGCGGCTTCCCGCGCTGCTGCGCCAGTGCCTGGTGTGCGCTGCG 180
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGluLeu 80
 Db 181 GAGCAGCGCGCGCGCGCGCGCGCGCGCTCTCCGCGCAGGTGTCTGCTGAGAGAGCTG 240
 QY 81 ValAlaArgValLeuGlnArgLeuGlyValArgGlyValAlaValSerValLeuAlaPheGly 100
 Db 241 GTGGCCCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGAGAACCTGTGCGCTTGGG 300
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 Db 301 TTGGCGGTGCTGAGCGGGGCGCGCGGGGCGCGCGCGCGCGCTTCCAGCAGCGGTGCG 360
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
 Db 361 AGCTACCTGCGCCAAACAGGTGACCGAGCCTGCGGGGAGCGGGGCGGTGGGCGTGTG 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 421 CTGGCGCGCGGTGGCGAGAGGTGTCTGCTGCTGCTGCGAGCGGTGCGGCTCTTGTG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 481 CTGGTGGCTCCAGCTCGGCTTCCAGGTGTGGGGCGCGCGGTGACAGCTCGGGGCT 540
 QY 181 AlaThrGlnAlaArgProProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 Db 541 GCCACTAGGCGCGCGCGCGCGCGCGCGCGCGCTAGTGAGACCCGAGAGGCTCTGGAG 600
 QY 201 ArgAlaThrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CCGGCGCTGGAACCTAGCGTCCGAGGAGCGGGGTCCCTTGGCGCTGCGAGCCCGGGT 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db 661 GCGAGGAGGCGCGGGGCGAGTCCAGCGGAAGTCTGCGTGGCCCAAGAGGCCAGCGGT 720
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260

Db 721 GCGCTGCGCTCGAGCCGAGCGGAGCGCGCGCTTGGCGAGGGGTCTTGGGCCCGCGGCG 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 Db 781 AGGAGCGGTGAGCCAGTGAACCGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAAGCACCTCTTTGGAGGGTGGCGCTCTGGCAGCGCCCACTCCCACTCCCTGGGGC 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
 Db 901 CGCCAGACCAACGCT 960
 QY 321 CysProProValTyrAlaGlnThrThrHisPheLeuTyrSerSerGlyAspLysGlnGln 340
 Db 961 TGTCCCCCGGTGTAGCGGAGAGCAAGCACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1021 CTGGCGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
 QY 361 ValGlnThrThrPheLeuGlySerArgProTyrMetProGlyTThrProArgArgLeuPro 380
 Db 1081 GTGGAGACCATCTTCTTGTGGTTCAGGCCCTGTGATGCCAGGAGACTCCCGCAGGTGGCC 1140
 QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 Db 1141 CGCTTGCCTCCAGCGCTACTGCGAATGGCGCCCTGTTCTGGAAGCTGTGGAAACAC 1200
 QY 401 AlaGlnCysProTyrGlyValLeuLeuValThrHisCysProLeuAlaAlaValThr 420
 Db 1201 GCGAGTGCCTCTAGCGGGGTGCTCTCAAGAGCAGCTGCGCGCTCGAGTCCGCTGAC 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
 Db 1261 CCAGAGCGCGGTGTGTGTCCGAGAGAGCCAGAGGCTGTGTGGCGCGCCCGAGAGAG 1320
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 Db 1321 GAGGACACAGACCCCGGTGCTGTGTGCGAGCTGCTCCGACACAGAGCGCCCTGGGAG 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
 Db 1381 GTGTAGCGCTTGT 1440
 QY 481 ArgHisAsnGlnAspArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
 Db 1441 AGGCACAGAGAGCGCGCTTCTTCAAGAACACAGAGAGTCACTTCTTGGGAGAGCAT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaThrLeu 520
 Db 1501 GCCAAGCTCTCGTGTGAGAGGTGACGTGGAAGATGAGGTGCGGGAGCTGCCCTTGGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlu 540
 Db 1561 CCGAGAGGCGCGAGGGGT 1620
 QY 541 LeuAlaLysPheLeuHisThrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 Db 1621 CTGGCCAGTCTCTGACCTGAGCTGATGATGTGTGATGCTGCTGAGCTGCTCAGGTCTTTC 1680
 QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
 Db 1681 TTTTATGTACCGAGAGCAAGTTTCAAAAGAACAGGCTCTTTTCTTCAACGGAAGTGTTC 1740
 QY 581 TrpSerLysLeuGlnSerLysLysLysLysLysLysLysLysLysLysLysLysLysLys 600
 Db 1741 TGGAGCAAGTTGCAAGCAATTGGAATCAGACAGCACTTAAAGAGGTGTGAGCTGCGGAG 1800
 QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGTCCGAGAGAGGTCAAGGACATCGGAGAGCCAGGCGCGCTGCTGAGCTGCACA 1860

QY 621 LeuArgPheIleProLySerProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 Db 1861 CTCGGCTTCATCCCAAGCCTGACGGGCTGGCGCATTTGTGAACATGACATCGTCG 1920
 QY 641 GlyAlaArgThrPheArgArgGlyValArgAlaGlyLeuThrSerArgValValVal 660
 Db 1921 GGAGCCAGAACCTTCGCGAGAAAAGAGGGCGGAGCTCTCACTCGAGGCTGAAGGCA 1980
 QY 661 LeuPheSerValLeuAsnTyrGlyValArgAlaArgArgProGlyLeuLeuValValSerVal 680
 Db 1981 CTGTTACAGGTCTCAACTACACAGCGGCGCGCGCTCGGCTCTCTGAGCGCTCTG 2040
 QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGGCTCTGAGATTCACAGGGGCTGGCGGCACTTGTCTGCTGCTGGGCGGCGG 2100
 QY 701 AspProProGlyLeuLeuTyrPheValValValAspValThrGlyValTyrAspThrIle 720
 Db 2101 GACCGCGCGCTGAGCTGACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATC 2160
 QY 721 ProGlnAspArgLeuThrGlyValIleAlaSerIleIleLeuProGlnAsnThrTyrCys 740
 Db 2161 CCCAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAACCCCAAGAACGTAATG 2220
 QY 741 ValArgArgTyrAlaValValGlyValAlaHisGlyHisValArgValAlaPheVal 760
 Db 2221 GTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 Db 2281 AGCCACGTCTCTACCTTACAGACCTCCAGCCGTACATGACAGATTCGTGCTGCTG 2340
 QY 781 GlnGlnThrSerProLeuArgAspAlaValValIleGlnGlnSerSerSerLeuGln 800
 Db 2341 CAGGAGACAGGCGCGGTGAGGATGCGGTGATGACAGAGCTCTCCCTGAAATGAG 2400
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValAlaArgIle 820
 Db 2401 GCCAGCAGTGGCTCTTCACTCTTCTTCACTCTTCACTCTTCACTCTTCACTCTTCA 2460
 QY 821 ArgGlyLySerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db 2461 AGGGGGAAGTCTCTACGTCAGTCCAGGGGATCCGCAAGGCTCCATCTCTTCAAG 2520
 QY 841 LeuGlySerLeuGlyTyrGlyValAspMetGlyAsnValLeuPheAlaGlyIleArgAsp 860
 Db 2521 CTCTGAGCTGTGTGCTACGCGCACATGAGAAACAGCTGTGCGGGGATTCGCGCGG 2580
 QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHisAla 880
 Db 2581 GGGCTGCTCTCTGCTTGTGATGATTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
 QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGlyTyrGlyCysValValAsnLeu 900
 Db 2641 AAAACCTTCTCTACAGACCTGTGTCGAGGTGTCTCGATGATGAGTGGCGGTGAA 2700
 QY 901 ArgLyThrValValAsnPheProValGlyAspGlyAlaLeuGlyGlyThrAlaPheVal 920
 Db 2701 CGGAAGACAGTGTGAATCTTCTCTGTGAAGAAGAGGCTGTGGTGCAAGGCTTTT 2760
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrGlyValLeuLeuLeuAspThrArgThrLeu 940
 Db 2761 CAGATGCGGCGCCACGCTATTCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820
 QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db 2821 GAGGTGACAGGACCTACCTACGCTATGCGGAGCTCTCATACAGACCGATCTCACT 2880
 QY 961 AsnArgGlyPheValAlaGlyArgAsnMetArgArgLyLeuPheGlyValLeuArgLeu 980
 Db 2881 AACCGGCTCTTAAAGGCTGGAGGAAATGCGTGTGCAAACTTTTGGGGCTTTGCGGCT 2940

QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValLysThrAsn 1000
 Db 2941 AAGTGTACAGGCTCTTCTGTGATTTGAGGTAAGGTAACAGCTCTCAACGCTGTGCAACA 3000
 QY 1001 IleTyrIleIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db 3001 ACTTACAAAGATCTCTCTGTGAGGCGTACAGGTTTACGCAATGTGTGTGTGTGTGT 3060
 QY 1021 PheHisGlnGlnValTyrPheAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db 3061 TTTCATCAGCAAGTTTGAAGAAGCCCACTTTTCTCTGCGGTATCTCTGACACGGGC 3120
 QY 1041 SerLeuCysTyrSerIleLeuValAlaValAsnAlaGlyMetSerLeuGlyValValGly 1060
 Db 3121 TCCCTGTGTAATCTCATCTTCACTTCAAGCAAGGAGTGTCTGTGGGCGCAAGGCG 3180
 QY 1061 AlaAlaGlyProLeuProSerGlyAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
 Db 3181 GCCGCGGCGCT 3240
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3241 AAGCTGACTGACACCGGTCTACCTTACGCTTCTGAGGTCACTCTGACAGCCCG 3300
 QY 1101 ThrGlnLeuSerArgLyLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 Db 3301 ACGCAGCTGAGTGGAGAGCTCCCGGGAGAGAGCTGAGCTGCTGTGAGGCGCAGC 3360
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 Db 3361 CCGGCACTGCT 3396

RESULT 8
 ABL91685
 ID ABL91685 standard; DNA; 3399 BP.
 AC ABL91685;
 XX
 DT 28-MAY-2002 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 28.
 XX
 KM Human; HIV; HCV; gene expression; oligonucleotide; tumour; pathogen;
 KM Plasmidum; virus; viroid; cytokine; prion; antisense oligonucleotide;
 KM cytosolic; virotoxin; protozoan; antibacterial; ds.
 OS Homo sapiens.
 XX
 PN DE10100586-Cl.
 XX
 PD 11-APR-2002.
 XX
 PF 09-JAN-2001; 2001DE-01000586.
 XX
 PR 09-JAN-2001; 2001DE-01000586.
 XX
 PA (RIBO-) RIBOPHARMA AG.
 XX
 PI Kreutzler R, Limmer S, Rost S, Hadwiger P;
 DR WPI; 2002-270454/32.
 XX
 PT Inhibiting gene expression in cells, useful for e.g. creating tumors, by
 PT introducing double-stranded complementary oligonucleotide having unpaired
 PT terminal bases.
 PS Claim 13; Page 27-28; 104pp; German.
 CC The invention relates to a method for inhibiting expression of a target
 CC gene (ABL91685-AB91797) in a cell by introducing at least one
 CC oligonucleotide that has a double-stranded structure consisting of at
 CC most 49 sequential nucleotide pairs, with at least part of one strand
 CC complementary with the target gene and has at least one end a single-

CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC antisense inhibition of gene expression useful e.g. for treating tumours
CC but the oligoribonucleotides may also be directed against genes present
CC in pathogen (e.g. plasmidium or viruses/viroids, pathogenic on humans,
CC animals or plants) or against cytokine, id, developmental or prion genes.
CC The method provides more effective inhibition of gene expression than use
CC of known oligonucleotides, probably because the unpaired overhang
CC increases stability and thus intracellular concentration

XX Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) x ABL91685 (1-3399)

```
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATGCGCGCGCTCCCGCTGCGAGCGCTGCTCCCTGCTGCGAGCACTACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheArgLeuValGln 40
DB 61 GTGCTGCGCTGCGAGCTTCTGTCGCGCGCTGCGCGCCCGAGGCTGCGCGCTGTCAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGGCGGAGACCGCGCGCTTCCGCGCTGTCGAGCGCGCTGAGCTGTCGCTGCG 180
QY 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuArgGlnLeu 80
DB 181 GAGCGACGCGCGCGCGCGCGCGCGCGCTTCCGAGGTCGCTGCTGAGAGAGCTG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyValAlaCysValLeuAlaPheGly 100
DB 241 GTGCGCGAGTCTGCTGCGAGGCTGTGTCGCGCGCGCGAGAACGTCGCTTCCGCG 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGCGCGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCTTCCACACGAGCTGCGC 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
DB 361 AGCTACCTGCGCAACGAGTACCGAGCACTGCGGCGAGCGGCGGCTGAGCTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGCGCGCGCTGCGCGAGCGAGCTGTGTCACCTGTCGCGAGCGCTGCTTGTG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGCTGCTCCAGCTGCGCTACAGGTGTGCGCGCGCGCTGTACACGCTGCGGCT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCCACTAGGCGCGCGCGCGCGCGCAACGCTAGTGAACCGCGAGGCTGTGAGATGGAA 600
QY 201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGGCGCTGGAACCACTACGCTGAGGAGCGCGGCTCCCTGCGCTGCGAGCCCGCGCT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCGAGGAGCGCGCGCGCGCGAGTGCAGCGCAAGTCTGCTGCTGCGCAAGAGCGCGCT 720
QY 241 GlyAlaAlaProGlnProGlnArgGlyThrProValGlyGlnGlySerThrAlaHisProGly 260
DB 721 GCGCGCTGCGCTGAGCGAGCGGAGCGCGCTGAGGAGGAGGCTGAGGCGCGCGCGCT 780
```

```
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 AGGACGCGTGAACCGAGTGAACCGTGTGTCGTGAGTGTGCTGACCTGCGAGACCGCGCAA 840
QY 281 GlnAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAAGCGACCTCTTTGAGAGGAGGCTGCTGTCGAGCGCGCACTCCACCGCATCTGAGGCT 900
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProArgProTyrAspThrPro 320
DB 901 CGCGAGACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 960
QY 321 CysProProValTyrAlaGlnThrLysPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 961 TGTCCCGCGGTATGCGCGAGACCAAGCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyValAlaArgArgLeu 360
DB 1021 CTGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
DB 1081 GTGAGACCATCTTCTGTGAGTTCAGGCGCTGATGCGAGGACTCCCGCGAGTTCGCC 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuHis 400
DB 1141 CGCTGCGCGCGAGCTGCTGCGCAATGCGCGCGCGCTTCTGAGCTGCTGAGAACAC 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCGCAGTGCCTCTACGAGGAGTGTCTCTCAAGAGCACTGCGCGCTGAGCTGCGGTCACC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGlnGlu 440
DB 1261 CAGCAGCGCGGTGTCTGTGCGCGAGAGAGCGCGCGCTGTCGCGCGCGCGCGCGCGAG 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1321 GAGGACACAGACCGCGCTGCTGCTGAGCTGCTCCGCGAGCAAGACCGCTGCGCAG 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrGlySer 480
DB 1381 GTGTAGGCTGTGTGAGGCTGCTGCTGCGCGCGCTGAGTGCCTCCAGCGCTCTGAGGCTCC 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheIleSerLeuGlyLysHis 500
DB 1441 AGGCAACAAGAACCGCGCTCTCTCAGAACACCAAGAGTTATCTCCCTGCGGAAAGCAT 1500
QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
DB 1501 GCCAAGCTCTCGCTGAGAGCTGACGTGAGATGACGCTGCGGAGACTGCGCTTGGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlu 540
DB 1561 CGCAGAGCGCGAGGAGTGTGCTGCTCCGCGCGAGACACGCTGTGAGTGAAGAGATC 1620
QY 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
DB 1621 CTGCGCAAGTCTCTGACTGCTGAGTGAATGATGATGATGATGATGATGATGATGATGAT 1680
QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerVal 580
DB 1681 TTTTATGTACGAGAGCACGTTTCAAAGAACAGGCTCTTTTCTAACCGGAAGAGTCTC 1740
QY 581 TyrSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB 1741 TGGAGCAAGTTGCAAGCACTTGTGAACAGCACTTGAAGAGGTTGAGCTGCGGAGG 1800
QY 601 LeuSerGluAlaGlyValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
DB 1801 CTGTGGAAGCAGAGGTACGAGCACTCGGAAAGCAGGCGCGCTGCTGTCAGTCAACA 1860
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
```



```

1861 CTCCCTTCATCCCAAGCCTGACGGGCTGCGCGCATGTGAAACATGACATACGCGTG
1862
1863 G1A1AAGTGTPhenArgArgGluLysArgAlaGluArgLeuThrSerArgAlaLysAla
1864
1865 GAGGCGAAGACCTTCGCGAGAGAAAGAGGCGCGCTCCATCCTCGAGGGGTGAAGGCA
1866
1867 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyValSerVal
1868
1869 CTGTTCAAGGTGCTCACTACAGAGCGGCGCGCGCTCCCTGAGGCCCTCTG
1870
1871 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln
1872
1873 CTGGGCTCGAGCATATCCACAGGCGCTGCGCACCTTGCTGCTGCTGCGGCGCCAG
1874
1875 AspProProGlnLeuTyrPheValLysValAspValThrGlyValArgThrPheIle
1876
1877 GACCGCGCGCTGAGCTGACTTTGTCAAGGTGATGACGCGCGCGCTGACACACCATC
1878
1879 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys
1880
1881 CCCAGAGACAGCTACGAGAGGTATCGCCAGCATCATAAACCCAGAAACAGTACTCC
1882
1883 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys
1884
1885 GTGCGTGGTATGCGGTGATCCAGAAAGCGCGCCCATGCGCACGTCCGCAAGGCTTCAAG
1886
1887 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu
1888
1889 AGCCACGCTCTTCACTTGAACAACCTCCAGCGGTACATGACAGTCTCTGCTCACTCCG
1890
1891 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGln
1892
1893 CAGAGAGACCAAGCCCGCTGAGGATGCCGTCTCATGACAGACAGCTCTCTCTGAATGAG
1894
1895 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle
1896
1897 GCCACAGAGTGCGCTCTTGCAGCGCTTCTTAACGCTTATGTCACACCGCGGCGCATC
1898
1899 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu
1900
1901 AGGGGCAAGTCTTACGTCAGAGGCGAGGCGGATCCCGCAGGGCTCCATCTCTCCACGCTG
1902
1903 LeuCysSerLeuCysTyrGlyValAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp
1904
1905 CTCTGACGCTGTGCTACGCGCAATGAGAAACAGCTTTTGGCGGATTCGCGCGGAC
1906
1907 G1LysLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla
1908
1909 GGGCTGCTCTGCTGTTGGTGAATGATTTCTTGTGGTGAACACTCACTCAACCCACGCG
1910
1911 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu
1912
1913 AAAACCTTCTTCAAGACCTGAGCTGAGGTGTCCTCGATATAGCGCTGAGTGAACCTTG
1914
1915 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal
1916
1917 CGGAAGACAGTGTGAATCTTCTCTGTAAGAGAGAGCCCTGGGTGGCACGCGCTTTGTT
1918
1919 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu
1920
1921 CAGATGCGCGGCCACAGGCTATATCCCTGATGGGCTGCTGCTGATACCCGAGACCTCG
1922
1923 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe
1924
1925 GAGGTGACAGAGCACTACTCCAGCTATGCGCGGACCTTCATAGACCCAGCTTCAACCTTC
1926
1927 AsnArgGlyPheLysValArgLysAsnMetArgArgLysLeuPheGlyValLeuArgLeu
1928
1929 AACCGCGGCTTCAAGGCTGGAGAGAACATGCGTCCGAACCTTTGGGGTCTTGGCGGCTG
1930
1931 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn
1932

```

```

2941 AAGTGTCAAGCCTGTTCTTGATTTGCAAGGTGAACAGCTTCCAGACGGTGTGACCAAC
1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro
3001 ATCTCAAGATCTCTCTGTCAGAGCGGTACAGGTTTACAGATGATGTGCTGACCTCCCA
1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla
3061 TTTCATCAAGCAAGTTTGAAGAACCCCAATTTTTCCTGCGGCTCATCTTCAACCGGCC
1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly
3121 TCCCTCTGTACTCTCATCTTGAAGCAAGCAAGAGGATGTCCCTGGGGCCCAAGGCG
1061 AlaArgLysProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu
3181 GCCGCGGCGCTCTCTCCCTCCAGGCGGTGAGTGCTGTGTCACCAAGCATTTCTGCTC
1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln
3241 AAGCTGACTCGACACCGGTGACCTACAGTGCACCTCTGGGCTCACTCAGAGCAAGCCAG
1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn
3301 ACGCAGCTGAGTGGAGAGCTCCCGGGAGAGACGCTGACTGCTCGAGGCGCCAGCCAAAC
1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp
3361 CCGGCACTGCGCTCAAGACTTCAAGACATCTTGAGC
RESULT 9
ADG90598
ID ADG90598 strand: DNA; 3399 BP.
AC ADG90598;
XX
XX 25-MAR-2004 (first entry)
DT
XX
XX Human TERT gene SEQ ID NO:1.
DE
XX
XX ds; gene; human; immune response; telomerase reverse transcriptase; TERT;
XX cytosolic; immunostimulant; cancer; cytotoxic T cell response.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..3399
XX FT /*tag= a
XX FT /product= "TERT"
XX
XX WO2004002408-A2.
XX
XX 08-JAN-2004.
PD
XX
XX 24-JUN-2003; 2003WO-US019844.
PF
XX 27-JUN-2002; 2002US-0393295P.
PR
XX
XX (GERO-) GERON CORP.
PA
XX
XX Majumdar A, Ferber IA, Frolkis M, Wang Z;
PI
XX
XX WPI: 2004-071946/07.
DR
XX
XX P-PSDB; ADG90599.
XX
XX Eliciting an immune response in a mammal specific for its own telomerase
XX reverse transcriptase (TERT), useful for treating or preventing cancer,
XX comprises administering a composition containing TERT of another
XX mammalian species.
XX
XX Disclosure; SEQ ID NO 1; 44pp; English.
PS
XX
XX The invention relates to a novel method for eliciting an immune response
XX

```

in a mammalian subject that is specific for its own telomerase reverse transcriptase (TERT), comprising administering an immunogenic composition containing a protein with at least 20 consecutive amino acids of TERT of another mammalian species, or a nucleic acid encoding the protein. A composition of the invention has cytotoxic, and immunostimulant activity. The protein or the nucleic acid encoding the protein is useful in the manufacture of a medicament for the treatment of cancer in a human or for eliciting a cytotoxic T cell response in a human.

Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:
 Prod. No.: 2,38e-218 Length: 3399
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 12 Indels: 0
 DB: Gaps: 0

US-10-044-692-2 (1-1132) x ADG90598 (1-3399)

Qy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
 Db 1 ArgCCGCGCGCTCCCGCTCCGACCGCTGCTCCCTGTCGACGACCTACCGCGAG 60
 Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 Db 61 GTGCTGCGCTGGCGCAGCTTGTGCGCGCTGCGCGCGCGCGCGCGCGCGCTGTCAG 120
 Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 121 CGCGCGAGCCCGCGCGCTTTCGCGCGCTGTCGCGCGCGCGCGCGCGCGCTGTCG 180
 Qy 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
 Db 181 GAGCCAGCTG 240
 Qy 81 ValAlaArgValLeuGlnValGluCysGlnArgGlyValAlaValAsnValLeuAlaPheGly 100
 Db 241 GTGCGCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGAGAACTGTGCTGCGCTTCCG 300
 Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 Db 301 TTCGCGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCAACACAGCGTCCG 360
 Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTTPGlyLeuLeu 140
 Db 361 AGCTACCTGCCCAACACAGCTGACCGACCTGCGCGCGAGCGCGCGCGCTGCTG 420
 Qy 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 421 CTGCGCGCGGTGGAGAGAGCTGTGCTTCACTGCTGCGACCTGCGCGCTTTTGTG 480
 Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 481 CTGCGCGCTCCAGCTGCGCTGACAGAGTGTGCGCGCGCGCGCTGTACAGCTGCGCGCT 540
 Qy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
 Db 541 GCCACTCAGCTTGGAGTGGAA 600
 Qy 201 ArgAlaTTPAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CGGCGCTGGACCAATGCGCTCAGAGAGCGCGCGCTCCCTGCGCTGCGCGCGCGCTG 660
 Qy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProValArgProArgArg 240
 Db 661 GGGAGAGAGCTG 720
 Qy 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
 Db 721 GCGCGCTGCGCTGAGCGCGAGCGAGCGCGCTTGGCGAGGAGGCTTGGCGCGCGCGCG 780

Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 Db 781 AGAGCGGTGAGCGAGTGAACCTGCTTCTGTGTGTGTCACTGCGAGCGCGCGCA 840
 Qy 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAAGCCACTCTTGGAGGAGTGGCTCTGCGACCGCGCGCGCGCGCGCGCGCTG 900
 Qy 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTTPAsnThrPro 320
 Db 901 CGCGAGACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 960
 Qy 321 CysProProValTyrAlaGlnThrTyrHisPheLeuTyrSerGlyValAspGlyGln 340
 Db 961 TGTCTCCCGGTGATGCGCGAGACCAAGCACTTCTCTTCACTGCGCGCGCGCGCG 1020
 Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1021 CTGCGCGCTCTCTTCTTCACTGAGCTCTGAGCGCGCGCGCGCGCGCGCTG 1080
 Qy 361 ValGlnThrThrPheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
 Db 1081 GTGAGACCACTTCTTGTGCTTCCAGCGCTGAGATGCGAGGACTCCCGCGAGTTGCCC 1140
 Qy 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuGlyAsnHis 400
 Db 1141 CGCTTGGAGACAC 1200
 Qy 401 AlaGlnCysProTyrGlyValLeuLeuTyrThrHisGlyCysProLeuArgAlaAlaValThr 420
 Db 1201 GCGAGTCCCGCTTGGAGGAGTCTCTCAAGAGGACTGCGCGCGCGCGCGCGCGCTG 1260
 Qy 421 ProAlaAlaGlyValCysAlaArgGlnAspProGlnGlySerValAlaAlaProGlnGlu 440
 Db 1261 CGAGAGCGCGGTCTGTGCGCGGAGAACCGCGAGGCTGTGAGCGCGCGCGCGAG 1320
 Qy 441 GlnAspThrAspProArgArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
 Db 1321 GAGGACACAGACCGCGCGCTGTGTCAGCTGTCCGCGAGACAGAGCGCGCGCGCG 1380
 Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer 480
 Db 1381 GTGTACGGCTTGTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCTTGGAGCTCC 1440
 Qy 481 ArgHisAsnGlnValArgPheLeuArgAsnThrTyrValSerPheLeuGlyValHis 500
 Db 1441 AGGCAACAAGAACCGCGCTTCTCAGAGAACCAAGAACTTCCTCTGAGAGAGAT 1500
 Qy 501 AlaTyrLeuSerLeuGlnGlnLeuThrTTPLeuMetSerValArgAspCysAlaTTPLeu 520
 Db 1501 GCCAAGCTTCTGCTGAGAGCTGACGTGAGAGATGACGTGCGGAGCTGCGCTTGGCTG 1560
 Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisValArgLeuArgGlnGlu 540
 Db 1561 CGAGAGAGCGCGAGGAGTGTGCTGCTGCGCGCGCGAGAGCAACCTCTCGTGAAGAGATC 1620
 Qy 541 LeuAlaTyrPheLeuHisTTPLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 Db 1621 CTGCGCAAGCTTCTGACCTGCGCTGATGAGTGTGAGTGTGAGCTGTGAGCTTTC 1680
 Qy 561 PheTyrValThrGlnThrThrPheGlnTyrAsnAspLeuPhePheTyrArgTyrSerVal 580
 Db 1681 TTTTATGTACGAGAGCAACGCTTCAAAAGAACAGGCTTTTCTACCGGAAAGTGTG 1740
 Qy 581 TTPSerTyrLeuGlnSerIleGlyIleArgGlnHisLeuValArgValGlnLeuArgGlu 600
 Db 1741 TGGAGCAAGTGGAAAGCAATGGATCAGACAGCACTTGAAGAGGCTGACGTGCGGAG 1800
 Qy 601 LeuSerGlnAlaGluValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGTGGAGACCAAGGTCAAGGAGCATGCGAGAGCGCGCGCGCGCTTGTGAGCTGAC 1860
 Qy 621 LeuArgPheThrProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640

This full-length cDNA clone codes for a human telomerase protein 2 (TP2, see AAW61350), a novel protein of the telomerase complex. The sequence was deduced from overlapping partial clones #32 (see AAV27872) and TP2-15 (see AAV27875), which were obtained from a human colon tumour cell line LIM863 CDNA. Expressing TP2 genes in a cell is used to increase telomerase activity and thus proliferation for treatment of e.g. HIV infection, AIDS and ageing disorders, while expressing an inactive mutant of TP2 (or molecule antitense to the gene) is used to decrease telomerase activity, e.g. for treatment of cancer. TP2 polypeptides can also be used to screen for agents that inhibit TP2 activity or its binding to TRP1 (see AAW61347) or telomerase RNA, potentially useful therapeutically, also to raise specific antibodies useful in immunoassays and as diagnostic probes for detecting/quantifying TP2 DNA. Also contemplated are transgenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or they are delivered from engineered cells or gene therapy vectors.
(Updated on 25-MAR-2003 to correct PR field.)

CC Sequence 3798 BP; 613 A; 1311 C; 1212 G; 662 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,63e-218	Length:	3798
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-044-692-2 (1-1132) x AAV27876 (1-3798)

```
QY 1 MetProArgAlaP-0A9GysArgAlaValArgSerLeuArgSerHisTyrArgIn 20
Db 68 ATGCGCGCGCTCCCGCTCCGAGCGCTGCGCTGCTGCGAGCCACTACCGGAG 127
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPAglLeuAlGln 40
Db 128 GTGCGCGCGTGGCGCAGTTCGTGCGCGCTGGGCGCCAGCGGCTGGCGGTGCGAG 187
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 418 CGCGCGGAGCCGCGCGCTTTCGCGCGTGGTGGCCAGTCTGCTGCTGCTGCTGCTG 247
QY 61 AspAlaArgProProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 80
Db 248 GACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
QY 81 ValAlaArgValLeuGlnArgLeuGlnArgGlyAlaArgGlyAlaAlaValAlaPheGly 100
Db 308 GTGCGCGGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGGAGAAAGTGTGCGCTTGGC 367
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
Db 368 TTCGCGCGTGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 427
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTTPGlyLeuLeu 140
Db 428 AGCTACCTGCGCCACACAGGCTGACCGACCTGCGCGGAGACGCGGCGCTGGGCGCTG 487
QY 141 LeuAlaArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 488 CTGCGCGCGGTGGGAGCAGCTGTGCTTACCTGCTGCGACGCTGCGCGCTTCTTGG 547
QY 161 LeuValAlaPheSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 548 CTGCGCGCTCCAGCTGCGCGCTTACAGGTGTGCGGCGCGCGCTTACAGCTGCGCGCT 607
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProProArgArgLeuGlyCysGln 200
Db 608 GCCACGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
QY 201 ArgAlaTTPAsnHisSerValArgGlnArgValProLeuGlyLeuProAlaProGly 220
```

```
Db 668 CGGCGCTGAGACCATATGCGTCAAGGAGCGCGGCGTCCCGCTGGGCG
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProArgIn
Db 728 GCGAGAGAGCGCGGCGGAGTGCACCGCAAGCTCCGCTTGGCCAAAGGCGCCAA
QY 241 GlyAlaAlaProGlnProGlnAlaGlyThrProValGlyGlnGlySerThrAlaHisProGly
Db 788 GCGCGCTCCCGCTTACGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
Db 848 AGAGCGCTGAGCAGGAGTACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 908 GAAACCACTCTTGTGGAGGCGCGCTTCTTGGAGCGCGCGCGCGCGCGCGCGCGCGCG 967
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro 320
Db 968 CGCAGGACCAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1027
QY 321 CysProProValTyrAlaGlyThrLysHisPheLeuTyrSerSerGlyAspGlyGln 340
Db 1028 TGTCCCGCGGTGAGCGCGAGACCAAGCACTTCTTACTTCTTCAAGCGCAAGAGAGAG 1087
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1088 CTGCGCGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1147
QY 361 ValGlnThrIlePheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
Db 1148 GTGAGACCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1207
QY 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuLeuGlyAlaHis 400
Db 1208 CGCTGCCCGCAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1267
QY 401 AlaGlnCysProTyrGlyValLeuLeuSerThrHisCysProLeuAlaValAlaThr 420
Db 1268 GCGAGTCCCGCTTACGAGGAGTGTCTTCAAGACGACTCCCGCTGCGAGCTGGGTAC 1327
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGly 440
Db 1328 CAGGAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1387
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
Db 1388 GAGGACACAGACCGCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1447
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer 480
Db 1448 GTGTACGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1507
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
Db 1508 AGGCACAAAGAGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1567
QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTTPLysMetSerValArgAspCysAlaTTPLeu 520
Db 1568 GCCAACCTCTGCTGAGAGCTGAGCTGAGTGAAGATAGAGCTGGGAGCTGGCTTGGCG 1627
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlyLe 540
Db 1628 CGAGAGAGCCAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1687
QY 541 LeuAlaLysPheLeuHisTTPLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1688 CTGGCCAAAGTCTTCACTGAGTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1748 TTTTATGTACGAGAGCAACAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1807
```

QY 581 TTPSerLysLeuGlnSerIleGlyIleArgGlnIleuLysArgValGlnLeuArgGlu 600
 DB 1808 TGGAGCAAGCTTCAGAAAGCATTTGGATTCAGACAGCATTCAGAGGGTGCAGCTCGCGAG 1867
 QY 601 LeuSerGlnValGlnValArgGlnIleSarGlnValAargProAlaLeuLeuThrSerArg 620
 DB 1868 CTGTGGAGAGCAGAGGTCCAGCATCGGAGAGCCAGGCCCGCTGTGACGTCCAGA 1927
 QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 DB 1928 CTCCCTTCATCCCAAGCCTGACGGCTGCGCGCATTTGTGAACATGACATGACGTCTGG 1987
 QY 641 GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
 DB 1988 GGAGCCAGAACCTTCGCGAGAAAGAGAGGCCGAGCGCTCACTCCGAGGGTGAAGGCA 2047
 QY 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyValAserVal 680
 DB 2048 CTGTTCAAGGTCTCAACTACAGAGCGGCGCGCGCCCTCTGGGCGCTCTGTG 2107
 QY 701 AspProProGlnLeuTyrPheValLysValAspValThrGlyValTyrAspThrIle 720
 DB 2168 GACCCGCGCTGAGCTGTACTTGTCAAGGTGAGATGAGCGGCGCGTACAGACATC 2227
 QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 DB 2228 CCCAGGAGCAGGCTCAGGAGGTCCGCGACATCATCAACCCAGAACAGTACTGC 2287
 QY 741 ValAlaArgGlyTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
 DB 2288 GTGCGCTGGTATGCGGTGTCCAGAAAGCGCCCATGGGCGACGTCCGCAAGGCTTCAAG 2347
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 DB 2348 AGCCACGCTCTCAACTTCAGACAGCTCCAGCCGTACATCGACAGATTCGTGGCTACCTG 2407
 QY 781 GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
 DB 2408 CAGGAGACACAGCCCGGTAGGATGCGGTGCATGACAGACAGCTCCCTCGATATGAG 2467
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 DB 2468 GCCACAGTGGCTCTTCGACGCTTCCTACCTTCATGTGCCACCAACCCGCTGCGCATC 2527
 QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 DB 2528 AGGGGCAAGTCTTACGTCAGAGCCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTG 2587
 QY 841 LeuCysSerLeuCysTyrGlyAspMetGlnAsnLysLeuPheAlaGlyIleArgArgAsp 860
 DB 2588 CTCTCGACGCTGTGCTACGCGGACATGAGAACAGACTTTTTCGGGGATTCGCGCGGAGC 2647
 QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 DB 2648 GGGCTGCTCTCGTGGTGGATGATTTCTTGTGGTGAACCTCACTCAACCCACGCGG 2707
 QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrGlyCysValValAsnLeu 900
 DB 2708 AAAACCTTCTCAGAGCCTCTGATCCAGAGGTGTCCGATATAGCTGCGCTGGGAACCTTG 2767
 QY 901 ArgLysThrValValAsnPheProValGlnAspGlnAlaLeuGlyValYThrAlaPheVal 920
 DB 2768 CGGAAGACAGCTGTGAACCTTCTGTGAAGAAGAGAGGCCCTGGGTGCACGCGTTTGTGTT 2827
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 DB 2828 CAGATGCGCGGCCACAGGCTATTCCTCGGTGTGCGGCTGTGTGATATCCGAGACCTTG 2887

QY 941 GlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 DB 2888 GAGGTGACAGAGGACTATCTCCAGCTATGCCGGACTCCATCATGAGGCCAGTCTCACTTC 2947
 QY 961 AsnArgGlyPheLeuAlaGlyArgAsnMetArgGlyValLeuPheGlyValLeuArgLeu 980
 DB 2948 AACCCGGCTTCMAAGCTGGGAGAAAGCGTCCCAAACTTTTGGGTCTTGGGGCTG 3007
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 DB 3008 AAGTGTCAAGCTTTCTTGTGATTTGAGGTGAAGAGCTTCACAGCGGTGCAAC 3067
 QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 DB 3068 ATCTCAAGATCTCTCTGCTGAGCGGTACAGGTTTCAAGCATGTGTCTGACAGCTCCA 3127
 QY 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 DB 3128 TTTCAATCAGCAAGTTTGGAGAACCCCAATTTCCTGCGGTCAATCTGTACACAGGCGC 3187
 QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
 DB 3188 TCCCTGTCTACTCTCATCTGAAAGCCAGAAACGAGAGATGTCTGTGGGGCCAAAGGGC 3247
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
 DB 3248 GCGCGCGGCTCTCTGCTCCGAGGCCGTGACGTGGTCTGTGCCAACATTCCTGTCTC 3307
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 DB 3308 AAGCTGACTCGACACCGTGTCACTACGTGCCACCTCTGGGGTCACTCAGGACAGCCCG 3367
 QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnValAlaAsn 1120
 DB 3368 ACGCAGCTGAGTGGAGAGCTCCCGGGAGACAGCTGACTGCTGTGAGGCGCGAGCCAA 3427
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 DB 3428 CCGGCACTGCCCTCAGACTTCAGAACATCTCGAGC 3463

RESULT 11
 AAV22379
 ID AAV22379 standard; cDNA; 3955 BP.
 XX
 AC AAV22379;
 DT 13-AUG-1998 (first entry)
 DE Human telomerase reverse transcriptase encoding cDNA.
 XX
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 cell proliferation; cancer; ageing; ribonucleoprotein; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 56..3454
 FT /tag= a
 FT /product= "telomerase reverse transcriptase"
 PN GB2317891-A.
 PD 08-APR-1998.
 XX
 XX 01-OCT-1997; 97GB-00020890.
 XX
 PF 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.

PR 14-AUG-1997; 97US-00915503.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Czech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 DR WPI, 1998-171633/16.
 DR P-PSDB; AAM46957.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 PS Claim 5; Fig 16; 387pp; English.
 XX
 CC The present sequence encodes human telomerase reverse transcriptase
 CC (hTERT), which is a ribonucleoprotein. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein preparation
 CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
 CC protein in a sample by binding a relevant probe to the sample and
 CC detecting the complex formed or in the case of RNA detection, amplifying
 CC the product with presence of hTERT in the sample; and (D) increasing the
 CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
 CC the use of an agent that causes an increase in cell vertebrate cell
 CC proliferation to create a medicament that inhibits ageing. A protein
 CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
 CC the manufacture of medicaments for inhibiting the effect of ageing or
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions
 CC that are associated with high telomerase activity. A protein preparation
 CC of hTERT can also be used in the new methods
 XX
 SQ Sequence 3955 BP; 648 A; 1353 C; 1251 G; 703 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 2.73e-218 Length: 3955
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-044-692-2 (1-1132) x AAV22379 (1-3955)
 QY 1 MetProAlaGAlaProArgCysAlaGAlaValAlaArgSerLeuLeuArgSerHisTyrArgGlu 20
 DB 56 ATGGCGCGGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGCAGCATACCGGAG 115
 QY 21 ValLeuProLeuAlaThrPheValAlaArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
 DB 116 GTGCTGCGCGCTGCGCAGCTTCTGTGCGGCGCTGCGGAGCCCGAGGCTGCGCTGCGAG 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 DB 176 CGGGGAGACCGCGCGCTTCCGCGGCTGTGCGCCAGTGTGCTGTGCTGCTGCTG 235
 QY 61 AspAlaArgProProProAlaAlaPheSerPheArgGlnValSerCysLeuGlyGluLeu 80
 DB 236 GACGACCGGCGCGCGCGCGCGCTTCCGCGCAGGTCTCTGCTGAGGAGCTG 295
 QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaValAsnValLeuAlaPheGly 100
 DB 296 GTGGCCCGAGTGTGAGAGGCTGTGCGAGCGGCGGCGAAGACGTGTGCTTCCG 355
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
 DB 356 TTGGCGCTGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCTTCAACGACGCGTGGC 415

QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
 DB 416 AGCTACTGCTCCCAACAGGTGACCGACATGCGGGGAGCGGGCGCTGGGGCTGCTG 475
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 DB 476 CTGGCGCGCGTGGGCGAGCAGCTGTGCTGTTCACCTGTGACAGCTGCGGCTTGTG 535
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 DB 536 CTGGTGTCTCCAGCTGTGCTGCTTACAGGTGTGCGGGCGCGCTGTACAGCTCGGCGCT 595
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 DB 596 GCCACTAGGCG 655
 QY 201 ArgAlaTyrPheHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB 656 CGGGCTGTGAACCATACATGCTGAGGAGCGGGGCTCCCTGTGAGCTGCGCGCGGCT 715
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB 716 GCGAGAGCGCGGGGCGAGCTGCGACCGCAAGTCTGCTTGGCCCAAGAGCGCGCGCT 775
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
 DB 776 GCGCGTGCCTTGAAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 835
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 DB 836 AGGAGCGCTGACCGAGGACCGGTGTTCTGTGTGTGTCACTTGCAGACCGCGCGGA 895
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 DB 896 GAGGCACTCTTGTGAGAGGTGCGCTCTGTGAGCGCGCACTCCACCACTCCGTGAGC 955
 QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
 DB 956 CGCCAGACACACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1015
 QY 321 CysProProValTyrAlaGlyThrLysHisPheLeuTyrSerSerGlyAspGlyGln 340
 DB 1016 TGTCCCGGTGTACCGGAGCAGACCAATCTCTCACTCCAGGCGAGCAAGAGAGAG 1075
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 DB 1076 CTGGCGCGCTCTCTCACTCACTCACTCTCACTCACTCACTCACTCACTCACTCA 1135
 QY 361 ValGlnThrIlePheLeuGlySerArgProTyrPheCysProGlyThrProArgArgLeuPro 380
 DB 1136 GTGGAGACCATCTTCTGTGAGTTCAGGCGCTGTGATGCCAGGAGCTCCCGCAGGTGCGC 1195
 QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuGlyLysHis 400
 DB 1196 CGCTCTCCCGAGGCTACATGGAAATGCGGCGCTGTGTGTGAGACTGCTGTGGAAACAC 1255
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
 DB 1256 GCCCAGTGCCTTACCGGAGTCTCTCAAGACGACATGCGCGCTGCACTGCGACTGCGTCA 1315
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
 DB 1316 CAGACACCGGTGTCTGTGCGCGGAGAACCCAGAGGCTGTGTGGCGCGCGCGCGAG 1375
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 DB 1376 GAGGACACAGACCCCGCTGCTGTGCGAGCTGCTCCGACAGCAGCGCGCTTGGCAG 1435
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
 DB 1436 GTGTACGCTTGTGAGGCGCTGTGCTGTGCGCGCTGTGCTGTGCGCGCTGTGCGCTCC 1495
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500


```

Db 1496 AGGCACACGAACGCCGCTTCTCAGAAACACCAAGATTATCTCCCTGGGAAAGCAT 1555
Qy 501 AAlaylsleuSerLeuGlnGluLeuThrTrpPlysmetSerValArgAspCysAlaIrrpleu 520
Db 1556 GCCAAGCTCTCGCTCAGAGAGCTGAGAGATGAGGCTGCGGACCTGCGGCTGGGCTG 1615
Qy 521 ArgAspSerProGluValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540
Db 1616 CGCAGAGACCCAGGGGTTGGCTGTGTTCCGAGCCGAGACCCGCTCTGCTGAGAGATC 1675
Qy 541 LeuAlaylsPheLeuHisIrrPleuMetSerValTyrValValGluLeuLeuArgSerPhe 560
Db 1676 CTGGCCAAAGTTCTCTCAGCTGGCTGATGAGTGTGATGCTGCTGAGCTGCTCAAGCTTTTC 1735
Qy 561 PheTyrValThrGlnThrThrPheGlnLysAsnaArgLeuPhePheTyrArgLysSerVal 580
Db 1736 TTTTATGTCAACGAGAACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGAGTGC 1795
Qy 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisIleuLysArgValGlnLeuArgGlu 600
Db 1796 TGGACCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAAGAGGTGCACTGCGGAG 1855
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaIleuLeuThrSerArg 620
Db 1856 CTGTGGAAGACGAGAGTCAAGCATCGGAGATCGGAAAGCCAGGCCGCTGCTGACGTCCAGA 1915
Qy 621 LeuArgPheIleProLysProArgGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db 1916 CTCCCTTCATCTCCCAAGCCTGACGGGCTGCGGCGCATTTGTGAACATGACATACGTCTG 1975
Qy 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1976 GGAGCAGAACCTTCGCAAGAAAGAGGCGGAGCGCTCACTCAGCGGGTGAAGGCA 2035
Qy 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyValAspSerVal 680
Db 2036 CTGTTCAAGGTCTCACTACAGAGCGGGCGCGGCCGCTCTGCGGCCCTCTGTG 2095
Qy 681 LeuGlyLeuAspAspIleHisArgAlaIrrPargThrPheValLeuArgValArgAlaGln 700
Db 2096 CTGGGCTCGAGAGATATCCAGAGGGGCTGGCGCACCTTGCTGTGCTGTGCGGGCCAG 2155
Qy 701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
Db 2156 GACCCGCGCGCTGAGCTGACTTGTGCAAGGTGATGATGACGGGCGCGTACACACCATC 2215
Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db 2216 CCCAGAGACAGGCTCAAGAGGTCTCGCCAGCATATCAAAACCCAGAACACGTRCTGC 2275
Qy 741 ValArgArgTyrAlaValaValaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2276 GTGCTCGGTATGCGGTGGTCCAGAAAGCGGCCCATGGGCACTCGGCAAGGCTTCAAG 2335
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
Db 2336 AGCCACGCTCTTCACTTGAACAACCTCCAGCGGTATGAGCAAGTTCGTGCTCACTG 2395
Qy 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuLeuGln 800
Db 2396 CAGAGAGACAGCCCGCTGAGGAGATGCGCTGCTCATGAGACAGACTCTCTCTGAATGAG 2455
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2456 GCCACACAGTGGCTCTTCAAGCTTCTTAACCTTATGTGCACCAACCCGCTGCGCATC 2515
Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2516 AGGGGCAATCTTCACTTCAAGTGCAGGGGATGCCCAAGGCTCCATCTCTCCACGCTG 2575
Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

```

```

Db 2576 CTCTGACGCTGTGCTTACGGGACATGAGAACAAAGCTTTTCCGGGGATTTCGCGGAC 2635
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisIleuThrHisAla 880
Db 2636 GGGCTGCTCTGCGTTGGTGGATATTTCTGTGTGACACCTCACTCAACCCAGCG 2695
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2696 AAAACCTTCTCAGGACCCCTGGTCCGAGGTGCCCTGTAGTATGCTGGGTGTGAACCTTG 2755
Qy 901 ArgLysThrValAlaAsnPheProValGluAspGluAlaIleuGlyGlyThrAlaPheVal 920
Db 2756 CGGAAGACAGTGTGAACCTTCCCTGTAGAACGAGGCGCTGGGTGGACCGGCTTTTGT 2815
Qy 921 GlnMetProAlaHisGlyLeuPheProThrProCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2816 CAGATGCGGCGCCACAGGCTATTTCCCTGTGCGGCGCTGCTGCTGATACCCGAAACCTTG 2875
Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGACAGAGGACTTACTCCAGCTATGCGGACCTTCATCAGAGCCAGTCTCACTTC 2935
Qy 961 AsnaArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2936 AACCGCGCTTCAAGGCTGGAGAAATGCGCTCCAAACTTTTGGGGCTTTGGCGGCTG 2995
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValaAsnSerLeuGlnThrValLysThrAsn 1000
Db 2996 AAGTGTCAAGCTTCTTCTGTGATTTGACAGGAAACAGCTTCAACAGGTGTGCACCAAC 3055
Qy 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTCAAGATCTCTCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGTGACGTCCCA 3115
Qy 1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTCAACAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGGCTCATCTGACACGCGCC 3175
Qy 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnaAlaGlyMetSerLeuGlyValLysGly 1060
Db 3176 TCCCTCTCTACTCATCTGTAAGCAAGCAAGCAAGGAGTCTCTGGGGCGCAAGGGCC 3235
Qy 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrPLeuCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCGCGCGCGCTCTGCTCCGAGGCGTGCAGTGGCTGTGCCACCAAGATTCCTGCTC 3295
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACCGTGTCACTACGTCACATCTCTGGGTCACTCAGACAGCCAG 3355
Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTCCGAAAGCTCCCGGGAGCAAGAGCTGAGCTGCGCTGAGAGGCCAGCAAC 3415
Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGACGTGCTCTCAGACTTCAAGACCATCTGAGAC 3451

```

RESULT 12
 AA200724
 ID AA200724 strand: DNA; 4015 BP.
 XX
 AC AA200724;
 XX
 DT 06-OCT-1999 (first entry)
 XX
 DE Human telomerase catalytic domain DNA.
 XX
 KW Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
 KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
 KW acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
 KW breast cancer; ss.
 XX

OS Homo sapiens.
 XX DE19804372-A1.
 XX
 XX
 PD 05-AUG-1999.
 XX
 PF 04-FEB-1998: 98DE-01004372.
 XX
 PR 04-FEB-1998: 98DE-01004372.
 XX
 PA (DAHM/) DAHM M W.
 XX
 PI Dahm MW;
 XX
 DR WPI, 1999-431408/37.
 XX
 PT Quantifying tumor cells by amplifying mRNA encoding the catalytic subunit
 of telomerase.
 XX
 PS Example, Fig 1A-B, 26pp; German.
 XX
 CC This invention describes a novel method for the quantitation of tumor
 CC cells in a body fluid which comprises (1) enrichment or isolation of
 CC tumor cells in the sample, (2) amplification of mRNA from these cells
 CC that encodes the catalytic subunit of telomerase and (3) quantifying the
 CC amount of amplified mRNA. The method is applied to tumor cells derived
 CC from (micro)metastases, e.g. associated with a wide range of tumors such
 CC as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia,
 CC melanoma, pulmonary carcinoma, cancer of colon or breast etc. This
 CC sequence encodes a human telomerase protein catalytic domain
 XX
 SO Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,76e-218 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-044-692-2 (1-1132) x AA200724 (1-4015)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
 DB 56 ATGCGCGCGCTCCCGCTGCGAGCCGCTGCGCTCCTGCTGCGAGCCATACCGGAG 115
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPargLeuValGln 40
 DB 116 GTGCTGCGCTGCGGCACTTGTGCGGCGCTGGGGCCCAAGGCTGGCGGTGTGAG 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValProTyr 60
 DB 176 CGCGGGGACCGCGGCGCTTCCGCGCGCTGGTGGCCAGTGCCTGCTGCTGCTGG 225
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
 DB 236 GACCGACGCGCGCGCGCGCGCGCGCGCTTCTTCCGCAAGGTGTCTTCCGAGAGAGCTG 235
 QY 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyValAlaValAsnValLeuAlaPheGly 100
 DB 296 GTGCGCGGAGTGTGAGAGGCTGTGCGAGGCGCGCGCGCAAGACGTGCTGCGCTTGGC 355
 QY 101 PheAlaLeuLeuArgGlyValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 DB 356 TTCCTGCGCTGTGAGCGGGGCGCGGGGCGCGCGCGCGCGCTTCCACACCAAGGTGTGCGC 415
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATPGLYLeuLeu 140
 DB 416 AGCTACTGCTCCCAACAGGTGACGACGACCTGCGGGGAGAGCGGGGCTGTGGGCTCTG 475
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

DB 476 CTGGCGCGCGTGGGCGAGCAGCTGTGTTCACTGTGGGACGCTGCGGCTTGTG 535
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyValAla 180
 DB 536 CTGGTGGCTCCACCTGCGCTACAGAGTGTGGGCGCGCGCTGTATACAGCTGGGCGCT 595
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGln 200
 DB 596 GCCACTCAGGCGCGCGCGCGCGCGCGCGCGCTAGTGAGACCCGAGAGCGCTGGAGTGCAG 655
 QY 201 ArgAlaTyrPheAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB 656 CGGGCTGTGAACATAGCTGAGGAGGCGCGGGGTCCCTGGGCTGTGCGAGCGCGCGGCT 715
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB 716 GCGAGAGAGCGCGGGGAGAGTGTCCAGCGGAGTCTGCGCTTGTCCAGAGGCGCGAGGCT 775
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrPheAlaHisProGly 260
 DB 776 GCGCTGCGCGCTGAGCGGAGGAGCGCGCGCTGGGAGGGGTCTGGGCGCGCGCGGCT 835
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGln 280
 DB 836 AGGACGCTGTGACCGAGTGCAGCGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
 QY 281 GlnAlaThrSerLeuGlnGlyValLeuSerGlyThrArgHisSerHisProSerValGly 300
 DB 896 GAAAGCACTCTTGTGAAGGTGTGCTTCTGTGACGCGCGCTCCACCACTCGGTGGG 955
 QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrPheThrPro 320
 DB 956 GCGCAGACACAGCGCGGCT 1015
 QY 321 CysProProValTyrAlaGlyThrTyrHisPheLeuTyrSerSerGlyAspLysGlnGln 340
 DB 1016 TGTCCCGCGGTGTACCGCAGACCAAGACCTTCTTACTCTTCTGAGGAGCAGAGAGCAG 1075
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 DB 1076 CTGGCGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1135
 QY 361 ValGluThrTyrPheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
 DB 1136 GTGAGAGACCATCTTCTGCGTTCAGCGCGCTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1195
 QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlyLeuLeuGlyAsnHis 400
 DB 1196 CGCTGTCCCGAGCGCTACTGGCAATGCGGCGCGCTGTCTGTGAGCTGTGGAGACCA 1255
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLeuTyrHisCysProLeuArgAlaAlaValThr 420
 DB 1256 GCGCAGTGCCTTACGCGGGGTGTCTCTCAAGAGCAGCTGCGCGCTGAGCTCGGTGACCC 1315
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGln 440
 DB 1316 CCAGCAGCGCGGT 1375
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 DB 1376 GAGGAGACAGACCCCGT 1435
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgValProProGlyLeuTyrGlySer 480
 DB 1436 GTGTAGCGCTGT 1495
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheHisSerLeuGlyLysHis 500
 DB 1496 AGGCACACAGAACGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1555
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
 DB 1556 GCCAAGCTCTGCTGAGGAGGCTGAGCAGATGAGCGTGTGGGAGCTGTGGCTTGTGCTG 1615

QY 521 ArgArgSerProGlyValGlyCysValProAlaIleAGlnHisArgLeuArgGlnGluIle 540
 DB 1616 CGCAGAGACCCAGGGGTTGGCTGTTCGGCCGCGAGACACCTCTGGGTAGAGAGATC 1675
 QY 541 LeuAlaIysPheLeuHisIleTrieuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 DB 1676 CTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTAAGTCTGTCAGAGCTGCTTCTTC 1735
 QY 561 PheTyrValIleThrGlnThrThrPheGlnIlysaMaArgLeuPhePheTyrArgIlySerVal 580
 DB 1736 TTTTATGTCACGGAACACCGTTTCAAAAGACAGGCTTTTCTTACCGGAAGAGTGTTC 1795
 QY 581 TPSSerIlyLeuGlnSerIleGlyIleArgGlnHisIleuLysArgValGlnLeuArgGln 600
 DB 1796 TGGACCAAGTTCACAAAGCATTTGGATCAGACAGCACTTGAAGGGGTGACGCTCGCGAG 1855
 QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaIleuLeuThrSerArg 620
 DB 1856 CTGTGGAAGCAGAGGTGACGAGCATCGGAAGCCAGGCCCTGCTGACGTCACAG 1915
 QY 621 LeuArgPheIleProIlySerProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 DB 1916 CTCCGCTTCATCCCAAGCCTGACGGGCTGCGCGCATTTGTGAACATGACATCACTGCTG 1975
 QY 641 GlyAlaArgThrPheArgArgGlnIlysaArgIleuArgLeuThrSerArgValIlysaIa 660
 DB 1976 GGAGCCAGAACCTTCGCGAGAAAGAGGGCCGAGCGCTCACTCGAGGGGTGAAGGCA 2035
 QY 661 LeuPheSerValIleuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlnIlysaSerVal 680
 DB 2036 CTGTTCAAGGTGCTCAACTACGAGCGGGGCGCGGCCCTGCGCTGGGGCCCTCTGTGG 2095
 QY 681 LeuGlyIleuAspAspIleHisArgAlaTyrArgThrPheValIleuArgValArgAlaGln 700
 DB 2096 CTGGGCTCGAGACGATATCCAGAGGGCTGGCCGACCTTGTGTGTGTGGGGCCGACG 2155
 QY 701 AspProProGlnLeuTyrPheValIlysaValAspValThrGlyAlaTyrAspThrIle 720
 DB 2156 GACCCGCGGCTGAGCTGTACTTGTTCAGAGTGATGAGCGGGCCGTCACACACCATTC 2215
 QY 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 DB 2216 CCCAGAGACAGGCTCAAGAGGTCACTCCGACATCATCAAAACCAGAACGTCATCTGC 2275
 QY 741 ValAlaArgTyrAlaValAlaGlnIlysaIleAlaHisGlyHisValArgIlysaIlePheIys 760
 DB 2276 GTGCGTGGTATGCGGTGTCCAGAGGCGCGCCCATGGGCACTCGGCAAGGCTTCAAG 2335
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
 DB 2336 AGCCACGTCCTCACTTGAACAACCTCCAGCCGTCATCGAACAGTTCCTGGCTCACTCG 2395
 QY 781 GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
 DB 2396 CAGAGAGACAGGCCCGGTGAGGATGCCGTGTCATCGAACAGAGCTCCTCCCTGATGAG 2455
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 DB 2456 GCCACAGAGTGGCTCTTCAACGCTCTTCACTTCATGTGCACACACCCGCTGCGCATTC 2515
 QY 821 ArgGlyIlySerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrIleu 840
 DB 2516 AGGGGCAAGTCTACGTCACAGTCAGGGGATCCGACAGGGCTCCATCTCTCCACGCTG 2575
 QY 841 LeuCysSerLeuCysTyrGlyAspMetGlnAsnIlysaLeuPheAlaGlyIleArgArgAsp 860
 DB 2576 CTCTGCAAGCTGTGCTAGCGGACAGCATGAGAACAGAGCTTTTGGGGGATTCGGCGGAGC 2635
 QY 861 GlyLeuLeuLeuValAspAspPheLeuValThrProHisIleuThrHisAla 880
 DB 2636 GGGCTGCTCTCGCTGTGGTATGATTTCTTGTGTGTGACACTCACTCACTCCACGCGG 2695

QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrGlyCysValIleAsnLeu 900
 DB 2696 AAAACCTTCCTCAGAGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGGGTGTAACCTTG 2755
 QY 901 ArgIlyThrValIleAsnPheProValGlnAspGlnAlaLeuGlyGlyThrAlaPheVal 920
 DB 2756 CCGAAGACAGGTGTCAACCTTCCTGTAGAACGAGGGCCGTGGGGTGACAGGCTTTTGT 2815
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuAspThrArgThrLeu 940
 DB 2816 CAGATGCGGCCACAGGCTTATTCCTGTGTGCGGCTGTGCTGTGATACCGGACCTTG 2875
 QY 941 GlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 DB 2876 GAGGTGACAGAGGACTTACTCCAGTCATGCGCGGACCTTCATCAGAGCCAGTCTCACTTC 2935
 QY 961 AsnArgGlyPheIlysaIleGlyArgAsnMetArgGlyIleuPheGlyValIleuArgLeu 980
 DB 2936 AACCCGCGCTTCAGGCTGGGAGAACATGCTCCCAAACTTTGGGGTCTTGGCGCTG 2995
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 DB 2996 AAGTGTCAAGCTGTCTTCTGATTTGAGTGAAGTGAACGCTTCAGACGCTGTGCACCAAC 3055
 QY 1001 IleTyrIlyIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValIleuGlnLeuPro 1020
 DB 3056 ACTTACAAAGATCTCTCTGTGACGGCGTACAGGTTTCAACGATGATGTGTCAGAGTCCCA 3115
 QY 1021 PheHisGlnGlnValIlysaAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 DB 3116 TTTTCATCAGCAAGTTTGGAGAACCCCACTTTTCTCGCGGTATCTCTGACACAGGCGC 3175
 QY 1041 SerLeuCysTyrSerIleLeuIlysaIleAsnAlaIlysaAsnAlaGlyMetSerLeuGlyAlaIlyGly 1060
 DB 3176 TCCCTCTGTACTCATCTCTGTAAGCCCAAGAACGAGGATGTCCCTGGGGGCCAAAGGSC 3235
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
 DB 3236 GCGCGCGGCTCTCTGCTCCGAGGCCGTGACGTGGCTGTGCAACAGCATTCCTGCTGC 3295
 QY 1081 LysLeuThrArgHisArgValIleThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 DB 3296 AAGCTGACTCGACACCGGTGTCACTACGTGCCACTCTGGGGTCACTCAGACAGCCGACG 3355
 QY 1101 ThrGlnLeuSerArgIlysaLeuProGlyThrThrIleuThrAlaLeuGlnAlaIleAsn 1120
 DB 3356 AGCAGCTGAGTGGAGAACTCCGGGGAGACGAGCTGACTGCTGGAGGCCGACGCAAC 3415
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 DB 3416 CCGGCACTGCCCTCAGACTTCAAGACATCTCGAAC 3451

RESULT 13
 AA220279
 ID AA220279 standard; cDNA; 4015 BP.
 XX
 AC AA220279;
 XX
 XX 17-JAN-2000 (first entry)
 DT
 XX Human telomerase reverse transcriptase (hTERT) cDNA.
 DE
 XX Telomerase reverse transcriptase; human; hTERT; cell proliferation;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 56..3454
 FT /tag= a
 XX
 PN W09950386-A2.

PD 07-OCT-1999.
 XX 31-MAR-1999; 99WO-US007097.
 PF 31-MAR-1998; 98US-00052864.
 PR 03-AUG-1998; 98US-00128354.
 XX (GERO-) GERON CORP.
 PA Morin GB;
 PI
 XX WPI: 1999-610842/52.
 DR P-PSDB; AA132090.
 XX
 PT New catalytic polypeptide and polynucleotide, useful for increasing
 catalytic activity in a cell.
 PS Disclosure; Fig 2; 24pp; English.
 XX This is the nucleotide sequence of cDNA encoding human telomerase reverse
 transcriptase (hTERT, see AA132090). Human telomerase is a target for
 CC diagnosing and treating diseases relating to cell proliferation and
 CC senescence, such as cancer, or for increasing the proliferative capacity
 CC of a cell. A claimed method for increasing the proliferative capacity of
 CC a vertebrate cell, especially a human or other mammalian cell, involves
 CC introducing into the cell a recombinant hTERT polynucleotide encoding an
 hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-
 CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
 CC claimed method for reducing telomerase activity in a cell involves
 CC introducing a recombinant polynucleotide encoding an hTERT variant having
 CC a deletion of amino acids 192-450, 560-565, 637-660, 748-764 or
 CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT
 CC coding sequence
 XX
 SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,76e-218 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 US-10-044-692-2 (1-1132) x AA20279 (1-4015)
 QY 1 MetProAlaAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
 Db 56 ATGCGCGCGCTCCCGCTGCGAGCGCTGCGCTCTGCTGCGCAGCCACTACCGGAG 115
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 Db 116 GTGCTGCGCGTGGCGCAGTGTGCGGCGCTGAGGCGCCAGGAGCTGCGCTGCGAG 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 176 CGCGGGGAGCCGGCGGCTTTCGCGCGCTGCTGCGCAGTGCCTGAGTGCCTCGG 235
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
 Db 236 GAGCCACGCGCGCGCGCGCGCGCTTTCGCGCAGGAGTGTCTGCTGAGAGACTG 295
 QY 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyAlaLysAsnValLeuAlaPheGly 100
 Db 296 GTGGCCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGGAGAGACGTGTGCTTGGC 355
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 Db 356 TTGCGGCTGTGCGAGCGGCGCGCGCGGCGCGCTTTCACACACAGCGGTGCGC 415
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATTTGGLLeuLeu 140
 Db 416 AGCTACCTGCGCAACACGCTGACGACGCTGCGGGGAGCGGCGGTGTGGGCTGCTG 475

QY 141 LeuArgProValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 476 CTGCGCGCGCGTGGCGAGAGAGTGTCTTCACTTGTGCGACCGCTCTTGTG 535
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 536 CTGGTGGCTTCCACCTGCGCTTACAGAGTGTGCGGCGCGCTGTACAGCTCGCGCT 595
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGln 200
 Db 596 GGCACCTACGCGCGCGCGCGCGCGCTGAGAGAGCGAGAGCGCTTGGAGAGCGGA 655
 QY 201 ArgAlaTyrAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 656 CGGCGCTGGAACATAGCTAGTGAAGAGCGCGGGTCTCCCTGGCGCTGCCAGCCG 715
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db 716 GCGAGAGAGCGCGGGGCGAGTGCAGCGCAGAGTGTGCGCTGCGCAGAGCGCGCT 775
 QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
 Db 776 GCGCTGCGCTGAGCGCGAGCGAGCGCGCTTGGGCGAGGGGTCTTGGCGCCACCG 835
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 Db 836 AGGAGCGCTGGACGAGAGCGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
 QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 896 GAAGCCACTCTTTTGAAGGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
 QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProArgProTyrAspThrPro 320
 Db 956 CGCCAGACACAGCGCGCGCGCGCGCGCGCTTCACTTGTGTGTGTGTGTGTGTGT 1015
 QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGln 340
 Db 1016 TGTCCCGCGGTATGACCGGAGACCAAGCACTTCTCTCTCTCTCTCTCTCTCTCT 1075
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1076 CTGCGCGCT 1135
 QY 361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
 Db 1136 GTGAGACCATCTTCTGTGCTTCCAGGCGCTGTGAGTCCAGGAGACTCCCGCAGT 1195
 QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlnHis 400
 Db 1196 CGCTGCGCGCGAGCTACTGCGCAATGCGCGCGCTGTGTGTGTGTGTGTGTGT 1255
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
 Db 1256 GCGCACTGCGCGCTACGAGGAGTCTCTCAAGAGCACTGCGCGCTCGAGCTCGG 1315
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGln 440
 Db 1316 CAGAGCGCGGT 1375
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 Db 1376 GAGAGACAGACCGCGCTGCTGTGCGAGTGTCTCCGACACAGAGCGCGCTTGG 1435
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
 Db 1436 GTTACGCGCTTGTGCGGCGCTGCTGCGCGCGCTGCTGCGCGCGCTTGGGCTCC 1495
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
 Db 1496 AGGCACACAGAGAGCGCGCTTCTCTCAGAGACACCAAGAGATTATCTCTCTGG 1555

501 AAlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaIleuLeu 520
1556 GCCAAGCTCTGCTGCTGAGAGCTGACGTGGAAGATGAGCTGCGGAGCTGCCCTGGCTG 1615
551 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLe 540
1616 CGCAGAGAGCCCGAGGGGTGGCTGTGTCTCGGCGCAGACACCGTCTGCTGAGGAGATC 1675
541 LeuAlaLysPheLeuHisIleTrpLeuMetSerValIleValValGluLeuLeuArgSerPhe 560
1676 CTGGCCAAAGTCTCTGACTGCGCTGAGAGTGTGACGTGCTGAGCTGCTCAGGCTTTTC 1735
561 PheIleValIleThrGluThrThrPheGlnLysAsnArgLeuPhePheIleArgLysSerVal 580
1736 TTTTATGTCACGGAGACACCGTTTCAAAGAACAGGCTTTTCTACCGGAAGAGTGC 1795
561 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGluLeuArgGlu 600
1796 TGGACCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAAGGGGTGACGCTGCGGAG 1855
601 LeuSerGluAlaGluValArgIleHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
1856 CTGTGGAAGCAGAGGTCAGGAGCATCGGAAAGCCAGGCGCGCTGCTGACGTCCAGA 1915
621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspIleValVal 640
1916 CTCCGCTTCATCCCAAGCTGACGGGCTGCGGCGCATTTGTGAACATGGAACATACGTCTG 1975
641 GlyAlaArgThrPheArgArgGluLysArgAlaGluLysArgLeuThrSerArgValIleVal 660
1976 GGAGCCAGAACCTTCGCGAGAAAAGAGGGCGGAGCGCTCTCAGCTCGAGGGTGAAGGCA 2035
661 LeuPheSerValLeuAsnTrpGluArgAlaArgArgProGlyLeuLeuGluValAsnSerVal 680
2036 CTGTTACGCTCTCACTACCTACGAGCGGCGCGCGCGCGCTCTCTGCGCTCTCTG 2095
681 LeuGlyLeuAspAspIleHisArgAlaIleTrpArgThrPheValLeuArgValArgAlaGln 700
2096 CTGGGCTCTGAGCATTCACAGGGGCTGGCGCACCTTGTCTGTGTGTGGCGGCGCAG 2155
701 AspProProProGluLeuLeuTrpPheValLysValAspValIleThrGlyAlaIleTrpAspThrIle 720
2156 GACCCGCGCGCTGACTGACTGACTTGTCAAGGTGATGTGACGGGCGCGTACACACACATC 2215
721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTrpCys 740
2216 CCCGAGACAGGCTCAGCGAGGTCACTCGCAGCATCATCAAAACCCCAAGAACGTAATGC 2275
741 ValArgArgIleValValGluLysAlaHisGlyHisValArgLysAlaPheLys 760
2276 GTGCTCTGGTATGCCGTGTCCAGAAAGCCGCCCATGGACGTCGCGAAGGCTTCAAG 2335
761 SerHisValSerThrLeuThrAspLeuGlnProIleTrpMetArgGlnPheValAlaHisLeu 780
2336 AGCCACGTCTTACCTTACCAACCTCCAGCCGTACATGACGACAGTTCGTGCTCAACCTG 2395
781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuLeuGlu 800
2396 CAGGAGACACAGCCCGCTGAGGATGCCGTCACTGACAGCAAGCTCTCCCTGATATGAG 2455
801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisIleAlaValArgIle 820
2456 GCCAGCAGTGGGCTCTTGCAGCTCTTCTTACCGTTTATGTGCCACACCCGCTGGCAGTC 2515
821 ArgGlyLysSerTrpValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
2516 AAGGGCAAGTCTCTACGTCAAGTCCAGGAGATCCCGCAGAGGCTCCATCTCTCCACAGCTG 2575
841 LeuCysSerLeuCysTrpGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
2576 CTCTGAGGCTGTGTGCTACGAGCAATGAGAAACAAGCTTTTGGCGGAGATTGGCGGAGAC 2635
861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValIleProHisLeuThrHisAla 880

2636 GGGCTGCTCTGCGTGTGGATGATTTCTGTGGTGAACACTCAGCTCACCCACGCG 2695
881 LysThrPheLeuArgThrLeuValArgGlyValProGluTrpGlyCysValValLeuLeu 900
2696 AAAACCTTCTCAGAGACCTGTGTCGAGGTGTCCCTGAGTATGAGCTGCGGTGTGAACCTG 2755
901 ArgLysThrValIleAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheVal 920
2756 CGGAAGACAGTGTGTAACCTTCTGTAGAAACAGAGCCCTGTGGTGGACAGGCTTTGT 2815
921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940
2816 CAGATGCCGGCCACAGGCTATATCCCTGTGTGCGGCTGCTGCTGATATACCGGACCTG 2875
941 GluValGlnSerAspTrpSerSerTrpAlaArgThrSerIleArgAlaSerLeuThrPhe 960
2876 GAGGTGACAGAGCACTACTCCAGCTATGCCCCGAGCTTCATCAGAGCCAGTCTCACCTTC 2935
961 AsnArgGlyPheLysAlaGlyValArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
2936 AACCCGCTTCAAGGCTGGAGGACATGCGTCCGAACCTTTTGGGGTCTTGGCGCTG 2995
981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
2996 AAGTGTACAGCTCTGTTCTGTGATTTGACAGGTGAACAGCTCCAGACGGTGTGACCAAC 3055
1001 IleTrpLysIleLeuLeuLeuGlnAlaIleTrpPheHisAlaCysValLeuGlnLeuPro 1020
3056 ATCTACAAAGATCTCTCTGTGACGGGTACAGATTTCACGATGTGTGTGACGTCCCA 3115
1021 PheHisGlnGlnValTrpLysAspProThrPhePheLysArgValIleSerAspThrAla 1040
3116 TTTTCATCAGCAGATTGTGAAGAACCCACATTTTCTGTGCGGTATCTTCAACAGGCTC 3175
1041 SerLeuCysTrpSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaArgGly 1060
3176 TCCCTCTGCTACTCATCTGATCCGAACCAAGAACGAGGATGCTCGTGGGCGCAAGGCTC 3235
1061 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
3236 GCCGCGCGCCCTCTCCCTCCGAGGCGGTGACGTGTGTGCAACAGCATTCCTGTCTC 3295
1081 LysLeuThrArgHisArgValThrTrpValProLeuLeuGlySerLeuArgThrAlaGln 1100
3296 AAGCTGACTCGACACGGTCACTTACGTCGCTCTGAGGCTCACTGAGCAGCCAG 3355
1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
3356 ACGCAGCTGAGTCGGAAGCTCCCGGAGACAGACGTGACGTGCCCTGTGAGGCCGACCAAC 3415
1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
3416 CCGGCACTGCCCTCAGACTTCAAGACATCTCGAGC 3451
RESULT 14
AAZ30154
ID AAZ30154 standard; cDNA; 4015 BP.
XX AAZ30154;
AC
XX
XX
DT 26-JAN-2000 (first entry)
XX
XX
DE cDNA encoding a human telomerase reverse transcriptase (TRT).
XX
XX Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease; ss.
XX
XX Homo sapiens.
OS
XX
XX
FH
FT Key Location/Qualifiers
CDS 56..3454

```
/*tag= a
/product= "telomerase reverse transcriptase"
```

W09950392-A1.

07-OCT-1999

30-MAR-1999; 99WO-US006898.

31-MAR-1998; 98US-0112006P.

(GERO-) GERON CORP.

Gaeta FCA;

WPI: 1999-610845/52.

P-PSDB; AAY43621.

Eliciting an in vivo immune response for prevention and treatment of cancers.

Disclosure; Fig 2; 26pp; English.

The present sequence encodes a human telomerase reverse transcriptase (TERT) polypeptide. The protein is used in the method of the invention. The specification describes a method for activating a T lymphocyte, comprising contacting the T lymphocyte with a dendritic cell that expresses a TTR peptide in the context of a MHC class I or MHC class II molecule. The protein causes induction of an in vivo immunological response to telomerase activity. Cancer cells are characterized by expression of endogenous TTR gene and the presence of detectable telomerase activity. Therefore, by eliciting a specific immune response to TTR or to TTR-expressing cells, it is possible to selectively target proliferating cells for immunological destruction. The method is used for eliciting an in vivo immune response to telomerase by activating a T lymphocyte, and is useful for prevention and treatment of cancers and other proliferation diseases/conditions

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	2,76e-218
Score:	4015
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	2
Length:	4015
Matches:	11320
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-044-692-2 (1-1132) X AA230154 (1-4015)

QY	1	MeCProArgAlaProArgCysValnroAlaValArgsserleuAAssertrHsryrArgGlu	20
Db	56	ATGCGCGCGCTCCCGCTGCGCGAGCGGCGCCTCTCTGCGAGCCACTACCGGAG	115
QY	21	ValIleuProIleuAlaThrPheValArgArgIeuGlyProGlnIYTPArgIeuValGln	40
Db	116	GTGCTGCGCTGCGCCAGCTTCGCGCGCCCTCGGGGCCCCAGGGCTGCGCGCTGGTCAG	175
QY	41	ArgGlyAspProAlaAlaPheArgAlaIeuValAlaGlnCysIeuValCysValProTyr	60
Db	176	CGCGGGAGCCCGGGGCTTTCGCGCGCTGAGTGGCCAGTGCCTGAGTGGTGGTCCCTGG	235
QY	61	AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysIeuIysGluIeu	80
Db	236	GACCCACGGCGCGCCCCCGCGCCCTCTTCGCGAGGTCTCTGCTGTAAGAACTG	295
QY	81	ValAlaArgValIeuGlnArgIeuCysGluArgGlyAlaIysAsnValIeuAlaPheGly	100
Db	296	GTGCGCCGAGTGCCTGCAGAGCGTGTGCGAGCGGGGCGAAGAAGCTGCTGGCTTGGCG	355
QY	101	PheAlaIeuIeuAspGlyAlaArgGlyGlyIyrProProGluAlaPheThrThSerValArg	120
Db	356	TTGCGCGTGTGAGCGGGGCGCGCGGGGGCCCCCGAAGCTTACACACAGGCTGCC	415

Oy	121	SetTYLeuPProaSnhrThValThraSpAlaLeuAArgGlySeGlyValATrGlyLeuLeu	140
Db	416	AGCTAaCTGGCCAAACAGGGTGAACGCACTGGCGGGAGAGCGGGGCTGGGGCTGCTG	475
Oy	141	LeuAArgThArgValGlyValAspAspValLeuValAhiSLeuLeuAlaArgCysAlaLeuPheVal	160
Db	476	CTGGGGCGGCTGGGGCCAGACGAGCGTGGTTCAACTGTGGCAAGCGCTGGCGCTCTTTGTG	535
Oy	161	LeuValAlaProSeCySalATyGlnValCySgLyProProLeuThyGlnLeuGlyAla	180
Db	536	CTGTGTGCTCCCAAGCTGGCTGCCTTCAAGAGTGTGGGGCCGCGCTGTACACGCTCGAGCT	595
Oy	181	AlaThrGlnAlaArgProProProhiSAIsSeGlyProArgArgThLeuGlyCysGln	200
Db	596	GCCACTACAGGCGGAGCCCCCGCCACACGCTAAGTGAACCCGAAAGGCGTCTGGAGATGCCAA	655
Oy	201	ArgAlaTrpAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly	220
Db	656	CGGGCGTGGAAACCTACCTACGTCAAGAGAGCGGGAGTCCCCCTGGCTGGCACCCCGAGT	715
Oy	221	AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
Db	716	GCGAGAGAGCGCGGGGGAAGTGCACAGCGCAAGTCTGCTGTCCTGGCCAAAGCGCCAGGCGT	775
Oy	241	GlyAlaAlaProGlnProGlnArgThProValGlyGlnGlySerTrpAlaHisProGly	260
Db	776	GGCGGTGCTCCCTGAAGCCGAGCGGAGCCCGCTTGGGAGAGGGCTCTGGGCGCCACCGGAGC	835
Oy	261	ArgThraArgGlyProSerSerAspArgGlyPheCyValValSerProAlaArgProAlaGln	280
Db	836	AGGAGCGCTGAGCCGAGTGAACCGTGGTTCTGTGTGTGTGTCACTGTCCACACCGCGCA	895
Oy	281	GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
Db	896	GAAAGCACTCTTTTGAAGGGTGGGCTCTGTGGACGCGGCACCTCCACCATCTGTGGGG	955
Oy	301	ArgGlnHisSHIbaGlyProProSerThSerArgProProArgProTrpAspThrPro	320
Db	956	CGCCGACGACACAGCGGGGCCCCCATCCACATCGGGGACACACGCTCTGGACAGGCT	1015
Oy	321	CysProProValTYrAlaGluThThyHisPheLeuTySerSerGlyAspLysGlnGln	340
Db	1016	TGTCCCCCGAGTGTAGCCGACCAACCAACTCTCTACTCTCAGGCGCAAGAGGAG	1075
Oy	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
Db	1076	CTGGCGGCTCTCTTCTCACTCAGGCTCTGTAGGGCCAGCGCTGAATGGCGCTCGAGGCTC	1135
Oy	361	ValGluThrThIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
Db	1136	GTTGGAGAACCATTTCTGTGGTTCAGAGGCCCTGGATGCCAGGAACTCCCGCAGGTTGCC	1195
Oy	381	ArgLeuProGlnArgTYrTYrPGLmMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis	400
Db	1196	CGCTGTCCCAAGCGCTACTGGCAATATGGGCCCCCTGTTCTGAGAGCTGCTTGGAGACAC	1255
Oy	401	AlaGlnCysProTYrGlyValLeuLeuLysThrHisCysProLeuAlaArgAlaAlaValThr	420
Db	1256	GCGCAATGCCCCCTACCGGGGTGCTCTTCAAGAGCACTCCCGCTGGAGCTCGAGTCAAC	1315
Oy	421	ProAlaAlaGlyValCyAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGln	440
Db	1316	CAAGCAGCGGTGTCTGTGCCGGGAGAAAGCCCAAGGCTGTGTGTGGGCCCCCGAGAG	1375
Oy	441	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
Db	1376	GAGGACACAGACCCCGTGTGGCTGGTGAAGCTGCTCCACAGCAACAGACGCCCTGGGAG	1435
Oy	461	ValTYrGlyPheValAlaArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
Db	1436	GTTGTAGCGCTTGTGTGGGAGCTGCTTGGCGCGGCTGTGTGTGCCCAAGGCTCTGGGGGCTCC	1495

481 ArgHisaEngluAArgArgPheLeuArgAsnThrLysPheIleSerLeuGlyLysHis 500
 1496 AGGCAACAGAACGGCGCTTCTCCAGAACACCAAGAACTTATCTCCCTGGGAGAACAT 1555
 501 AAlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
 1556 GCCAAGCTCTCGCTCAGAGAGCTGACGTGGAAGATGAGCGTGGGAGACTGCGCTTGGCTG 1615
 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnIle 540
 1616 CGCAGAGACCCCGAGGAGTGGCTGTGTCTCGCCGAGACACCGTCTGCTAGAGAGATC 1675
 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 1676 CTGGCAAGTCTCTGCTGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTTTC 1735
 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
 1736 TTTTATGTCACGGAGACCGCTTTCAAAAGAACAGGCTTTTCTTCAACGGAAAGATGTC 1795
 581 TrpSerLysLeuGlnSerIleGlyTleArgGlnHisLeuLysArgValGlnLeuArgGln 600
 1796 TGGACCAAGTTGGCAAGCATTTGAAATCAGACAGCACTTGAAAGAGGTGCGCTGGGAG 1855
 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
 1856 CTGTGGAAAGAGAGGTGACGAGCATCGGGAAGCCAGGCGCGCTGCTGCTGCTGCTGCA 1915
 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 1916 CTCCCTTCATCCCAAGGCTGACGGGCTGCGGCGCATTTGTGAACATGTGACATACGCTG 1975
 641 GlnValaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
 1976 GAGGCAAGACCTTCGCGAGAAAGAGGCGCGCTGCTCACCCTGAGGCTGAGAGCA 2035
 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlnValaSerVal 680
 2036 CTGTTCAAGCTCTCACTACAGAGCGGCGCGCGCGCTCTGCTGCTGCTGCTGCTGCTG 2095
 681 LeuGlyLeuAspAspIleHisArgAlaTyrPheArgThrPheValLeuArgValArgAlaGln 700
 2096 CTGGGCTCTGAGATATCCACAGGCGCTGCGCACCTTGTGCTGCTGCTGCTGCTGCTG 2155
 701 AspProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
 2156 GACCGCGCGCTGACCTGATCTTGTTCAGAGTGTGATGTGACGGGCGCTGACACACCATC 2215
 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 2216 CCCAGAGACGGCTCACGGAGGTATCGCCAGCATCATCAACCCAGAACAGCTGCTGC 2275
 741 ValaArgArgTyrAlaValaValaGlnLysAlaAlaHisArgLysValaArgLysAlaPheLys 760
 2276 GTGGCTCGGTATGCGGTGTTCAGAAAGCGCGCCCATGGGCACTCGGCAAGGCTTCAAG 2335
 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 2336 AGCCACGCTCTTACCTTGCACAGACCTCCAGCCGCTACATCGACAGTTCCTGCTCACCTG 2395
 781 GlnGlnThrSerProLeuArgAspAlaValaValIleGlnGlnSerSerSerLeuAnglu 800
 2396 CAGGAGACACCGCCGCTGAGGAGTGCCTGCTCATTCGACAGACTCTCTCCCTGAATGAG 2455
 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValaArgIle 820
 2456 GCCAGCAGTGGCTCTTGCACGCTTCTTACGCTTATGTGCAACACCGCGGCGCATC 2515
 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 2516 AGGGGCAACTCTTACCTTGCACGAGGCGGAGATCCCGCAGAGGCTCTTCTTCCACGCTG 2575
 841 LeuCysSerLeuCysTyrGlyAspMetGlnAsnLysLeuPheAlaGlyIleArgArgAsp 860

2576 CTCTCAGACCTGTGTTACGGGACATGAGAGAACAGCTGTGTGGCGGAGTTGGCGGGAC 2635
 861 GlnLeuLeuLeuArgLeuValaAspAspPheLeuLeuValaThrProHisLeuThrHisAla 880
 2636 GGGCTGCTCTCGCTGTGTGTATGATTTCTTGTGTGAGACCTCCACCTCACCCAGCGG 2695
 881 LysThrPheLeuArgThrLeuValaArgGlyValaProGlnTyrGlyCysValaValaAsnLeu 900
 2696 AAAACCTTCTCAGAACCTTGTGCTGAGGTCTCTGAGTATGCTGCTGCTGCTGCTGCTG 2755
 901 ArgLysThrValaValaAsnPheProValaGlnAspGlnAlaLeuGlyGlyTyrAlaPheVal 920
 2756 CGGAAGACAGGTGTGAATCTCCCTGTGAAGAAGCGAGCGCTGGGTGGACCGGCTTTTGT 2815
 921 GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940
 2816 CAGATGCCGGCCACAGGGCTATTCCCTGTGTGGCGGCTGTGCTGTGATAACCCGAGCCCTG 2875
 941 GlnValaGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 2876 GAGGTGACAGGAGCTTACTCCAGCTATGCGGACCTTCATAGAGCCAGTCTACCTTC 2935
 2936 AACCGGGCTTCAAGCGCTGGAGAGAACATGGCTGCCAACTTTGGGGCTTTCGGGCTG 2995
 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValaLeuArgLeu 980
 981 LysCysHisSerLeuPheLeuAspLeuGlnValaAsnSerLeuGlnThrValaCysThrAsn 1000
 2996 AAGTGTCAAGCTCTTCTGTGATTTGACAGGTGAACAGCTTCCACACCGTGTGCACCAAC 3055
 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValaLeuGlnLeuPro 1020
 3056 ATCTTCAAGATCTCTCTGCTGACGCGTACAGGTTTACAGCATGTGTGTCTGACACTCCA 3115
 1021 PheHisGlnGlnValaTrpLysAspProThrPhePheLeuArgValaIleSerAspThrAla 1040
 3116 TTTTATCAGCAAGATTGGAGAGAACCCACATTTTTCCTGGCGGTATCTGTACACGGGC 3175
 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlnValaLysGly 1060
 3176 TCCCTCTGCTATCTCATCTCTGAAGCCAAAGCAAGAGGATTCCTGTGGGGCCCAAGGGC 3235
 1061 AlaAlaGlyProLeuProSerGlnAlaValaGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
 3236 GCGGCGGGCTCTGCTCTCCAGGCGGTGACGTGCTGTGTGCTGACCAACATTCCTGCTC 3295
 1081 LysLeuThrArgHisArgValaThrTyrValaProLeuLeuGlySerLeuArgThrAlaGln 1100
 3296 AAGTGAATCCGACACCGGTGTCATACGTGCCACTCTGGGGTCACTCAGACAGCCGAG 3355
 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAlaAla 1120
 3356 ACGCAGCTGAGTGGAGAACTCCCGGGGAGAGAGCTGAGTCCCTGTGAGGCCCGCAGCAAC 3415
 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 3416 CCGGCACTGCTCTCAGACTTCAAGACATCTCTGGAC 3451

RESULT 15

AAH45901 strand: DNA; 4015 BP.

AAH45901;

06-SEP-2001 (first entry)

Human hTERT gene.

Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;

detection; beta-region; diagnosis; cancer; de.

Homo sapiens.

```

XX Key Location/Qualifiers
FH exon 1..274
FT /*tag= a
FT /number= 1
FT 275..1628
FT /*tag= b
FT /number= 2
FT 1629..1824
FT /*tag= c
FT /number= 3
FT 1825..2005
FT /*tag= d
FT /number= 4
FT 2006..2185
FT /*tag= e
FT /number= 5
FT 2186..2341
FT /*tag= f
FT /number= 6
FT complement(2309..2325)
FT primer_bind
FT /*tag= g
FT /note= "primer SYC1076 (AAH45902) binding site"
FT complement(2311..2325)
FT primer_bind
FT /*tag= h
FT /note= "primer SYC1118 (AAH45905) binding site"
FT 2342..2437
FT /*tag= i
FT /number= 7
FT complement(2345..2374)
FT misc_binding
FT /*tag= j
FT /bound moiety= "hybridisation probe CS3"
FT /note= "AAH45908"
FT complement(2427..2456)
FT misc_binding
FT /*tag= k
FT /bound moiety= "hybridisation probe CS12"
FT /note= "AAH45906"
FT 2438..2523
FT /*tag= l
FT /number= 8
FT complement(2458..2487)
FT misc_binding
FT /*tag= m
FT /bound moiety= "hybridisation probe CS1"
FT /note= "AAH45907"
FT 2489..2506
FT primer_bind
FT /*tag= n
FT /note= "primer SYC1097 (AAH45904) binding site"
FT 2524..2637
FT /*tag= o
FT /number= 9
FT 2615..2631
FT primer_bind
FT /*tag= p
FT /note= "primer SYC1078 (AAH45903) binding site"
FT 2638..2709
FT /*tag= q
FT /number= 10
FT 2710..2898
FT /*tag= r
FT /number= 11
FT 2899..3025
FT /*tag= s
FT /number= 12
FT 3026..3087
FT /*tag= t
FT /number= 13
FT 3088..3212
FT /*tag= u
FT /number= 14
FT 3213..3350
FT /*tag= v
FT /number= 15
FT 3351..4015
FT /*tag= w

```

```

FT /number= 16
XX EP1108789-A2.
XX 20-JUN-2001.
PD 15-DEC-2000; 2000EP-00127228.
XX 16-DEC-1999; 99US-00465491.
XX (HOF ) HOFFMANN LA ROCHE & CO AG F.
XX Chang SP, Santini CD;
XX WPI; 2001-376930/40.
DR Quantitating expression of mRNA encoding hTERT, the catalytic subunit of
PT telomerase, as an indicator of cancer, by amplifying RNA using primers
PT complementary to hTERT gene sequence and quantitating amplified products.
XX Claim 1; Page 5-7; 29pp; English.
XX The present sequence is that of the hTERT gene encoding the catalytic
CC subunit of the human telomerase, comprising 16 exons, which is useful in
CC a method for quantitating hTERT mRNA. The method is useful for detecting
CC the presence of beta-region (a 182 nucleotide region consisting of exons
CC 7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
CC of cancer. The method provides an accurate measure of telomerase activity
CC by selectively measuring mRNA that encodes an active hTERT protein
XX
XX SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
XX
XX Alignment Scores:
Pred. No.: 2,76e-218 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 4
XX
XX US-10-044-692-2 (1-1132) x AAH45901 (1-4015)
QY 1 MetProAaGAlaPProAaGcYsAaGAlaValaAaGserLeuAaGserHisTyraGlu 20
DB 56 ATGCGCGCGCTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 115
QY 21 ValLeuPProLeuA1aThaPheValaAaGArgLeuGlyProGlnGlyTyraGluValaGln 40
DB 116 GTGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 175
QY 41 ArgGlyAspProA1aAlaPheAaGAlaLeuValaAaGlnCyAaLeuValaCyAaValaProTTP 60
DB 176 CGCGGGGAGCGCGCGCGCTTCCGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 235
QY 61 AspAlaAaGProProProA1aAlaAaProSerPheAaGlnValaSerCyAaLeuGlyGluLeu 80
DB 236 GACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 295
QY 81 ValAlaAaGValLeuGlnAaArgLeuCyAaGlyA1aAaValaAaValaAaPheGly 100
DB 296 GTGGCCCGAGGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 355
QY 101 PheAlaLeuLeuAaSp1yA1aAaGlyGlyProProGlnA1aPheThaThaSerValaArg 120
DB 356 TTGCGCGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
QY 121 SerTyLeuProAaThaValaThaAspAlaAaGlySerGlyA1aAaTTPGlyLeuLeu 140
DB 416 AGCTACCTGCCCAACGCGTGAACGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 475
QY 141 LeuAaGArgValaG1yAaSpAaPValaLeuValaH1sLeuLeuA1aAaGcYsA1aLeuPheVal 160
DB 476 CTGGCGCGCGGTGGGCGACGAGCTGTGCTTCACTGCTGCGACGCTGCCGCGCTTTTG 535

```

QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB CTGGTGGCTCCCAAGCTGCGCTTACCAAGGTGTGCGGGCCGCTGTACCAAGCTGGCGCT 595
QY 181 AlaThrGlnAlaArgProProBroHisaIaSerGlyProArgArgArgLeuGlyCysGlu 200
DB GGCACTCAAGGCCGGCCCCCGCCACACGCTAGTGAGCCCGAAGGGGTGTGGGATCGGA 655
QY 201 ArgAlaTyrPheAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB CGGGCTGTGAACATAGCTCAGGAGAGCGGGGTCTCCCTGTGGCTGTGCACCCCGGGT 715
QY 221 AlaAcGArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB GCGAGAGAGCGCGGGGGAGTGTCCAGCCGAGTCTTCCTTCCCAAGGCCCAAGGCT 775
QY 241 GlyAlaAlaProGluProGluLysArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB GGGCTGTGGCTGTAGCGGAGCGGACGCCGTGGGCAAGGGGTCTGGGCCCAACCGGGG 835
QY 261 ArgThrArgGlyProSerArgArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB AGGACGCGTGACCAAGTACCGTGGTTCGTGTGTGTCACTGTCCAGACCCCGCGAA 895
QY 281 GluAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB GAGGCCACTCTTTGGAGGGTGTGCTCTGTGACCGCCACTCCCAACCATTCGTGGGC 955
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrPheAspThrPro 320
DB CGCCAGCACACACGGGGGCCCCCATTCACATCGCGGCCACCAAGTCTCTGGGACAGGCT 1015
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyLysPylsGln 340
DB TGTCCCCCGGTGTACGCCAGACCAAGCACTTCTCTACTCTCCAGGCCACAAAGAGCAG 1075
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB CTGCGGGCTCTCTCTACTCAAGCTCTCTGAGGCCAGCCCTGATGTGGCCCTGGAGGCTC 1135
QY 361 ValGluThrLysPheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
DB GTGAGACACATCTTCTGGGTTCCAGGCCCTGGATGCCAGGAGCTCCCGCAGGTTGGCC 1195
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB CGCCTGCCCCACCGCTACTGGCAATGCGGCCCTGTCTGTGAGCTGTGGGAAACCAAC 1255
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaThr 420
DB GGGCAGTGTCCCTTACGGGGTGTCTCTCAAGACGACATGCCCCGTGGACCTGGGTCACC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGln 440
DB CCAGCAGCGGGTGTGTGTGCCCCGGGAGAGCCCGAGGCTGTGTGGCGGCCCGCAGAG 1375
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB GAGGACACAGACCCCGTGTGCTGTGCTCCGACAGCTGTCCGACACAGCAGCCCTGGCAG 1435
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB GTGTACGGCTTGTGTGGGGCTGTGCTGCGCGCGCTGTGTCCCCCAGGCTCTGGGGCTCC 1495
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
DB AAGCACAACGAAGCGGCTTCTCCAGGAACCAAGAAATTCATCTCCCTGGGGAAGCAT 1555
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
DB GCGCAGCTCTCGCTGACGAGCTGACGTGGAAGATGACGTGGGAGCTGCGCTGGCTG 1556
1556 GCGAAGCTCTCGCTGACGAGCTGACGTGGAAGATGACGTGGGAGCTGCGCTGGCTG 1615

QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLe 540
DB CGCAGAGACCCAGGGGTTGGGTGTTCGGGCCGACAGACACCGTGTGGTGAAGGAGATC 1616
QY 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValGlnLeuLeuArgSerPhe 560
DB CTGGCCAAAGTCTCTGACCTGAGTGTGATGTGTACGTGTGCAGCTGTCAAGTCTTTC 1676
QY 561 PheTyrValThrGlnThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB TTTATGTACGAGAACCAAGTTTCAAAAGACAGGCTTTTCTTACCGGAAGAGTGT 1736
QY 581 TrpSerLysLeuGlnSerLysGlyLysArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB TGGACCAAGTTTCCAAAGCATTTGGAATCAGACGACTTGAAGAGGTTGACGTGGGGAG 1796
QY 601 LeuSerGluAlaGlnValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
DB CTGTGGAAGCAGAGGTACGAGCATCGGGAAGCCAGGCCCGCTGTGACGTCCAGA 1856
QY 621 LeuArgPheLysProLysProAspGlyLeuArgProLysValAsnMetAspTyrValVal 640
DB TTTTCTTATCTCCCAAGCTGTGACGCGCTGTGGCCGATTTGTGAACATGTGACTACGTG 1916
QY 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
DB GGAAGCCAAAGCTTCCGAGAGAAAGAGGCCAGCGTCTACCTCCAGGGTTGAAGGA 1976
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
DB CTGTTCAAGGTCTCAACTACAGAGCGGCGCGGCCCGCTCGGGCCCTCTGTG 2036
QY 681 LeuGlyLeuAspAspLysHisArgAlaTyrArgThrPheValLeuArgValAlaArgAlaGln 700
DB CTGGGCTGTGAGAAATGCACAGGGCTGTGGCCACTTGTGTGTGTGTGGGGCCAG 2096
QY 701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrLys 720
DB GACCGCGCGCTGAGCTGTACTTGTCAAGGTGTGTGTGACGGGGCGGTACGACACCATC 2156
QY 721 ProGlnAspArgLeuThrGluValLysAlaSerLysLeuLysProGlnAsnThrTyrCys 740
DB CCCGAGACAGGCTACCGAGGGTATCGCCAGCATCATCAAAACCCAGAACAGATCTGC 2216
QY 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
DB GTGCGTGGTATGCGGTGTCCAGAGCGCGCATGGCGACGTCCGCAAGGCTTTCAG 2276
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
DB AGCCAGTCTTCACTTGAACAGCTCCAGCCGTACACACATTCGATTCGTGGCTCACCTG 2336
QY 781 GlnGluThrSerProLeuArgAspAlaValValLysGlnGlnSerSerSerLeuGln 800
DB CAGGAGACAGCCCGCTGAGGATGCCGTGCTGATCGACAGAGCTCTCCCTGAATGAG 2396
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLys 820
DB GGCACAGTGGCTTGTGACGCTTCTTACACCTTCAATGTGCACACACGCGTGGGCATC 2456
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyLeuProGlnGlySerLysLeuSerThrLeu 840
DB AGGGCAGTCTTACGTCAAGTCCAGGGGATCCCGCAGGCTCATCTCTCCAGCTG 2516
QY 841 LeuCysSerLeuCysTyrGlyLysPheMetGluAsnLysLeuPheAlaGlyLysArgArg 860
DB CTCTCAGGCTGTGTGACGGGACATGAGGAACAAGCTTTTGGCGGGATTTGGCGGGAC 2576
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisGluThrHisAla 880
DB GGGCTGTCTTGTGGTGTGATGATTTCTTGTGTGTGACACCTCATCTCAACCGGG 2636
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900

```
Db ||||| 2696 AAAACCTTCCTCAGGACCTCGTGGATGTCCTGATGATGCTGCGTGGTGAATTG 2755
Qy ||||| 901 ArgIysThrValIAsnProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db ||||| 2756 CGGAGACAGTGTGACTTCCTCTGAGAGACGAGGCCCTGGGTGGACCGGCTTTGTT 2815
Qy ||||| 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db ||||| 2816 CAGATCCGAGCCCA CGGCTAATCCCTGCTGCGGCTGCTGCTGATACCGGACCCCTG 2875
Qy ||||| 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db ||||| 2876 GAGGTCAAGCTCACTTCAGCTAAGCCGAGCTTCATCAGACCACTCCTCATTG 2935
Qy ||||| 961 AsnArgGlyPheIysAlaGlyArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu 980
Db ||||| 2936 AACCGCGGCTTCAAGGCTGGAGGAACATGCGCGCAACTCTTGCGGCTTGCGGCTG 2995
Qy ||||| 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db ||||| 2996 AAGTGCACAGCCTGTTCTTGATTTGCAAGTGACAGCTCCAGACGGGTGTGCACCAAC 3055
Qy ||||| 1001 IleTyrIleSerIleLeuLeuLeuGlnAlaIleArgPheHisAlaCysValLeuGlnLeuPro 1020
Db ||||| 3056 ATCTACAGAGATCCCTCGCTGACGGCTACAGATGTTTCAACGATGTGCTGACGCTCCA 3115
Qy ||||| 1021 PheHisGlnGlnValIlePylsAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db ||||| 3116 TTTCATCAGCAAGTTTGAGAGAACCCCACTTTTCTGCGCGCTCATCTCTGACAGGCC 3175
Qy ||||| 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
Db ||||| 3176 TCCCTCGCTACTCCATCTGAAAGCCAGAGACGAGGATGTGCTGGGGGCCAAGGGC 3235
Qy ||||| 1061 AlaAlaGlyProLeuProSerGluAlaValGlnIlePheLeuCysHisGlnAlaPheLeuLeu 1080
Db ||||| 3236 GCCGCCGGCCCTCGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC 3295
Qy ||||| 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db ||||| 3296 AAGCTGACTCGACACCGTGTCACTACAGTGCACCTCTGGGGGTCACTCAGAGACAGCCAG 3355
Qy ||||| 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db ||||| 3356 ACGCAGCTGAGTCCGAGAGCTCCGGGAGACAGCCTGACTGCTGCCCTGGAGGCCGACCAAC 3415
Qy ||||| 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db ||||| 3416 CCGGCACTGCCCTCAGACTTCAGAGCACTCCTGGAC 3451
```

Search completed: October 28, 2004, 13:10:02

Job time : 1416 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 10:29:52 : Search time 11545 Seconds
(without alignments) 12672.631 Million cell updates/sec

Title: US-10-044-692-1

Perfect score: 4015

Sequence: 1 GCACGCGCTCCCTCCCTGCTGC.....TTTTCACTTTGAAAAA 4015

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1584	39.5	1826	9	AY407349 Homo sapi
2	1308.6	32.6	1584	9	AY407350 Pan trogl
3	911.4	22.7	1835	9	AY407351 Mus muscu
4	806	20.1	925	4	BM453198 AGEMCOURT
5	500.2	12.5	851	5	BU702370 UI-M-FIO-
6	465.4	11.6	468	2	AM270031 x57603. x
7	445	11.1	492	4	BM824748 K-EST0036
8	419	10.4	851	4	BG917907 602820830
9	416	10.4	416	2	AM276315 x11012. x
10	385.8	9.6	389	1	AA281296 zt08902. x
11	381.4	9.5	409	7	CN274427 170005313
12	346.2	8.6	688	7	CN274427 170005313
13	340.4	8.5	649	7	CF531069 UI-M-FYO-
14	322	8.0	599	2	CF531069 UI-M-FYO-
15	317.8	7.9	664	5	BB618671 BB618671
16	305.4	7.6	340	1	BQ258274 NISC_kp11
17	290.8	7.2	614	2	AA811084 ca85c05.8
18	284.4	7.1	315	1	BB651920 BB651920
19	267	6.7	866	2	AA748707 nv02605.8
20	252.2	6.3	715	2	BE371943 601217728
21	249.6	6.2	409	1	BE396925 601250610
22	248.8	6.2	679	1	AA311750 EST182469
23	243.2	6.1	649	2	BE396606 601289077
24	243	6.1	610	2	BE514070 601316575
					BE514188 601316376

25	214	5.3	344	7	CF531258	CF531258 UI-M-FYO-
26	208.6	5.2	779	2	BE268183	BE268183 601125261
27	203.8	5.1	336	6	BY775178	BY775178 BY775178
28	203.2	5.1	343	6	BY783093	BY783093 BY783093
29	200.6	5.0	338	6	BY784804	BY784804 BY784804
30	192.2	4.8	326	5	BY149368	BY149368 BY149368
31	189.2	4.7	753	5	BU452535	BU452535 603767927
32	186.8	4.7	1424	3	CR688161	CR688161 Tetradodon
33	182.6	4.5	347	2	AM244516	AM244516 BR. END06B
34	180.2	4.5	880	5	BU377259	BU377259 603811228
35	167.6	4.2	775	4	BI388013	BI388013 BFL26_002
36	162.4	4.0	703	5	BX868589	BX868589 BX868589
37	155.4	3.9	619	7	CK392784	CK392784 K0850A03-
38	154.8	3.9	696	5	BU139751	BU139751 603134527
39	150.4	3.7	668	6	CA380121	CA380121 659344. NC
40	140	3.5	148	1	A1824948	A1824948 WB04C01.X
41	132	3.3	641	8	A2972318	A2972318 2M0246F07
42	128.8	3.2	875	5	BU122597	BU122597 603148441
43	128	3.2	846	7	CNS05902	CNS05902 AGENCOURT
44	123.8	3.1	813	4	BG198331	BG198331 RST17589
45	116.8	2.9	632	6	CA353864	CA353864 625469 NC

ALIGNMENTS

RESULT 1	AY407349	1826 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY407349				
DEFINITION	Homo sapiens TERT gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY407349				
VERSION	AY407349.1	GI:39763320			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1826)				
AUTHORS	Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civeleto, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1826)				
AUTHORS	Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civeleto, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..1826				
gene	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	<1..>1826				
	/gene="TERT"				
	/locus_tag="HCM2861"				
ORIGIN					
Query Match	39.5%	Score 1584:	DB 9:	Length 1826:	
Best Local Similarity	86.7%	Pred. No. 0:			
Matches 1584:	Conservative	0:	Mismatches 242:	Indels 0:	Gaps 0:
OY	1629	GGATTGCGTGTTCGCGCCGACGACCGCTGCGTGGAGAGATCTCGCAAGTTCC	1688		

Db	1	GGGTTGGCTGGTGGTTCGGGCGGAGAGCAACGTCGTGGGTGAGAGATCCTGGCCAAAGTTC	60
OY	1689	TGCACTGGCTGATGATGTGTGATCGTCGTGAGCTGCTCAGGTCCTTTCTTTATGTCAAG	1748
Db	61	TGCATGGCTCATGTGTGTGTGATCGTCGTGAGCTGCTCAGGTCCTTTCTTTATGTCAAG	120
OY	1749	AGACCAGCTTTCAAAAGAAAGAGGCTCTTTTCTACCGAAGAGTGTGAGAGCAAGTTC	1808
Db	121	AGACCACTTTCAAAAGAAAGAGGCTCTTTTCTACCGAAGAGTGTGTGAGAGCAAGTTC	180
OY	1809	AAAGCATTTGAATCAGACGCACTTTGAAGAGGTGACCTGCGGAGCTGTCCGAAGCAG	1868
Db	181	AAAGCATTTGAATCAGACGCACTTTGAAGAGGTGACCTGCGGAGCTGTCCGAAGCAG	240
OY	1869	AGGTGAGCAGCATGCGGAGCGAGGCGCGCGCTGCTGACGTCACGATCCCGCTTCATCC	1928
Db	241	AGGTGAGCAGCATGCGGAGCGAGGCGCGCGCTGCTGACGTCACGATCCCGCTTCATCC	300
OY	1929	CCAAAGCTGACGGGCTGGCGGCGATTGTGAACATGACCTACGTGCTGGAAGCCAGAAGT	1988
Db	301	CCAAAGCTGACGGGCTGGCGGCGATTGTGAACATGACCTACGTGCTGGAAGCCAGAAGT	360
OY	1989	TCCGCAAGAAAAGAGGGCCGAGGCTCTCACTCGAGGCTGAAGGCACTGTTCAAGCTGC	2048
Db	361	TCCGCAAGAAAAGAGGGCCGAGGCTCTCACTCGAGGCTGAAGGCACTGTTCAAGCTGC	420
OY	2049	TCAACTAGACGGGCGGGCGGCGCCCGGCGCTCTGTGAGGCGCTCTGTGCTGGGCGTGAAG	2108
Db	421	TCAACTAGACGGGCGGGCGGCGCCCGGCGCTCTGTGAGGCGCTCTGTGCTGGGCGTGAAG	480
OY	2109	ATATTCACAGGAGCTTGGCGGCACCTTTCGTGCTGCTGTGCGGAGCCAGGACCCGCGCTG	2168
Db	481	ATATTCACAGGAGCTTGGCGGCACCTTTCGTGCTGCTGTGCGGAGCCAGGACCCGCGCTG	540
OY	2169	AGCTGTACTTGTCAAGAGTGATGTGAAGGAGGGTGAACAACATCCCGAGAGCAGGC	2228
Db	541	AGCTGTACTTGTCAAGAGTGATGTGAAGGAGGGTGAACAACATCCCGAGAGCAGGC	600
OY	2229	TCACGGAGGTCAATCGCAGCATCATCAACCCAGAACACGTAATGCGTGCCTGCGTATG	2288
Db	601	NN	660
OY	2289	CCGTGGTCCAGAAAGCGCGCCCATATGGGCAACGTCCGGAAGCCTTCAAGAGCCACGTCTCA	2348
Db	661	NN	720
OY	2349	CCTTGACAGACCTCCAGCCGCTACATGTCAGACAGATTGCTGCTCACTCGCAGAGACACAGCC	2408
Db	721	CCTTGACAGACCTCCAGCCGCTACATGTCAGACAGATTGCTGCTCACTCGCAGAGACACAGCC	780
OY	2409	CGCTGAGGGATGCGGTCGTCAATCGACAGAGCTCCTCCCTGAATGAGGCCAGCTGACC	2468
Db	781	CGCTGAGGGATGCGGTCGTCAATCGACAGAGCTCCTCCCTGAATGAGGCCAGCTGACC	840
OY	2469	TCTTCGACGTCTCTCACTTCAATGTGCAACAAGCGTGCGATCAAGGGCAAGTCCCT	2528
Db	841	NN	900
OY	2529	ACGTCACAGTCCAGGGAGTCCCGACAGGGCTCATCTCTCCAGCTGCTGACAGCTGT	2588
Db	901	ACGTCACAGTCCAGGGAGTCCCGACAGGGCTCATCTCTCCAGCTGCTGACAGCTGT	960
OY	2589	GCTACGGGACATGAGAAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCTGCTCTGC	2648
Db	961	GCTACGGGACATGAGAAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCTGCTCTGC	1020
OY	2649	GTTTGATGATGATTTCTTTGTGTGACACCTCACTTCACCCAGCGCAAACTTCTCTCA	2708
Db	1021	GTTTGATGATGATTTCTTTGTGTGACACCTCACTTCACCCAGCGCAAACTTCTCTCA	1080
OY	2709	GGACCCCTGGTCCGAGGTCTCCCTGAATATGGCTGCTGTGTGAACCTTGCGGAACAAGTGC	2768
Db	1081	GGACCCCTGGTCCGAGGTCTCCCTGAATATGGCTGCTGTGTGAACCTTGCGGAACAAGTGC	1140

QY	2769	GGAACTTCCCTGTAGAAAGACGAGGCGCCCTGGGTGGCACAGGCTTTTGTTCAGATGCGCGGCC	2822		
Db	1141	TGAATCTTCCCTGTAGAAAGACGAGGCGCCCTGGGTGGCACAGGCTTTTGTTCAGATGCGCGGCC	1200		
QY	2829	AOCGCTTAATTCCTCCGTGTGCGGCGCTGCTGTGATACACCGGACCTCGAGAGTGCAGAGCG	2888		
Db	1201	ACGGGCTTAATTCCTCCGTGTGCGGCGCTGCTGTGATACACCGGACCTCGAGAGTGCAGAGCG	1260		
QY	2889	ACTACTCCAGCTAATGCCCGGACCTTCACATCAGAGCAGATCTCACTTCAACCGCGGCTTCA	2948		
Db	1261	ACTACTCCAGCTAATGCCCGGACCTTCACATCAGAGCAGATCTCACTTCAACCGCGGCTTCA	1320		
QY	2949	AGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGGCTTGGCGGTGAAAGTGCAGAGCC	3008		
Db	1321	AGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGGCTTGGCGGTGAAAGTGCAGAGCC	1380		
QY	3009	TGTTTCTGATTTTGCAGGTGAACAGCCTTCAGACGATGTGACCAACATCTACAGATCC	3068		
Db	1381	TGTTTCTGATTTTGCAGGTGAACAGCCTTCAGACGATGTGACCAACATCTACAGATCC	1440		
QY	3069	TCTTGTCTGCAGGCGGTACAGGTTTACAGCATGTGTGTCTGCAGCTCCCATTTTCATGACAG	3128		
Db	1441	TCTTGTCTGCAGGCGGTACAGGTTTACAGCATGTGTGTCTGCAGCTCCCATTTTCATGACAG	1500		
QY	3129	TTTGGAAAGAACCCGACATTTTTCCTGGGCGGTCACTGTGACAGGGGCGCTCCCTGTCACT	3188		
Db	1501	TTTGGAAAGAACCCGACATTTTTCCTGGGCGGTCACTGTGACAGGGGCGCTCCCTGTCACT	1560		
QY	3189	CCATCTGTAAAGCCACAGAACGACAGGAGATGTGCTGTGGGGGCGCAAGGGCGCGGCCCTC	3248		
Db	1561	CCATCTGTAAAGCCACAGAACGACAGGAGATGTGCTGTGGGGGCGCAAGGGCGCGGCCCTC	1620		
QY	3249	TGCGCTTCGAGGCGCGTGCATGTGGCTGTGTGCCACCAAGATTCTCTGAAGCTGACTGCAC	3308		
Db	1621	TGCGCTTCGAGGCGCGTGCATGTGGCTGTGTGCCACCAAGATTCTCTGAAGCTGACTGCAC	1680		
QY	3309	ACCCTGTACACTACGTCGCACTCCTGGGGGTCACTCAGAGACAGCCACAGCAGCTGAGTC	3368		
Db	1681	ACCCTGTACACTACGTCGCACTCCTGGGGGTCACTCAGAGACAGCCACAGCAGCTGAGTC	1740		
QY	3369	GGAAGCTTCCCGGGGACGACGCTGACTGCTCCCTGAGAGGCGGACGACCAACCCGGCACTGCCT	3428		
Db	1741	GGAAGCTTCCCGGGGACGACGCTGACTGCTCCCTGAGAGGCGGACGACCAACCCGGCACTGCCT	1800		
QY	3429	CAGACTTCAAGAACCATCTCTGCACTGA	3454		
Db	1801	CAGACTTCAAGAACCATCTCTGCACTGA	1826		
RESULT 2					
LOCUS	AY407350	1584 bp	DNA linear GSS 15-DEC-2003		
DEFINITION	Pan troglodytes TERT gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY407350				
VERSION	AY407350.1	GI:39763321			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferrieria,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1584)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,				

QY 3360 AGCTGAGTGGAGAGCTCCCGGGAGACGACGCTGAGCTCCCTGAGAGCGGACCAACCCG 3419
DB 1741 TGCTGTGCGGAGAGCTCCCGAGGGGAGCAATGACATCTTAAGTGTGAGCGACCGCAG 1800
QY 3420 CACTGCGCTCAAGATTCAAGACCATCTCTGACTGA 3454
DB 1801 CCTAAGCAGACATTTTCAGACCATTTTGGACTAA 1835

RESULT 4
BM453198
LOCUS BM453198 925 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840
5', mRNA sequence.
ACCESSION BM453198
VERSION BM453198.1 GI:18502238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 925)
NIH-MGC http://mgi.mgi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bhs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12208 row: P column: 01
High quality sequence scop: 646.
Location/Qualifiers
1..925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5529840"
/issue_type="leiomycosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN
Query Match 20.1%; Score 806; DB 4; Length 925;
Best Local Similarity 99.2%; Pred. No. 1.7e-157;
Matches 821; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 2149 GGGCCGAGACCGCGCTGAGCTGACTTGTTCAGAGTGTGATGACGGGCGGTACGA 2208
DB 2 GGGCCGAGACCGCGCGCTGAGCTGACTTGTTCAGAGTGTGATGACGGGCGGTACGA 61
QY 2209 CACCATCCCCCAGAGACGAGCTCAAGAGTTCATCGCCAGCATCATCAAAACCCAGAAC 2268
DB 62 CACCATCCCCCAGAGACGAGCTCAAGAGTTCATCGCCAGCATCATCAAAACCCAGAAC 121
QY 2269 GATCTGCGTGGTGGTATGCGGTATGCTCCAGAAAGCGCCCATGGGCAAGTCCGCAAGGC 2328
DB 122 GATCTGCGTGGTGGTATGCGGTATGCTCCAGAAAGCGCCCATGGGCAAGTCCGCAAGGC 181
QY 2329 CTTCAAGAGCAGAGTCTTACCTTGAAGACCTCCAGCCGTACATCGCAAGTTCGTGCG 2388
DB 182 CTTCAAGAGCAGAGTCTTACCTTGAAGACCTCCAGCCGTACATCGCAAGTTCGTGCG 241
QY 2389 TCACCTGAGAGACAGCCCGCTGAGGAGATGCGGTGATGAGCAGAGCTCTCTCCCT 2448
DB 242 TCACCTGAGAGACAGCCCGCTGAGGAGATGCGGTGATGAGCAGAGCTCTCTCCCT 301

QY 2449 GAATGAGCCAGACAGTGGAGCTCTTGCAGCTCTTCTTACGCTTCAATGACCAACAGCCGT 2508
DB 302 GAATGAGCCAGACAGTGGAGCTCTTGCAGCTCTTCTTACGCTTCAATGACCAACAGCCGT 361
QY 2509 GCGCATCAGGGGCAAGTCTTCAAGTCCAGTCCAGGGAGATCCCGAGGCTCATCTCTTC 2568
DB 362 GCGCATCAGGGGCAAGTCTTCAAGTCCAGTCCAGGGAGATCCCGAGGCTCATCTCTTC 421
QY 2569 CAGCTGCTCTGACAGCTGTGTAGCGGAGCATGAGAACAGCTGTTGGGGGATTCG 2628
DB 422 CAGCTGCTCTGACAGCTGTGTAGCGGAGCATGAGAACAGCTGTTGGGGGATTCG 481
QY 2629 GCGGAGCGGAGCTCTCTGCTGCTTGTGATGATTTCTTGTGTGACACCTCACTCAG 2688
DB 482 GCGGAGCGGAGCTCTCTGCTGCTTGTGATGATTTCTTGTGTGACACCTCACTCAG 541
QY 2689 CCAGCGGAAACCTTCTCAGAGACCTGTGTCGAGGTCTCTGATGATGCTGCTGTGT 2748
DB 542 CCAGCGGAAACCTTCTCAGAGACCTGTGTCGAGGTCTCTGATGATGCTGCTGTGT 601
QY 2749 GAATCTGCGGAGAGAGTGTGAATCTTCCCTGTAGAACGAGGCGCTGGGTGGACGCGC 2808
DB 602 GAATCTGCGGAGAGAGTGTGAATCTTCCCTGTAGAACGAGGCGCTGGGTGGACGCGC 661
QY 2809 TTTTGTGATGATGCGGCGCCAGGCTATTTCCCTGTGCGGCTGTGCTGATATCCCG 2868
DB 662 TTTTGTGATGATGCGGCGCCAGGCTATTTCCCTGTGCGGCTGTGCTGATATCCCG 721
QY 2869 GACCTTGAAGTGCAGAGAGTACTTCAAGTATGCGGAGCTTCATCAGAGCCAGTCT 2928
DB 722 GACCTTGAAGTGCAGAGAGTACTTCAAGTATGCGGAGCTTCATCAGAGCCAGTCT 781
QY 2929 CACCTTCAACCGCGCTTCAA--GGCTGGAGAGAACATGCGTCCGAAA 2974
DB 782 CACCTTCAACCGCGCTTCAAAGGCTGGAGAGAACATGCGTCCGAAA 829

RESULT 5
BU702370
LOCUS BU702370 851 bp mRNA linear EST 15-JUL-2003
DEFINITION UI-M-F10-byx-f-12-0-UI-r1 NIH_BMAP_F10 Mus musculus cDNA clone
IMAGE:6400523 5', mRNA sequence.
ACCESSION BU702370
VERSION BU702370.1 GI:23627105
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 851)
NIH-MGC http://mgi.mgi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bhs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5.
Location/Qualifiers
1..851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6400523"

Db 288 GCCAGCTTTCTCCACACGAGAGCCGGCTTCCACCTCCACATAGGAATAGTCATCCCC 229
 QY 3783 AATATGCGCATTTGTCACACCCCTGCGCCCTCCCTCTTGGCTTCCACACCCACATCCAG 3842
 Db 228 AATATGCGCATTTGTCACACCCCTGCGCCCTCCCTCTTGGCTTCCACACCCACATCCAG 169
 QY 3843 GTGAGAACCCCTGAGAAAGACCCCTGAGAGCTGTGGAAATTTGAGTAGCAACCAAGGTGTGCC 3902
 Db 168 GTGGAGAACCCCTGAGAAAGACCCCTGAGAGCTGTGGAAATTTGAGTAGCAACCAAGGTGTGCC 109
 QY 3903 CTGTACACAGGCGAGAGACCCCTGACACCTGTGATGAGGAGGTCCCTGTGAGTCAATTTGGGAGGA 3962
 Db 108 CTGTACACAGGCGAGAGACCCCTGACACCTGTGATGAGGAGGTCCCTGTGAGTCAATTTGGGAGGA 49
 QY 3963 GGTGCTGTGGAGTAAATATCTGAATATATGATTTTTCAGTTTGA 4010
 Db 48 GGTGCTGTGGAGTAAATATCTGAATATATGATTTTTCAGTTTGA 1

RESULT 7

BM824748 492 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0096335 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-99-E07
 DEFINITION 5', mRNA sequence.
 ACCESSION BM824748
 VERSION BM824748.1 GI:19181161
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 492)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,Y.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

TITLE Genome Research Center
 JOURNAL Korea Research Institute of Bioscience & Biotechnology
 COMMENT 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 99 row: E column: 07
 High quality sequence stop: 492.
 Location/Qualifiers
 1..492
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S22SNUI6n1-99-E07"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-16"
 /lab_host="DH10B"
 /clone_lib="S22SNUI6n1"
 /note="Organ: Stomach; Vector: pT713-Pac; Site 1: EcorI;
 Site 2: NotI; The S22SNUI6 library was constructed as described by
 Soares laboratory and it was constructed as described by
 Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
 Research 6(9): 791-806. RNA was prepared from harvested
 cells of SNU-16 culture. SNU-16 cell was obtained from
 Korean Cell Line Bank (KCLB). SNU-16 was established from
 ascitic fluids of Korean patients by Park J.G. et al.
 (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 11.1%; Score 445; DB 4; Length 492;
 Best Local Similarity 100.0%; Pred. No. 3.7e-82;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2768 GTGAATTCCTCTGTAGAAAGACAGGCGCCGTGGGCACGGCTTTTGTTCAGATGCCGCC 2827
 Db 1 GTGAATTCCTCTGTAGAAAGACAGGCGCCGTGGGCACGGCTTTTGTTCAGATGCCGCC 60
 QY 2828 CACGGCTATTTCCCTGTGGCGGCTGTGTGATATCCCGAGACCCCTGAGGTGACAGAC 2887
 Db 61 CACGGCTATTTCCCTGTGGCGGCTGTGTGATATCCCGAGACCCCTGAGGTGACAGAC 120
 QY 2888 GACTACTCCAGTATAGCCCGGACCTTCATCAGAGCCAGTCTCACTTCAACCGCGGCTTC 2947
 Db 121 GACTACTCCAGTATAGCCCGGACCTTCATCAGAGCCAGTCTCACTTCAACCGCGGCTTC 180
 QY 2948 AAGGCTGGAGGAACATGCGTGCAGAACTTTTGGGGTCTTGCAGGTGAAGTGCACAGC 3007
 Db 181 AAGGCTGGAGGAACATGCGTGCAGAACTTTTGGGGTCTTGCAGGTGAAGTGCACAGC 240
 QY 3008 CTGTTTCTGATTTTGACGTGAACAGCTTCAGACGGTGTGACCAACATCTACAGATC 3067
 Db 241 CTGTTTCTGATTTTGACGTGAACAGCTTCAGACGGTGTGACCAACATCTACAGATC 300
 QY 3068 CTCCTGCTGACAGCGGTACAGGTTTCAACGATGTGTGTGACAGTCCCATTTTATCAGCA 3127
 Db 301 CTCCTGCTGACAGCGGTACAGGTTTCAACGATGTGTGTGACAGTCCCATTTTATCAGCA 360
 QY 3128 GTTTGGAAGACCCCAATTTTCTGCGGCTCATCTGTGACACGGCCCTCCCTGTCTAC 3187
 Db 361 GTTTGGAAGACCCCAATTTTCTGCGGCTCATCTGTGACACGGCCCTCCCTGTCTAC 420
 QY 3188 TCCATCTGAAAGCCAGAACGACGAG 3212
 Db 421 TCCATCTGAAAGCCAGAACGACGAG 445

RESULT 8

BG917907 851 bp mRNA linear EST 05-JUN-2001
 LOCUS 602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
 DEFINITION mRNA sequence.
 ACCESSION BG917907
 VERSION BG917907.1 GI:14298383
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 851)
 NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10903 row: k column: 08
 High quality sequence stop: 753.
 Location/Qualifiers
 1..851

FEATURES

source
 1..851
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4949887"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Mam6"

ORIGIN

/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Query Match 10.4%; Score 419; DB 4; Length 851;
Best Local Similarity 71.9%; Pred. No. 1.1e-76;
Matches 579; Conservative 0; Mismatches 215; Indels 11; Gaps 2;

ORIGIN

2651 TTGGTGGATGATTTCTGTTGTGACACCTCACCCTCACCACCGCAAACTTCTCTCAG 2710
38 TTGTGTGATGACTTCTGTGTGAGGAGCCCTCATTGACCAAGCAAACTTCTCTCAG 97
2711 ACCCTGTCGAGAGTCTCTGTGATGATGCTGCTGTGATGAACTTTGGGAAAGCAGTG 2770
98 ACCCTGTCGAGAGTCTCTGTGATGATGCTGCTGTGATGAACTTTGGGAAAGCAGTG 157
2771 AACCTCCCTAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2830
158 AACCTCCCTAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 217
2831 GAGCTATTTCCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2890
218 TGCCTGTTTCCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 277
2891 TACTCCAGCTATGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2950
278 TACTCCAGCTATGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 337
2951 GCTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3010
338 GCTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 397
3011 TTCTGTGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3070
398 TTCTGTGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 457
3071 CTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3130
458 CTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 517
3131 TGGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3190
518 AGGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 577
3191 ATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3250
578 ATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 627
3251 CCGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3309
628 TCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 687
3310 CCGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3369
688 TTCTGTGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 747
3370 GAAAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3429
748 GAAAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 807
3430 AGAGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3454
808 AGAGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 832

RESULT 9
AM276315 416 bp mRNA linear EST 03-JAN-2000
LOCUS x110b12.x1 NC1_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
DEFINITION mRNA sequence.
ACCESSION AM276315

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AM276315.1 GI:6663345
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 416)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMI, at:
www.bio.lnlnl.gov/brp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 413.
Location/Qualifiers
1. 416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2759711"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/clone_1b="NCI_CGAP_Lu28"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: SalI,
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

ORIGIN

Query Match 10.4%; Score 416; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3594 AGGCTGCAATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3653
416 AGGCTGCAATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
3654 AAGGCTGAGTGTCCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3713
356 AAGGCTGAGTGTCCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 297
3714 CAGCCGAG 3773
296 CAGCCGAG 237
3774 TCCATCCCAAGATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3833
236 TCCATCCCAAGATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 177
3834 ACCATCCAGTGTGAGAGCCTGTGAGAGAGCCTGTGAGAGATTTGGAGTGACCA 3893
176 ACCATCCAGTGTGAGAGCCTGTGAGAGAGCCTGTGAGAGATTTGGAGTGACCA 117
3894 AGGTGTGCTCTGTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3953
116 AGGTGTGCTCTGTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 57
3954 TTGGGGGAG 4009
56 TTGGGGGAG 1

RESULT 10
AA281296 389 bp mRNA linear EST 14-AUG-1997
LOCUS AA281296

DEFINITION	zr08962.1 r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5', mRNA sequence.
ACCESSION	AA281296
VERSION	AA281296.1
KEYWORDS	GI:1924194
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997)
CONTACT	Contact: Robert Stransberg, Ph.D. Email: cgapbs-remail.nih.gov
FEATURES	This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert length: 2187 Std Error: 0.00 Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 385. Location/Qualifiers 1. .389

ORIGIN

	Query Match Best Local Similarity	9.6%; 99.5%;	Score 385.8;	DB 1;	Length 389;	
	Matches 387;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1679	GCCAAAGTTCCTGCACACTGGCTGATGATGATGTGTGTAACGTGCTGCAGCTGCTCAGGCTCTTTCTTT	1738			
Db	1	GCCAAAGTTCCTGCACACTGGCTGATGATGATGTGTGTAACGTGCTGCAGGCTGCTCAGGCTCTTTCTTT	60			
QY	1739	TATGTACGAGAGACCAAGCTTTCCAAAAGAACAGGCTCTTTTTCCTACCGGAAGTGTCTGG	1798			
Db	61	TATGTACGAGAGACCAAGCTTTCCAAAAGAACAGGCTCTTTTTCCTACCGGAAGTGTCTGG	120			
QY	1799	AGCAAGTTGCAGAAAGATTGGAATCGACAGACACTTGAAGAGGGTCACACTCCGGAGCTG	1858			
Db	121	AGCAAGTTGCAGAAAGATTGGAATCGACAGACACTTGAAGAGGGTCACACTCCGGAGCTG	180			
QY	1859	TCGGAAGCAGAGAGTCAAGGCAGCATCGGAGAGCCAGGCCGCTGCTACGCTCAGACTC	1918			
Db	181	TCGGAAGCAGAGAGTCAAGGCAGCATCGGAGAGCCAGGCCGCTGCTACGCTCAGACTC	240			
QY	1919	CGCTTCATCCCCAACCTTGACCGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGA	1978			
Db	241	CGCTTCATCCCCAACCTTGACCGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGA	300			
QY	1979	GCCAAACGTTCCGAGAGAAAAGAGGCCGACGCTCTCACTCGAAGGTTAAAGCACTG	2038			
Db	301	GCCAAACGTTCCGAGAGAAAAGAGGCCGACGCTCTCACTCGAAGGTTAAAGCACTG	360			

Oy	2039	TTTTCAGCTGCTCAACTACGACGGCGCCGC	2067
Dd	361	TTTCAGCTGCTCAACTACGACGGCGCCGC	389
RESULT 11	CN274427	409 bp	mRNA linear EST 16-MAY-2004
LOCUS	CN274427		
DEFINITION	17000531126763 GRN_ES Homo sapiens cDNA 5', mRNA sequence.		
ACCESSION	CN274427		
VERSION	CN274427.1	GI:47290841	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 409)		
JOURNAL	Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W. Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine Genon Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@genon.com Insert Length: 409 Std Error: 0.00.		
COMMENT			
FEATURES			
SOURCE	Location/Qualifiers		
	1..409		

ORIGIN

Query Match	Best Local Match	Similarity	9.5% 99.7%	Score	381.4	DB	7	Length	409
Matches	382	Conservative	0	Mismatches	1	Indels	0	Gaps	0
QY	1	GCAGCGCTCCGCTCCGCTGCGACAGTGGAAACCTTGACCCCGGCGCACCCCGCGATGCC							60
Db	27	GCAGGCGCTGCTCCGCTGCGACAGTGGAAACCTTGACCCCGGCGCACCCCGCGATGCC							86
QY	61	GCGGGCTTCCCGCTGCGGACGCTGCGCTCCCTCTCTGCGACGCCATACCCCGAGTGCCT							120
Db	87	GCGGGCTTCCCGCTGCGGACGCTGCGCTCCCTCTCTGCGACGCCATACCCCGAGTGCCT							146
QY	121	GCCGCTGGCCACGTTTCGTCGACGCGCCGCTGGAGGCCCCAGAGGCTGGGCGCTGGTGCACGCGG							180
Db	147	GCCGCTGGCCACGTTTCGTCGACGCGCCGCTGGAGGCCCCAGAGGCTGGGCGCTGGTGCACGCGG							206
QY	181	GAACCCCGCGGCTTTCGCGCGGCTGATGGCCAGTGCCTGGTGTGCTGCTGGAGGCGC							240
Db	207	GAACCCCGCGGCTTTCGCGCGGCTGATGGCCAGTGCCTGGTGTGCTGCTGGAGGCGC							266
QY	241	ACGGTCCGCCCCCGCGCGCCCTCTCTTCCGCGACAGTGTCTCTGATGAAGAGCTGTGGGC							300
Db	267	ACGGTCCGCCCCCGCGCGCCCTCTCTTCCGCGACAGTGTCTCTGATGAAGAGCTGTGGGC							326
QY	301	CCGAGTGTGCAGAGGCTGTGTCGAGCGCGGCGCGAAGAACGTGTGGCTTCCGCTTCGC							360
Db	327	CCGAGTGTGCAGAGGCTGTGTCGAGCGCGGCGCGAAGAACGTGTGGCTTCCGCTTCGC							386
QY	361	GCTGCTGACCGGAGCCGCGGGG 383							

Db 387 GCTGCTGAGACGGGCGCCGCGGG 409

|||||

RESULT 12
CF531121 688 bp mRNA linear EST 12-SEP-2003
LOCUS UI-M-FYO-CGP-m-21-0-UI-r1 NIH BMAP_FYO Mus musculus cDNA clone
DEFINITION IMAGE:30355988 5', mRNA sequence.

ACCESSION
CF531121
VERSION
CF531121.1 GI:34583085
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 688)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyx-5.
Location/Qualifiers

FEATURES

source

1..688
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355988"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5,dpcc"
/lab_host="DH10B (TI phage resistant)"
/note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 8.6%; Score 346.2; DB 7; Length 688;
Best local similarity 73.9%; Pred. No. 1.7e-61;
Matches 438; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 40 CCGGCGACCCCGCGATGCGCGCGCTCCCGCGCGAGCGCGTCCCGCTGCGG 99
Db 63 CCGGCGCTTGAGCAAAATGACCCCGCGCTCTGTTGCCCGCGGAGGCTCTCTGCTGCG 122
QY 100 CAGCCACTACCGCAGGTGTCTGCGCTGCGCCACCTTGTGCGGCGCTTGCGGCGCCCAAGG 159
Db 123 CAGCCACTACCGCAGGTGTCTGCGCTGCGCCACCTTGTGCGGCGCTTGCGGCGCCCAAGG 182
QY 160 CTGCGCGCTGTGACGCGCGGGAACCGCGCGCTTTCGCGCGCTGTGCGCCCAAGTGCCT 219

Db 183 CAGCGGCTTGTGCAACCCGCGGACCCGAGATCTACCGCACTTTGTTGCCCAATGCCT 242

QY 220 GGATGCGTGCCTTGAGGAGACGACGCGCGCCCGCGCCCTCTCTTCCGCAAGTGTG 279

Db 243 AGTGTGATGACACTGGGGCTCAGACCTCTCACTGCCAAGCTTCTTCCACGAGTGTG 302

QY 280 CTGCGTGAAGAGCTGTGGCGCCGAGTGTGCTGACAGAGCTGTGCGGCGCGGAGAA 339

Db 303 ATCCCTGAAGAGCTGTGGCGCGAGGTTGTGACAGACTCTGCGAGCCCAAGAGAA 362

QY 340 CGTGTGCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTT 399

Db 363 CGTGTGCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTT 422

QY 400 CACCAACAGCGTGCAGCTACCTGCGCCAGACAGCTGACCGACCTGCGGAGAGCGG 459

Db 423 CACTAGTACCGTGCCTTACCTGCGCCAGACCTGACCTGACCTGACCTGACCTG 482

QY 460 GCGTGTGGGCGTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 519

Db 483 TGCATGATGCTACTAGTGTGAGCGAGTGGGCGACGACCTGCTGTCTACCTGCTGCA 542

QY 520 CTGCGCGCTCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 579

Db 543 CTGTGCTCTTATCTTCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 602

QY 580 GTACCAAGCTGCGCGCTGACCTACAGCGCGCGCGCGCGCGCGCGCGCGCGCTAGTGC 632

Db 603 GTCTAACCCCTCATTTCCATCTACAGACGCTCAGCTTACTGCTGCGGCGCC 655

RESULT 13
CF531069 649 bp mRNA linear EST 12-SEP-2003
LOCUS UI-M-FYO-CGP-C-19-0-UI-r1 NIH BMAP_FYO Mus musculus cDNA clone
DEFINITION IMAGE:30355746 5', mRNA sequence.

ACCESSION
CF531069
VERSION
CF531069.1 GI:34583033
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 649)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyx-5.
Location/Qualifiers

FEATURES

source

1..649
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5,dpcc"
/lab_host="DH10B (TI phage resistant)"
/note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose

QY 62 CGCGCTCCCGCTGCGGAGCCGCTGCTCTGCTGCGGAGCCACTACCGCGAGGCTG 121
 DB 121 CGCGCTCTGCTGCTGCGGAGCCGCTGCTCTGCTGCGGAGCCACTACCGCGAGGCTG 180
 QY 122 CGCGCTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 181
 DB 181 CGCGCTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 240
 QY 182 GACCGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 241
 DB 241 GACCGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 300
 QY 242 CGCGCTCCCGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 301
 DB 301 GACCGCTCCGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 360
 QY 302 CGAGCTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 361
 DB 361 AGGCTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 420
 QY 362 CTGCTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 421
 DB 421 CTGCTTAACTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 480
 QY 422 CTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 481
 DB 481 TTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 540
 QY 482 CGCGCTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 539
 DB 541 CGAGCTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 598

RESULT 15
 LOCUS BQ258274 664 bp mRNA linear EST 06-MAY-2002
 DEFINITION NISC kpl1904.g3 Baker mouse embryo e7.5 Mus musculus cDNA clone
 IMAGE:5409222, mRNA sequence.

ACCESSION BQ258274
 VERSION BQ258274.1 GI:20459030
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 664)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bme-remail.nih.gov
 cDNA Library Preparation: J. Baker (Stanford University)
 DNA Sequencing by: The I.M.A.G.E. Consortium/LNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 info@image.lnl.gov
 MGI:1845958

FEATURES
 SOURCE Plate: L1AM12043 row: N column: 7
 Seq primer: SP6 primer.
 Location/Qualifiers

1. 664
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:5409222"
 /tissue_type="embryo, late gastrula"
 /dev_stage="embryo, 7.5 dpc"
 /lab_host="X11-Blue"

/clone_11b="Baker mouse embryo e7.5"
 /note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA
 made by oligo-dt priming. Directionally cloned into
 SalI/NotI sites using the following 5' adaptor:
 5'-TGACCTACCGCTCCG-3'. Size-selected for average insert
 size 1.8-1.9 Kb. Library constructed by J. Baker (Stanford
 University)."

ORIGIN

Query Match 7.9%; Score 317.8; DB 5; Length 664;
 Best Local Similarity 68.3%; Pred. No. 1.4e-55;
 Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;

QY 1108 GCCCAGCTGACTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 1167
 DB 9 GCTTAACTGAGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 68
 QY 1168 GATGCGAGGAGCTCCCGGAGGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 1227
 DB 69 GACATCAGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 128
 QY 1228 CCGTCTTCTGAGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 1287
 DB 129 CCGTCTTCTGAGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 188
 QY 1288 GCACTGCGGAGCCGCTGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGCGAGGCTG 1347
 DB 189 ACATTGCGGAGCTTTCGAGAGCAACCAAGGTGACAGATGCTGCTGCTGCGGAGGAGCC 232
 QY 1348 CCAAGGCTTGTGCGGAGCCGCTGCTGCTGCGGAGGAGGAGCAACAGCCGCTGCTGCTGCTG 1407
 DB 233 -----TGAACACAGAGCCGAGCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 263
 QY 1408 GCTCCGCGAGCAAGAGCCGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTG 1467
 DB 264 GCTCCGCGAGCAAGAGCTGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTG 323
 QY 1468 GCTGCTGCGGAGCCGCTGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTG 1527
 DB 324 GGTGCTG 383
 QY 1528 CAAAGAGTTCATCTCCGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTG 1587
 DB 384 AAAGAGTTCATCTCCGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTGCTG 443
 QY 1588 GATGAGCTGCGGAGCTGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTG 1647
 DB 444 GATGAGAGTATGAGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503
 QY 1648 CGCAGAGCAACGCTGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTGCTG 1707
 DB 504 TGCAGAGCAACGCTGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTGCTGCTG 563
 QY 1708 GTACGCTGCGGAGCTGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTGCTG 1767
 DB 564 ATACGCTGCGGAGCTGCTGCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTGCTGCTG 623
 QY 1768 CAGGCTCTTCTTCTACCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTGCTGCTG 1808
 DB 624 CAGGCTCTTCTTCTACCGGAGGAGTATGAGCTTCTGCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTG 664

RESULT 16
 LOCUS AA811084/c 340 bp mRNA linear EST 19-FEB-1998
 DEFINITION oas5c05.s1 NCI-CCAP GCB1 Homo sapiens cDNA clone IMAGE:1319048.3',
 mRNA sequence.

ACCESSION AA811084
 VERSION AA811084.1 GI:2880695
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLM8748 row: h column: 07
 High quality sequence stop: 639.

FEATURES
 source
 1. 866
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH II"
 /db_xref="taxon:10090"
 /clone="IMAGE:3586614"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 /lab_host="DH10B"
 /note="Organ: lung; Vector: PCMV-SPORT6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt. library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 6.7%; Score 267; DB 2; Length 866;
 Best Local Similarity 75.2%; Pred. No. 6.1e-45;
 Matches 333; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

2466 GCCTCTTGACGCTCTTCTACGCTTCATGTGCACACGCGTGCAGCAGGGCACT 2525
 2 GGCTGTTGACCTTCTTCGCACTTCGTCGTCACAGTGTGTAAGATTGGTGAAGT 61

2526 CCTAGCTCAGTCCAGGAGGAGTCCGCGAGGCTCCATCTCTTCACGCTCTTGAAGC 2585
 62 GGTATACGACAGTCCAGGAGGATCCCAAGGCTCCAGCTTATCCCTGCTCTGACATC 121

2586 TGTGCTACGGGACATGAGAACAGCTGTTGGGGGAGTTGGGGGGGAGCGGGTGTCC 2645
 122 TGTGTTTGAGACATGAGAACAGCTGTTGGGGGAGTTGGGGGGGAGCGGGTGTCC 181

2646 TCGGTTTGGTGAATATTTCTTGTGTGACACCTCACTCAACCCAGCAAAACCTTCC 2705
 182 TACGTTTGTGATGATCTTCTGTTGTGACGCTCACTTGAACCAAGCAAAACCTTCC 241

2706 TCAGACCTCTGTCGAGGTGTCCTGAGTATGCTGCTGTGAACTTGGCGAAGACAG 2765
 242 TCAGACCTCTGTCGAGGTGTCCTGAGTATGCTGCTGTGAACTTGGCGAAGACAG 301

2766 TGTGTAATCTTCCCTGTAAGAACAGAGCCCTGCTGTCGACCGCTTTTGTTCAGATCCCG 2825
 302 TGTGTAATCTTCCCTGTAAGAACAGAGCCCTGCTGTCGACCGCTTTTGTTCAGATCCCG 361

2826 CCAAGGCTATTTCCCTGTCGAGGCTGCTGCTGATACCGGACCTTGAAGTGCAGA 2885
 362 CTCATGCTCTTGTTCCTGTCGAGGCTGCTGCTGATACCGGACCTTGAAGTGTCT 421

2886 GCGACTACTCCAGCTATGCGCG 2908
 422 GTGACTACTCAGGTAAGCAG 444

RESULT 20
 BE396925 715 bp mRNA linear EST 21-JUL-2000
 LOCUS BE396925
 DEFINITION 601290610P1 NIH_MGC_8 Homo sapiens cDNA IMAGE:3621050 5',
 mRNA sequence.

ACCESSION BE396925
 VERSION BE396925.1 GI:9342290
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 JOURNAL 1 (bases 1 to 715)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLM294 row: c column: 03
 High quality sequence stop: 634.

FEATURES
 source
 1. 715
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3621050"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 8"
 /note="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 6.3%; Score 252.2; DB 2; Length 715;
 Best Local Similarity 93.9%; Pred. No. 7.3e-42;
 Matches 307; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

1627 AGGGTGGCTGTCTTCCGGCGGACAGACCGCTCTGCTGAGAGATCTCCCAAGT 1686
 372 AGGGTGGCTGTCTTCCGGCGGACAGACCGCTCTGCTGAGAGATCTCCCAAGT 431

1687 CCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTAGTCTTCTT-TATGTCA 1745
 432 CCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTAGTCTTCTT-TATGTCA 491

1746 CCGAAGCAAGCTTTCAAAAGAACAGGCTTTTCTACCGAAGAGTGTCTGAGCACT 1805
 492 CCGAAGCAAGCTTTCAAAAGAACAGGCTTTTCTACCGAAGAGTGTCTGAGCACT 551

1806 TCGAAGCAAGCTTTCAAAAGAACAGGCTTTTCTACCGAAGAGTGTCTGAGCACT 1864
 552 TCGAAGCAAGCTTTCAAAAGAACAGGCTTTTCTACCGAAGAGTGTCTGAGCACT 611

1865 GCGAGGTGACGACATCGAGG--AAGCGAGCCCGGCTGCTGAGAGTCAAGTCCGCT 1922
 612 GCGAGGTGACGACATCGAGGAAAGCCAGGCTGCTGAGAGTCAAGTCCGCT 668

1923 TCAATCCCAAGCTGACGCGCTGCGGC 1949
 669 TTCATCCCAAGCTGAGGCTGCGGC 695

RESULT 21
 AA311750 409 bp mRNA linear EST 19-APR-1997
 LOCUS AA311750
 DEFINITION EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA

sequence.
 accession AA311750
 version AA311750.1 GI:1964077
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 409)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullmer,R.A., Bult,C.J., Lee,N.H., Kirsnes,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Claydon,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fene,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geochagen,N.S., Glodok,A., Gnehm,C.L., Hanna,W.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,D.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bedaric,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Haefliger,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,D., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl.), 3-174 (1995)
 JOURNAL Nature 377 (6547 Suppl.)
 MEDLINE 96026280
 PUBMED 7566098
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
 Seq primer: M3 Reverse.
 Location/Qualifiers
 1..409
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):158964"
 /db_xref="taxon:9606"
 /cell_type="T-lymphocyte"
 /clone_lib="Jurkat T-cells VI"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
 Query Match 6.2%; Score 249.6; DB 1; Length 409;
 Best Local Similarity 97.7%; Pred. No. 2.3e-41;
 Matches 252; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 2649 GTTTGGTGAATGATTTTGTGTGACACCTCACTCAACGCAAGAAACCTTCTCA 2708
 1 GTTTGGTGAATGATTTTGTGTGACACCTCACTCAACGCAAGAAACCTTCTCA 60
 2709 GAAACCTGATCCGAGATGCTCCGAGATGAGCTGCGTGAAGAACTTGGAGACAGTGG 2768
 61 GAAACCTGATCCGAGATGCTCCGAGATGAGCTGCGTGAAGAACTTGGAGACAGTGG 120
 2769 TGAATCTCCCTGATGAAGACGAGCCCTGCGTGAAGACGCTTTTGTTCAGATGCGGCCC 2828
 121 TGAATCTCCCTGATGAAGACGAGCCCTGCGTGAAGACGCTTTTGTTCAGATGCGGCCC 180
 2829 ACGGACCTATTCCTGATGAGGCTGCTGCTGATACCGGACCTTGAAGAGTGAAGCG 2888
 181 ACGGACCTATTCCTGATGAGGCTGCTGCTGATACCGGACCTTGAAGAGTGAAGCG 240

ORIGIN
 Query Match 6.2%; Score 248.8; DB 2; Length 679;
 Best Local Similarity 96.8%; Pred. No. 3.7e-41;
 Matches 275; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
 1627 AGGGGTGCTGCTGCTCCGGC-GCAGACACCGTGTGCTGAGAGATCTGCGCAAGT 1685
 371 AGGGGTGCTGCTGCTCCGGCCTGCGAGACACCGTGTGAGAGATCTGCGCAAGT 430
 1686 TCTGACATG-EGTATGATGTGTATCGTGTGACCTGCTCAAGTCTTTTATATGTC 1744
 431 TCTGACATGCTGTATGATGTGTATCGTGTGACCTGCTCAAGTCTTTTATATGTC 490
 1745 ACGGACACACGTTTAAAGAAACAGGCTTTTCTACCGAAGAGTGTGAGACAG 1804
 491 ACGGACACACGTTTAAAGAAACAGGCTTTTCTACCGAAGAGTGTGAGACAG 550
 1805 TTGCAAGATGATGATGACAGACGACCTTGAAGAGGTCAGCTGCGGAGCTGTGGA 1864
 551 TTGCAAGATGATGATGACAGACGACCTTGAAGAGGTCAGCTGCGGAGCTGTGGA 610
 1865 GCGAGGTACGAGCATGCGAAGACGAGCCCGCTGCTGAC 1908

FEATURES
 source 1..679
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3619674"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC-8"
 /note="Organ: lymph; Vector: pOT7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

REFERENCE
 AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LNCM290 row: 1 column: 19
 High quality sequence start: 2
 High quality sequence stop: 656.
 Location/Qualifiers
 1..679
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3619674"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC-8"
 /note="Organ: lymph; Vector: pOT7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
 Query Match 6.2%; Score 248.8; DB 2; Length 679;
 Best Local Similarity 96.8%; Pred. No. 3.7e-41;
 Matches 275; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
 1627 AGGGGTGCTGCTGCTCCGGC-GCAGACACCGTGTGCTGAGAGATCTGCGCAAGT 1685
 371 AGGGGTGCTGCTGCTCCGGCCTGCGAGACACCGTGTGAGAGATCTGCGCAAGT 430
 1686 TCTGACATG-EGTATGATGTGTATCGTGTGACCTGCTCAAGTCTTTTATATGTC 1744
 431 TCTGACATGCTGTATGATGTGTATCGTGTGACCTGCTCAAGTCTTTTATATGTC 490
 1745 ACGGACACACGTTTAAAGAAACAGGCTTTTCTACCGAAGAGTGTGAGACAG 1804
 491 ACGGACACACGTTTAAAGAAACAGGCTTTTCTACCGAAGAGTGTGAGACAG 550
 1805 TTGCAAGATGATGATGACAGACGACCTTGAAGAGGTCAGCTGCGGAGCTGTGGA 1864
 551 TTGCAAGATGATGATGACAGACGACCTTGAAGAGGTCAGCTGCGGAGCTGTGGA 610
 1865 GCGAGGTACGAGCATGCGAAGACGAGCCCGCTGCTGAC 1908

Db 611 GCAGAGTCAGCAGCATCGGAGCCAGCCGCTGTGACGTC 654

|||||

RESULT 23
LOCUS BE514070 649 bp mRNA linear EST 07-AUG-2000
DEFINITION 601316575F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634962 5',
mRNA sequence.
ACCESSION BE514070
VERSION BE514070.1 GI:9721282
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM330 row: f column: 19
High quality sequence stop: 628.
Location/Qualifiers
1. 649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3634962"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 6.1%; Score 243.2; DB 2; Length 649;
Best Local Similarity 98.2%; Pred. No. 5.4e-40;
Matches 267; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Db 1627 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCCTGCTGAGAGATCTGGCCAAATT 1686
367 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCCTGCTGAGAGATCTGGCCAAATT 426
1687 CTTGC-ACCTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAAGTCTTTTATATGTA 1745
427 CTTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAAGTCTTTTATATGTA 486
1746 CGGAGACACCGTTTCAAAAGAACAGGCTCTTTT-CTACCGGAAGAGTCTGGAGCAAG 1804
487 CGGAGACACCGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGGAGCAAG 546
1805 TTGCAAGCATTTGATCAGACAGCACTTGAAGAGGCTGACCTCGGAGCTGTGGA 1864
547 TTGCAAGCATTTGATCAGACAGCACTTGAAGAGGCTGACCTCGGAGCTGTGGA 606
1865 GCAAGGCTCAGCAGCATCGGAGAGCCAGGCC 1896
607 GCAGAGTCAGCAGCATCGGAGAGCCAGGCC 638

RESULT 24
LOCUS BE514188 610 bp mRNA linear EST 07-AUG-2000
DEFINITION 601316376F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634987 5',
mRNA sequence.
ACCESSION BE514188
VERSION BE514188.1 GI:9721400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM330 row: g column: 20
High quality sequence stop: 610.
Location/Qualifiers
1. 610
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3634987"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 6.1%; Score 243; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 5.9e-40;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1627 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCCTGCTGAGAGATCTGGCCAAATT 1686
368 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCCTGCTGAGAGATCTGGCCAAATT 427
1687 CTTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAAGTCTTTTATATGTA 1746
428 CTTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAAGTCTTTTATATGTA 487
1747 GGAGACACAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGGAGCAAGT 1806
488 GGAGACACAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGGAGCAAGT 547
1807 GCAAGCATTTGATCAGACAGCACTTGAAGAGGCTGACCTCGGAGCTGTGGA 1866
548 GCAAGCATTTGATCAGACAGCACTTGAAGAGGCTGACCTCGGAGCTGTGGA 607
1867 AGA 1869
608 AGA 610

RESULT 25
CF531258

LOCUS CF531258 344 bp mRNA linear EST 12-SEP-2003
 DEFINITION UI-M-FY0-csp-h-01-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:30355848 5', mRNA sequence.
 ACCESSION CF531258
 VERSION CF531258.1 GI:34583222
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 344)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP).
 Seq primer: pyx-5.
 Location/Qualifiers

FEATURES

1..344
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355848"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_1ib="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pyx-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Ronald, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGACGACG. This library was created for the University Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 5.3%; Score 214; DB 7; Length 344;
 Best Local Similarity 76.2%; Pred. No. 6.2e-34;
 Matches 262; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
 QY 2765 GTGTTGAATTCCTCTGTAAGAGAGAGCCCTGGTGTGACGCGTTTGTTCAGATGCGG 2824
 DB 1 GTGTGAATCTCCCTGTGAGAGCTGTATCCCTGGGTGTGAGTCAATACCAAGTCCCT 60
 QY 2825 GCCCAGGCGCTATTCCTCGTGGTGGCGCTGCTGTGATACCGGAGACCTTGAGAGTGCAG 2884
 DB 61 GCTACTGCTGCTTTCTCTGCTGTGCTGTGCTGTGACACATGAGCTTTGGAGTGTTC 120
 QY 2885 AGCGACTACTCCAGCTATGCCCCGAGCTTCATCGAGCCAGTCTACCTTCAACCGCGGC 2944
 DB 121 TGTGACTACTCAGGTATGCCCCAGACTCAATTAAGACGAGCTCACCTTCCAGAGTGTG 180
 QY 2945 TTGAAGCTGGAGAGACATCCCTCGCAAACTCTTGGGGCTTGGCGGCTGAAGTGTAC 3004
 DB 181 TTCAAACTGGAGAACCACTGCGAACAAGCTCTGTGCGTCTTGGCGGTGAAGTGTAC 240

QY 3005 AGCTGTTTCTGATTTTCAGGTGAACAGCCTCCAGACGCTGTGACCAACATCTTACAG 3064
 DB 241 GGTCTATTCTTACAGCTTCAGGTGAACAGCCTCCAGACGCTGTGATCATATATACANG 300
 QY 3065 ATCTCTGCTGCTGAGCGGTACAGGTTTCAAGCATGTGTGCTGCA 3108
 DB 301 ATCTTCTGCTTACAGCGCTTACAGGTTTCAAGCATGTGTGATCA 344

RESULT 26

BE268183
 LOCUS BE268183

DEFINITION 601125261P1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345111 5',
 mRNA sequence.
 ACCESSION BE268183
 VERSION BE268183.1 GI:9141784

KEYWORDS

EST.
 Homo sapiens (human)

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 779)

REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at: image.llnl.gov
 Plate: LLCM132 row: 1 column: 16
 High quality sequence stop: 535.

Location/Qualifiers

FEATURES

1..779
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3345111"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 5.2%; Score 208.6; DB 2; Length 779;
 Best Local Similarity 86.8%; Pred. No. 9.4e-33;
 Matches 289; Conservative 0; Mismatches 34; Indels 10; Gaps 5;

QY 1627 AGGGCTTGGCTGTGTTCCGGCCGAGAGACCGTCTGGTGAAGAGATCCTGCGCAAGTT 1686
 DB 365 AGGGCTTGGCTGTGTTCCGGCCGAGAGACCGTCTGGTGAAGAGATCCTGCGCAAGTT 424
 QY 1687 CTTGCACTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1746
 DB 425 CTTGCACTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
 QY 1747 GGAGACCACTTTCAAAAGAGAGAGCTCTTTTCTACCGGAAGAGTCTT- GAAGCAAT 1805
 DB 485 GGAGACCACTTTCAAAAGAGAGAGCTCTTTTCTACCGGAAGAGTCTTGGAGAGCAAT 544
 QY 1806 TGGAAACA-TTGGATTCAGACAGCACTT- GAAGAGGGTGC-----AGTGGGGAGGCT 1857
 DB 545 TGGAAACA-TTGGATTCAGACAGCACTTGGAAAGGGGTGCTGCTTGGGGAACTTG 604

ORIGIN

Oy		1858	GTCCGAAGCACAAGGTCACAGGCAGCAATCGGGAAAGCCAGGCCGCCCTGTGTGACGT-CCAGAC	1916
Dd		605	CTTGGAACCGACGTCCTCGGCGCGCTTCCGGAAAGCTCGGCCGCCCTGTGTGAGATGCTCCAAC	664
Oy		1917	TCCGCTTCATCCCCAAGCCTGACGGCGCTGCAGC	1949
Dd		665	TCCGTTTCATCCCCAAGACTGAGGGGTCTGGGCC	697
RESULT 27				
Bv775178				
LOCUS				
DEFINITION		'Bv775178 RIKEN full-length enriched, 17.5 days embryo whole body		
ACCESSION		Mus musculus cDNA clone U930091N09 5', mRNA sequence.		
VERSION		Bv775178		
KEYWORDS		Bv775178.1 GI:39701816		
SOURCE		EST.		
ORGANISM		Mus musculus (house mouse)		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 336)		
AUTHORS		Carninci,P., Waki,K., Shiraki,T., Kono,H., Shibata,K., Itoh,M., Aizawa,K., Arakawa,T., Ishii,Y., Saeki,D., Bono,H., Kondo,S., Sugahara,Y., Saito,R., Osato,N., Fukuda,S., Sato,K., Watanishi,A., Hirozane-Kishikawa,T., Nakamura,M., Shibata,Y., Yasunishi,A., Kiyuchi,N., Yoshiki,A., Kusabe,M., Gusticich,S., Beisel,K., Pavan,W., Aldinis,V., Nakagawa,A., Heid,W.A., Iwata,H., Kono,T., Nakauchi,H., Lyons.P., Wells.C., Hume,D.A., Fagioli,M., Hensch,T.K., Brinkmeier,M., Camper,S., Hirota,J., Mombaerts,P., Muramatsu,M., Okazaki,Y., Kawai,U. and Hayashizaki,Y.		
TITLE		Targeting a complex transciptome: the construction of the mouse full-length cDNA encyclopedia		
JOURNAL		Genome Res. 13 (6B), 1273-1289 (2003)		
MEDLINE		22703353		
PUBMED		12819125		
COMMENT		Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suicho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.jp/) for further details.		
FEATURES				
source		Location/Qualifiers		
		1..336		
		/organism="Mus musculus"		
		/mol_type="mRNA"		
		/strain="C57BL/6J"		
		/db_xref="taxon:10090"		
		/clone="U930091N09"		
		/tissue_type="whole body"		
		/dev_stage="17.5 days embryo"		
		/clone_id="RIKEN full-length enriched, 17.5 days embryo whole Body"		
ORIGIN				
Query Match		5.1%; Score 203.8; DB 6; Length 336;		
Best Local Similarity		77.2%; Pred. No. 8.3e-32;		
Matches 247; Conservative		0; Mismatches 73; Indels 0; Gaps 0;		
Oy		254	GCGGCCCCCTCTCCGCGCAGGTGTCGCGCGAAGAGAGCGTGTGGCCGAGTGTGAG	313
Dd		2	GCGGACCCTTTCCTCACCGAGGTGTCATCTCGAAGAAGCTGTGTGACCGAGGTGTGGAG	61

FEATURES	source
Db	314 AGGCTGTGCAGAGCGGGCGGGAAGAACTGTCTGACCTTCGAGCTTCGGCTGCTGACGAG 373
Db	62 AGACTCTGAGAGGCGCAACGAGAGAAAGCTGCTGCTTTTGGCTTTAGAGCTCTTAACGAG 121
Qy	374 GCCCGCGGGGGGCCCCCCCCGAGCCCTTCCACCAAGCGTGGCGACGTACCTGCGCCACAGC 433
Db	122 GCCAGAGGCGGGGCGCTCCCATAGGCTTCATCTAAGTGGTGAGTCACTTGCCCAACT 181
Qy	434 GTGACCGACGCACTGCGGGGAGAGCGGGGCGTGGAGGCTGCTGCTGCCCGCGTGGGCGAC 493
Db	182 GTTATTGAGACCCCTGCGCTGTCAGTGAGTGCAATGATGCTACTGTTGAGCCCAAGTGGGAGC 241
Qy	494 GAGCTGTGTGTTACCCGTGCTGGACCGGTGGCGCGCTCTTGTGCTGTGGTCCAGCTGC 553
Db	242 GACCTGCTGTGCTTACCTGCGGACACATGTGCTCTTATCTTCTGTGATCCCCCACTGT 301
Qy	554 GCCTACCAAGGTGTGCGGGCC 573
Db	302 GCCTACCAAGGAGATGCC 321
RESULT 28	
LOCUS	BY783093
DEFINITION	343 bp mRNA linear EST 23-MAR-2004
ACCESSION	BY783093
VERSION	BY783093
KEYWORDS	mus musculus CDNA clone J930172A03 5', mRNA sequence.
SOURCE	BY783093.1 GI:39709732
ORGANISM	EST.
	Mus musculus (house mouse)
	Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 343)
AUTHORS	Carninci, P., Waki, K., Shiraki, T., Komou, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watabiki, A., Hirozane-Kitahikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusabe, M., Gustincich, S., Beisel, K., Pavan, W., Aldini, V., Nakagawa, A., Held, W. A., Iwata, H., Kono, T., Nakanishi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
TITLE	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
JOURNAL MEDLINE PUBMED	Genome Res. 13 (6B), 1273-1289 (2003)
COMMENT	22703353 12819125 Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Shohiro-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.jp/) for further details.
FEATURES	Location/Qualifiers
source	1..343 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="J930172A03" /tissue_type="whole body" /dev_stage="17.5 days embryo" /clone_lib="RIKEN full-length enriched, 17.5 days embryo

Sulana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane, K., Ishikawa, T., Komori, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shimagawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

TITLE JOURNAL MEDLINE PUBMED COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Komori, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watabiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384 format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES source

Location/Qualifiers
1. 326
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930261L24"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_1fb="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN

Query Match 4.8%; Score 192.2; DB 5; Length 326;
Best Local Similarity 76.9%; Pred. No. 2.2e-29;
Matches 247; Conservative 0; Mismatches 73; Indels 1; Gaps 1;
254 GCCGCCCTCTCTCGCAGGTGCTCTGCTGAAGAGCTGTGCGCCGAGTGTGAG 313
|||||
2 GCCGACCTTCTCTCACCAGGTGCTATCCCTGAAGAGCTGTGCGCGGTTTGACAG 61
|||||
314 AGGCTGTGAGAGCGCGCGGAGAACTGTCTGTGCTGTGCGCTGTGAGACGGG 373
|||||
62 AGACTGTGAGAGCGCAACAGAGAAAGCTGTGCTGTGCTGTGAGCTTAACTGAG 121
|||||
374 GCCCGCGGGGCGCCCGCAGGCTTACACCAAGAGGTGCGAGTACCTG-CCCAAC 432

|||||
Db 122 GCACAGCGGGGCTCCCATGCTCTTCACTAGTACGTCGCTACTCTTGGCCCAAC 181
433 GGTGACCAACGACATGCGCGGGAGGGCGCGTGTGCTGCGCGCGCGTGGGCGA 492
Db 182 TGTATTGTGAGACCTTCGCTGTGAGTGTGCTGAGTGTGAGCGAGTGGCGA 241
|||
Qy 493 CGACCTGTGCTTCACTGCTGTGCGACGCTGCGCGCTTGTGTGTGTGCTCCAGCTG 552
Db 242 CGACTGTGCTGTCACTGCTGTGCGACACTGTCTTTATCTTGTGTGCGCCCGACGCTG 301
|||
Qy 553 CGCTTACGAGTGTGCGGCGC 573
|||
Db 302 TGCCTACCAAGGAGATGCGC 322

RESULT 31
BU452535 753 bp mRNA linear EST 29-NOV-2002
LOCUS 603767927F1 CSEQRBN14 Gallus gallus cDNA clone Chest696f7 5', mRNA
DEFINITION
sequence.
ACCESSION BU452535 GI:25941846
VERSION BU452535
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 753)
Boatman, P.E., Sanz-Ezquerro, J., Overton, I.M., But, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22353534
12445392

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
Location/Qualifiers
1. 753
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHS7696f7"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1fb="CSEQRBN14"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI. This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adaptors, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996) 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 4.7%; Score 189.2; DB 5; Length 753;
Best Local Similarity 61.2%; Pred. No. 1.1e-28;

Matches 305; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 2960 AATATGCGTGGAAATCTTTGGGGCTTGGCGCTAAGTGCACAGCCGTGTTCTGGAT 3019
 DB 8 AATATGAATGCAATGACTGAGTCTCAAACTAATAAGCCATCTTACTCTTGAC 67
 QY 3020 TTGAGGTGAACAGCTCCAGACGGTGTGCACCAATCAAGAATCCCTCTGCTGAC 3079
 DB 68 TTAAATATCAACAGCTCTGACAGATTCTAATTAACATCTACAAAGATTTTACTCAG 127
 QY 3080 GCGTACAGTTTACCGCATGTGTGTGACAGCTCCATTTCAATCAGCAAGTTTGAAGAAC 3139
 DB 128 GCTTACAGGTTTCATGCTGTGTGTCTTCAAGCTTCAATCAACGAAGTTAGAAATAT 187
 QY 3140 CCCACATTTTCTGCGCGTCTCTGACAGCGCCCTCTGCTACTCCATCCAGAA 3199
 DB 188 CCGATTTCTCTTAAGATCAATCTGATATGCTTCACTGCTATTTTATCTGAAA 247
 QY 3200 GCCAAGAACGACGAGATGTGCTGAGGAGCCAGGCGCCGCTCTGCTCCGAG 3259
 DB 248 GCTAAATATCAAGAGATTCTTTAGTAGCAAAAGATGCACTGTATGTTCCCTTTGAG 307
 QY 3260 GCGGTGAGTGTGTGTGACCAAGCATTTCTGCTAAGCTGACAGACCGTGTACC 3319
 DB 308 GCACAGAAATGGCTGTGTGCTACATGCTTCAATGTCAAACTGTCAACCAAGATTAAT 367
 QY 3320 TAGTGCACTCCGCGGTGCTACAGACAGCCAGCGAGCTGAGTGGAAAGCTCCG 3379
 DB 368 TACAAATGCTTACTTAAGCCCTTAAAGTATTAAGATGATCTGTTGGAAAGATCCA 427
 QY 3380 GGGACGACGCTGACTGCTGAGAGCGCAGCCACCCGCGACTGCTCTGACATTCAG 3439
 DB 428 AGGATATCTATGAACTGCTGAAGAGGTGACGGAACATCGCTTGTGTAAGATTTCAA 487
 QY 3440 ACCATCTGAGCTGATGG 3457
 DB 488 ACTATACTGACTAAGGG 505

RESULT 32
 CR688161 1424 bp mRNA linear HTC 12-AUG-2004
 LOCUS Tetraodon nigroviridis full-length cDNA.
 DEFINITION CR688161
 ACCESSION CR688161.1 GI:51186068
 VERSION HTC; cDNA; full-length; Tetraodon nigroviridis.
 KEYWORDS Tetraodon
 SOURCE Tetraodon
 ORGANISM Tetraodon
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae.
 REFERENCE 1 (bases 1 to 1424)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage - 2 rue Gaston Creteil, CP 5706 - 91057 EVRY cedex - FRANCE.
 COMMENT (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.
 FEATURES
 source
 1..1424
 /organism="Tetraodon"
 /mol_type="mRNA"
 /db_xref="taxon:47144"
 /tissue_type="Eyes"

ORIGIN
 Query Match 4.7%; Score 186.8; DB 3; Length 1424;
 Best Local Similarity 57.5%; Pval. No. 3.7e-28;
 Matches 377; Conservative 0; Mismatches 272; Indels 7; Gaps 2;

QY 2522 AAGCTTACGTCCAGTGTCCAGGAGATCCGACGGGCTCATCTCTCCAGCTGTCTGC 2581
 DB 150 AAAACATACAGACAGTGCAGAGGGGTTCTCAGGATCTGCTGTCTCAGTGTCTTGC 209
 QY 2582 AACCTGTGTACGGGACATGGAACAAAGCTGTTTGGGGGATTCGGCGGAC--GGG 2638
 DB 210 TCCCTCTGTATGTCTTATGGAACGCTCATTCAGAGCATATTAACAAAGGC 269
 QY 2639 CAGCTCCGCGTGGTGGATGATTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2698
 DB 270 TCTTTAATAGACTGT 329
 QY 2699 ACCCTTCTCAGACCTGT 2758
 DB 330 ACCCTTTTGAATATCTGT 389
 QY 2759 AAGACAGT 2818
 DB 390 AAGATGT 449
 QY 2819 ATGCGCGCCAGCGCTATTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2878
 DB 450 CTTCCTCTACGCTGCTCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 509
 QY 2879 GTGCAGAGCACTATCTCAGTATGCGCGACCTGCATCAGACCACTTCAAC 2938
 DB 510 ATCTATAAAGACTATCTATGATGTATGCAACCTGTCTTGTGTGTGTGTGTGTGTGTGT 569
 QY 2939 CGGGCTTAAAGCTGT 2998
 DB 570 CCTGTCACTGT 625
 QY 2999 TGTACAGCTGT 3058
 DB 626 TGCATGCTGT 685
 QY 3059 TACAAATCTCTCTGT 3118
 DB 686 TACAATTAATCTGCTGT 745
 QY 3119 CATCAGCAAGTTTGAAGAACCCCACTTTTCTGCGGCTCATCTGTACACAGGC 3174
 DB 746 GGTCAAGCTGT 801

RESULT 33
 AM244516/c 347 bp mRNA linear EST 25-JAN-2002
 LOCUS BR END06B09 Bain Rancourt retinoic acid induced ES cell neural
 DEFINITION differentiation subtraction library Mus musculus clone 06B09
 similar to gb|AF073311|AF073311 Mus musculus telomerase catalytic
 subunit mRNA, complete cds, mRNA sequence.
 REFERENCE 1
 AUTHORS AM244516
 VERSION AM244516.1 GI:8051265
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 347)
 AUTHORS Bain,G., Mansergh,F.C., Wride,M.A., Hance,J.E., Isogawa,A.,
 Rancourt,S.L., Ray,W.J., Yoshimura,Y., Tezuka,T., Gottlieb,D.I.
 and Rancourt,D.E.
 ES cell neural differentiation reveals a substantial number of
 novel ESTs
 JOURNAL Func. Integr. Genomics 1 (2), 127-139 (2000)
 MEDLINE 21652683
 PUBMED 11793228
 COMMENT Contact: Rancourt DE
 Department of Biochemistry and Molecular Biology
 University of Calgary
 3330 Hospital Drive N.W., Calgary, Alberta, T2N 4N1, Canada
 Tel: 403 220 2888

Fax: 403 283 8727
Email: rancourt@ucalgary.ca; [URL:http://www.acs.ucalgary.ca/](http://www.acs.ucalgary.ca/)
rancourt

DNA sequencing by: University Core DNA Services, University of Calgary. Submitted sequence has been trimmed at both ends to remove the adaptor oligos containing the EcoRI sites, i.e. GAATTCGACCTA (beginning) and TAGTCGAATTC (end) removed. Therefore, reported insert length is longer than actual EST sequence length.
Insert length: 359 Std Error: 10.00
Seq primer: T3 Or T7.

EcORI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., EMAS (1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 4.5%; Score 180.2; DB 5; Length 880;
Best Local Similarity 61.8%; Pred. No. 8.2e-27;
Matches 337; Conservative 0; Mismatches 203; Indels 5; Gaps 3;

```

QY 2898 GGTATGCGCGAGCTCCATCAGAGCCAGCTCACTTCAACCGCGGCTTCAAGCTGGGA 2957
DB 266 GTTATGCGCTTACTTCTATCAGATCAAGTCTTCTTCAATTCAGTAGAATAGCTGGGA 325
QY 2958 GGAACATGCTCGCAAACTTTTGGGGTCTTGGCGGTGAGTCAACAGCTTTCTGG 3017
DB 326 AAAACATGAATGCAATTAAGTCAAGTCTTCAAACTGAAATGCAATCTTACTTTG 385
QY 3018 ATTGCAAGTGAACAGCTTCCAGAGCTGTGACCAACATCTAAGATCTTCTGCTGC 3077
DB 386 ACTTAAAGATCAACAGCTTCAAGAGTCTTAATTAACATCTAAGATATTTTACTTC 445
QY 3078 AGGCGTACAGTTTCAAGCATGTGTGTGAGCTCCCATTTCAATCAAGAGTTTGAAGA 3137
DB 446 AGGCTTACAGTTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 505
QY 3138 ACCCAATTTTCTGCGGCTATCTGTACAAGGCTTCTTCTGCTTCAATCTTCA 3197
DB 506 ATCTGATTTCTTCTTAAAGATATCTGTAACTGTGTTATCTGCTATTTATCTGA 565
QY 3198 AAGCGAAGAACGAGGATGTGCTGGGGGCAAGGGCGCGGCTTCTGCTTCCG 3257
DB 566 AAGCTAATAATCAAGGAGTCTTCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 624
QY 3258 AGGCGGCTGAGTGTGCGTGTGCAACCAACATTTCTGCTCAAGTCAAGCTGTCA 3317
DB 625 AGGCGAGAGATGCTGTGCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCT 682
QY 3318 CTAAGTGCACCTCTGCGGCTCACTGACAGAGCC--AGACGAGCTGAGTGGAGCT 3375
DB 683 GTTATTTAAAGATCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 742
QY 3376 CCGCGGAGCAGAGCTGACTGCTGAGAGCGGAGCCAGCCAGCTGCTCAAGCTT 3435
DB 743 CCGAGGAGATCTTATGGAAGCTGCTGAAAGAGGAGCCAGCCAGCTGCTGAGAT 802
QY 3436 CAGA 3440
DB 803 CAAA 807

```

RESULT 35
BI388013
LOCUS 775 bp mRNA linear EST 26-AUG-2003
DEFINITION BFL26_002716 Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMG531) Branchiostoma floridae cDNA clone MPMG531A0937 5', mRNA sequence.
ACCESSION BI388013
VERSION BI388013
KEYWORDS EST.
SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.
REFERENCE 1 (bases 1 to 775)
AUTHORS Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J., Herwig, R., Vingron, M. and Lehrach, H.
TITLE New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Res. 13 (6A), 1056-1066 (2003)
22683279
12799346
Contact: Panopoulou G
Laboratory 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Institstr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: <http://www.molgen.mpg.de/amphioxus/>
Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (<http://www.rzpd.de>)
PCR Primers
FORWARD: 5' CCCAGGCTTACACTTATGCTCCGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACGCGAGCTGCGAAGAGGAGATGTG 3' (M13FSP)
Insert length: 1 Std Error: 0.00
Seq primer: 5'-CCGCTCCGGAATCCCGGAT-3' pSPORT3/86
High quality sequence stop: 775.
Location/Qualifiers
1..775
/organism="Branchiostoma floridae"
/mol_type="mRNA"
/db_xref="taxon:7739"
/clone="MPMG531A0937"
/issue_type="whole embryo"
/dev_stage="26 hrs (neural stage)"
/lab_host="E.coli, XL1 blue"
/clone_lib="Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMG531)"
/note="Vector: pSPORT1 (Gibco BRL); Site 1: SalI, KpnI, EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSPORT1 vector using a NotI (5')-pGACTAGTTCATGATCGGAGCGGCGCC (7)15-3' and a SalI 5'-TCGACCCAGCGCTCCG-3' adapters (Gibco BRL)."

FEATURES

source

ORIGIN

Query Match 4.2%; Score 167.6; DB 4; Length 775;
Best Local Similarity 54.3%; Pred. No. 3.4e-24;
Matches 366; Conservative 0; Mismatches 299; Indels 9; Gaps 1;

```

QY 2497 CCACGACGGCGGCGATCAGGGGCAAGTCTTACGTCAGTGCAGAGGATCCCGAGGG 2556
DB 17 CGATCAGGATCCAGATCGGGGGAGCTTACGCGAGATCAGGGAGATCAGTAAAG 76
QY 2557 CTCATCTCTCCACGCTGCTGACGCTTGTCTACGCGACATGAGAGAAAGCTGTT 2616
DB 77 ATCTGCTGCTGACACCTGCTCTGTAGCTTCTTCTACGCTAATGAGAGAGATCT 136
QY 2612 TCGGGGAGTTCCGCGGAGCGGCTGCTCTGCGTTTGTGTGATGTTCTTGTGTGAC 2676
DB 137 CTGTGGCATGACATGATGAGTGTGCTGCTGCGCTGTGTGATGACTTCTGTGTGAC 196
QY 2677 ACCTACCTCACCAGCGGCAAACTTCTCAAGACCTGATCCGAGAGTCTCTGAGTA 2736
DB 197 CCACACCTTGAGCAGAGCTTCAAGCTTCTGTATCAAGTGTGATGATGATGATGAT 256
QY 2737 TGGCTCGTGTGTAATCTGCGAAGACAGTGTGATCTTCTGTGAGAGAGAGAGCCCT 2796
DB 257 TGGGTACAGGTTTCAATCCGAGAAAGTCTGACCAATCTTCTGTACACAGAGATGC 316
QY 2797 GGGTGCACGGCTTTTGTTCAGATGCGGAGCCAGGCTTATTCCTGTGTGCGCTGCT 2856
DB 317 TGTGTGACATGT-----CAGCCAGACAGTGGCTGTTCCTGTGTGCGCATGTCT 367

```

QY 2857 GCTGATACCCGGACCTGGAGTGCAGAGCACTACTCCAGCTAATGCCGAGACCTCCAT 2916
 DB 368 GTTCACTCTCTCTGCTGAGGGGTATGAGAGCTACACAAATATGCAACCTGATAT 427
 QY 2917 CAGAGCCAGTCTACCTTCACACCGGGCTTCAAGGCTGGAGGAAATGCTGCAAACT 2976
 DB 428 CAGGTAACCTTGACCTTTCAGCTCCATGAGACTCCGGTCAAGGCATGAAACAGAGCT 487
 QY 2977 CTTGGGGCTTGGCGCTGAAGTTCACAGCCTGTTTCTGATTTGACAGTGAACAGCT 3036
 DB 488 GATGAACACTGTCAAGGCGAAGTTCATCCTTCTCTGAGGCCCAAGTGAATTCACG 547
 QY 3027 CCAGACGGTGTGACCAACATCTTCAAGATTCCTGCTGAGGGGTACAGGTTTCAGGC 3096
 DB 548 AGCTGTATTCACAGACCTCTCTACAGGCAATTCCTGTTACAGACCCACAGTTTCCAGG 607
 QY 3097 ATGTGTGCTGACCTCCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCG 3156
 DB 608 CTACAACAGCTGTCTGCTCCATGTCATGTCAGAGGCTCAAGCAACCTGCAATTCCTCTAC 667
 QY 3157 CGTCACTCTGACA 3170
 DB 668 AATGATCATGAGACA 681

RESULT 36
 BX886589 703 bp mRNA linear EST 27-JUL-2004
 LOCUS BX886589 tcdk Oncorhynchus mykiss cdna clone tcdk0036c.p.02 5prim,
 DEFINITION mRNA sequence.
 ACCESSION BX886589
 VERSION BX886589.2 GI:42819050
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 703)
 REFERENCE Govoroun,M., Guiguen,Y. and Le Gac,F.
 Construction and primary characterization of normalized cDNA
 libraries in rainbow trout, Oncorhynchus mykiss
 Unpublished (2003)
 JOURNAL On Dec 18, 2003 this sequence version replaced gi:40135983.
 COMMENT Contact: Guiguen Y
 INRA - SCRIBE
 Campus de Beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yam.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
 plate: 0036 row: p column: 2
 Seg primer: M13R

FEATURES
 Source
 Location/Qualifiers
 1..703
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="tcdk0036c.p.02"
 /issue_type="multi-issues"
 /dev_stage="from embryos to adults"
 /lab_host="DH10B"
 /clone_lib="tcdk"
 /note="Vector: pT73D-pac; AGENAS Rainbow trout
 multi-issues - normalized + 2 subtractions; Clone
 distribution: AGENAS Resource centre. Francois PIUMI,
 Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
 Etude du genome (LREB), Domaine de Vilvert, 78352,
 Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
 (0) 1.34.65.22.73"

ORIGIN

Query Match 4.0%; Score 162.4; DB 5; Length 703;
 Best Local Similarity 55.5%; Pred. No. 4,1e-23;
 Matches 333; Conservative 0; Mismatches 266; Indels 1; Gaps 1;

QY 2858 CTGATATCCCGGACCTGGAGTGCAGAGCACTACTCCAGCTAATGCCGAGACCTCCAT 2917
 DB 1 CTGATATCCCGGACCTGGAGTGCAGAGCACTACTCCAGCTAATGCCGAGACCTCCAT 59
 QY 2918 AGAGCCAGTTCACCTTCAACCGGGCTTCAAGGCTGGAGGAAATGCTGCAAACTC 2977
 DB 60 CCTACAGCTGTACCGCTAGGCTCCGCCCACTGCGGGGACCAATGAGAGAGAGCTC 119
 QY 2978 TTTGGGGCTTGGCGCTGAAGTTCACAGCCTGTTTCTGATTTGACAGTGAACAGCTC 3037
 DB 120 ATGTCATCTTGAATTCAGTGCACAGCGCTCTCTGAGACTCAAAACCAATCTCCG 179
 QY 3038 CAGAGGTGTGACCAACATCTTCAAGATTCCTGCTGAGGGGTACAGGTTTTCACGCA 3097
 DB 180 GAGGCTGTATAGCAAGCTCTATAGTTAGTTGCTGCAAGCGTTCAAGTTCCATGCC 239
 QY 3098 TGTGTGCTGACCTCCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGC 3157
 DB 240 TGTGACAGAGATTGCGCTTGTGTGTCAGAAAGTGGCGGAAACCACTGTAATCTCCAT 299
 QY 3158 GTCACTCTGACACGGCCCTCCTGCTACTCCATCTGAAAGCCAAAGCGAGGATG 3217
 DB 300 CTGATCTGGAGCTTGGCGGAGTACACCAACATCTAGTCACTGCAACAAAGGTGTG 359
 QY 3218 TCGCTGGGGGCAACAGGCGCCGCCGCCCTGCTGCGCTGCGAGCGGTGACGTGCTGTC 3277
 DB 360 TCTCTAGGCTGTAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 419
 QY 3278 CACCAAGCAATTCCTGCTCAAGCTGACCTGACACCGTACCTGACCTGCTGCGG 3337
 DB 420 TGTCTGGCGCTTCTGTTGTTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
 QY 3338 TCACTCAGACAGCCCAAGCAGAGCTGAGTCCGAAAGCTCCCGGAGCAGACGCTGATGCC 3397
 DB 480 CCGCTACGACACGTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
 QY 3398 CTGAGAGCGGAGCCCAACCGGCACTGCTGAGCTTCAAGACCTTCAAGCTGATG 3457
 DB 540 ATCAGACAGGCTGCCACACCAATGCTGTAAGCTTCAAGGCTTCAAGGCTTGAAG 599

RESULT 37
 CK392784 619 bp mRNA linear EST 29-DEC-2003
 LOCUS CK392784
 DEFINITION K0850A03-5 NIA Mouse 8.5-dpc whole Embryo cDNA library (long) Mus
 musculus cdna clone NIA:K0850A03 IMAGE:30083138 5', mRNA sequence.
 ACCESSION CK392784
 VERSION CK392784.1 GI:40383303
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 619)
 REFERENCE Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL MEDLINE PUBLISHED
 11544199
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0850 row: A column: 03

Seq primer: M13 Reverse
High quality sequence stop: 619
POLYA=No.

FEATURES

source

Location/Qualifiers

1. 619
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="NIA:K0850A03 IMAGE:30083138"
/issue="whole embryo including extraembryonic
tissues at 8.5-days postcoitum"
/dev_stage="8.5-days postcoitum"
/lab_host="DH10B"
/clone_lib="NIA Mouse 8.5-dpc whole Embryo cDNA Library
(Long)"

/note="Vector: pSPORT1 (Invitrogen); site 1: SalI; site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsn.gsc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). (PMD: 11541991). Total RNAs were
extracted from a pool of 13 embryos at 8.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-pGACTGCTTCTAGATCCGACGCGCCCTTTTCTTTT-3'] from
9.1 ug of total RNA, treated with R4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match 3.9%; Score 155.4; DB 7; Length 619;
Best Local Similarity 57.5%; Pred. No. 1.2e-21;
Matches 364; Conservative 0; Mismatches 251; Indels 18; Gaps 4;
QY 679 GAGAGCGGGGTCCTCCCTGAGGCTCCAGCCCGGGTGCAGAGAGGGCGGGGCGACTGC 738
DB 2 GGAAGCACCCGAAACCCCTGGCTTCGATCTCGAGGTAACAAGAGGATCTGAGTCTCAC 61
QY 739 CAGCCGAAGTCTGCGCTTGCCTCAAGAGGCGGAGCGGCTGCGCTGAGCGGAGCG 798
DB 62 CAGTACAAGTGTGCTTCAAGTAAAGAGGCAAGTCTATCTCTCCGAGAGTGAAGGA 121
QY 799 GAGCGCCGTTGGGAGGAGGCTCTGGGCTCAACCCGAGGAGAGCGGTGAGCCGAGTACCG 858
DB 122 GGAAGCCCAAGGAGGAGTACCAACCCATCAGGCAAAATCATGGGTGCAAGTCTGCG 181
QY 859 TGGTCTTGTGTGTGTCTCACTGCGAAGCCCGGAGAAAGCCACTTTTGGAGGGTGC 918
DB 182 TCGGTCTCCCGAGGTGCTACTGCA-----GAGAAAGATTGTTCTTAAAGAAA 232
QY 919 GCTCTCTGAGCAGGAGCACTCCCAACCATCGGTGGGCGGAGAGCGGAGCGGCGCC 978
DB 233 GGTGTCTGACTGAGTCTCTTGGG---TCGGTGTCTGTAAACAAGCCAGCTCTCAC 289
QY 979 ATTCACATCGGAGCAGCAGCTCCCTGGAGACGCTTGTCCCGGTGAAGCCGAGAC 1038
DB 290 ATCTCT---GCTGTACACACCCCGCAAAATGCTTTAGCTCAGGCAATTATTGAGAC 346
QY 1039 CAGACACTTCTCTACTCTCTAGGCGA---CAAGAGAGAGTGGGCGCTCTCTCTACT 1095
DB 347 CAGACATTCTCTTACTCTCAAGGAGAGTGGCCAAAGGCTTAAACCTCATATCTACT 406

QY 1096 CAGCTCTGAGAGGCCAGCTGACTGCGCTCGAGGCTCGTGAACCATCTTCTTGGG 1155
DB 407 CAGCAACTCTCAGGCTTACTTACTGCGGGCCAGAGAGATGGTGAAGATCATCTTCTGGG 466
QY 1156 TTCCAGGCGCTGATGATGCAAGGAGTCTCCCGAGAGTTGCCCGCTCCCGAGCGTACTG 1215
DB 467 CTCAAGGCGTATGATCATGAGGACCACTCTGAGGAGCAACCGTCTATGCGCTGACTACTG 526
QY 1216 GGAATAGGCGCCCGCTTGTGAGAGCTGTTGGGAACACGAGCGAGTCCCTTACGGGGT 1275
DB 527 GAGAGTGGGCGCCCTGTCTTCAACAGCTGTGTGAACCATGACAGTGTCAATATGTACG 586
QY 1276 GCTCTCAAGACGACTGCGCGCTGCGAGCTGC 1308
DB 587 ACTCTCAGGTCACTGAGGTTTGAACAGC 619

RESULT 38
BUI39751 696 bp mRNA linear EST 25-NOV-2002
LOCUS 603134527F1 CSEQCHL24 Gallus gallus cDNA clone CSEST116f8 5', mRNA
DEFINITION
sequence.
ACCESSION BUI39751
VERSION BUI39751.1 GI:25354188
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 696)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
2235534
12445392
PUBMED
MEDLINE
JOURNAL
TITLE
AUTHORS

CONTACT: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers

1. 696
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="CSEST116f8"
/dev_stage="16 day embryo"
/lab_host="DH10B"
/clone_lib="CSEQCHL24"
/note="Organ: Brain; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-primed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BspI and
BamHI sites [5'ggcgcgtcgacgccgcgacccgaaagaaag]
[5'aattcttttttcgataccggcgctcgcaagc]

ORIGIN

Query Match 3.9%; Score 154.8; DB 5; Length 696;
Best Local Similarity 56.0%; Pred. No. 1.6e-21;
Matches 319; Conservative 0; Mismatches 242; Indels 9; Gaps 1;
QY 28 GGAAGCCCTTGGCCCGGACACCCCGGATGCGCGCGCTCTCCCGTCCGAGCCGTCGCG 87

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: www.bio.1lnl.gov/bbrp/image/image.html
Insert Length: 423 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 137.
Location/Qualifiers

FEATURES

source

1. 148
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2304672"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI-CGAP GC6"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and as circles were made in vitro. Following RNP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.5%; Score 140; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3876 GGAATTGGAGTGCACCAAGGTGTCCTGTACACAGCGAGACCTCGACCTGTGATGG 3335
DB 148 GGAATTGGAGTGCACCAAGGTGTCCTGTACACAGCGAGACCTCGACCTGTGATGG 89
QY 3936 GGGTCCCTGTGGCAATATGGGGGAGGTGCTGTGGAGTAATATCTGAATATATGAG 3995
DB 88 GGGTCCCTGTGGCAATATGGGGGAGGTGCTGTGGAGTAATATCTGAATATATGAG 29
QY 3996 TTTTTCAGTTTGAATAAAA 4015
DB 28 TTTTTCAGTTTGAATAAAA 9

RESULT 41
AZ972318 641 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION 2M0246F07F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
ACCESSION AZ972318
VERSION
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 641)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0246 row: F column: 07
Seg primer: CATTGTAAACAGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 641.
Location/Qualifiers

FEATURES

source

1. 641
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0246F07"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.3%; Score 132; DB 8; Length 641;
Best Local Similarity 61.6%; Pred. No. 9.1e-17;
Matches 229; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

QY 963 ACCACCGCGGCGCCCATCCATCGCGGCCACCAAGTCCCTGGAGACGCTGTGCC 1022
DB 216 AACCAAGGCCAGCTCCATCATCTGTCTACACCCCGCAAAATGCTTCAAGCTCA 275
QY 1023 CGGTGACGCCGAGACCAAGCACTTCTCTACTCTCCAGGCGA---CAAGAGCAGCTGC 1079
DB 276 GGGCATTTATTTGAGACCAAGCAATTTCTTACTCCAGGAGATGGCCAAAGCGTCTAA 335
QY 1080 GGGCTCTCTTCTACTCAGCTCTGTGAGGCCAGCTGAGCTGGCGTGGAGGCTGTGG 1139
DB 336 ACCCTCATCTCTACTCAGCAAGCTCCAGCTTAAGCTGGGCGCAGAGACTGTGG 395
QY 1140 AGACCAATCTTGTGGGTTCCAGGCTCGATGTCAGAGCACTCCCGCAGTGGCCCC 1199
DB 396 AGATCATCTTCTTGCGGCTCAAGGCTTAAGGACATCAAGAGCACTCTCAGAGCACACCTG 455
QY 1200 TGCCCCAGGCTTCTGCAATATGGGCGCCCTGTTTCTGAGAGCTGTTGGAAACCAAGCCG 1259
DB 456 TATGCGCTCATATCTGGAGATCGGCGCCCTGTTTCAACAGCTGTGTGAACCAAGCAG 515
QY 1260 AGTGGCCCTTACGGGGTCTCTTCAAGACGACTGCCGCTGCGAGCTGGCGTACCCCA 1319
DB 516 AGTGCCAAATATGTCAGACTCTCTCAGGTTCATGTGAGAGTTCGAAACAGAAACCAAG 575
QY 1320 CAGCGGCTGTCT 1331
DB 576 TGACAGATGCTT 587

RESULT 42
 BUI22597 875 bp mRNA linear EST 25-NOV-2002
 LOCUS 603148441f1 CSEBCHL18 Gallus gallus cDNA clone CHEST151a2 5', mRNA
 DEFINITION
 ACCESSION BUI22597.1 GI:25332991
 VERSION BUI22597.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 875)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 2235534
 MEDLINE 12445392
 PUBMED
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 016122360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers

FEATURES

source

1..875
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton line 15T"
 /db_xref="taxon:9031"
 /clone="CHEST151a2"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEBCHL18"
 /note="Organ: small intestine; Vector: pBluescript II
 KS(+); Site_1: EcoRI; Site_2: NotI; Modification of
 pBluescript II KS(+) (Stratagene) vector to accommodate
 cDNA produced with the T-timed protocol (Construction of
 uni-directionally cloned cDNA libraries from messenger RNA
 for improved 3' end DNA sequencing by Glenn Fu, et al.
 U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
 NotI and EcoRI. Ligate in double stranded adaptor
 containing BglI and BamHI sites
 [5'ggcggtgcagcccgatccgaaaaaag]
 [5'aatcttttctcgatccggggtcgcacgc]"

ORIGIN

Query Match 3.2%; Score 128.8; DB 5; Length 875;
 Best Local Similarity 58.0%; Pred. No. 4.4e-16;
 Matches 246; Conservative 0; Mismatches 177; Indels 1; Gaps 1;
 166 GGTGTGTGAGCCGGGAGACCCGGGCTTTCCGGCGGTGTGTGGCCAGTGTCTGTGTG 225
 165 GGTGTGTGAGGCGGAGACGCTCACTGCTACCGGACCTTGTGTGCGAGTGTGTGTG 224
 226 CGTGGCCCTGGAGACGACGCGCGCGCGCGCGCGCGCGCTTCCGCGAGTGTCTGTGCT 285
 225 CGTCCCCCGGT 284
 286 GAGAGAGCTGT 345
 285 GAGCGAAGTCATACGAAGATGTTTCAAGAGGCTGTGTGAAAAAAGAAAGAAATCCT 344
 346 GGGCTTGGGCTTGGCTGT 405
 345 TGGGTATGATACCTCTGT 404

QY 406 CAGCTGCGCAGCTACTCTGCCCAACGCTGACCGACCTGCGGGGAGCGCGGCGCTG 465
 DB 405 GTGTATATACACTATCTGTGTCCATATCTGTACAGAAAGATTCGATCAGTGGCTCTG 464
 QY 466 GGGGCTGTCTGTGCGCGCGGTGGGAGACGCTGTGTGTACCTGTGTGACCGC-TGGG 524
 DB 465 GAGATACTGTGCTGAGTAGAGTAGGAGACGCTGTGTGTACCTGTGTGAGACGCTGTG 524
 QY 525 CGCTCTTGT 584
 DB 525 CACTCTTATGTCTGT 584
 QY 585 AGCT 588
 DB 585 AACT 588

RESULT 43
 CN505902 846 bp mRNA linear EST 28-APR-2004
 LOCUS AGENCOURT 22432746 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7267941
 DEFINITION 5', mRNA sequence.
 ACCESSION CN505902
 VERSION CN505902.1 GI:46818526
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 846)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Len Zon, Harvard
 cDNA library Preparation: Open Biosystems
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM15246 row: h column: 19
 High quality sequence start: 21
 High quality sequence stop: 756.
 Location/Qualifiers

FEATURES

source

1..846
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7267941"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC_7"
 /note="Vector: pXpress1; Site_1: NotI; Site_2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pXpress-1.
 Library was size-selected for >1 kb fragments and
 normalized. A non-normalized version of this library is
 also available (NIH ZGC 10). Library was constructed by
 Open Biosystems (Huntsville, AL)"

ORIGIN

Query Match 3.2%; Score 128; DB 7; Length 846;
 Best Local Similarity 57.3%; Pred. No. 6.5e-16;
 Matches 252; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 2463 GTGGCCCTTTCAGACGCTTCTCTTACGCTTCATGTCACCAACGCCGTGGCATTACGAGGCA 2522
 DB 97 GAGACGCTTTCAGGCTTCTTCCAGAAAGTGTCTCAGCAGTTTACGTCATTCATTCATTCAGCAG 156
 QY 2523 AGTCTTACGCTTCCAGTCCAGGAGGATCCCGAGAGGCTTCATCTCTCCAGCTGCTCTGCA 2582
 DB 157 AGATGTTCCGGAGGCTGTGTGGATCCCGAGAGGCTTCTGTGTCTTCTGTCTGTGA 216
 QY 2583 GCCTGTGTACGCGGACATGAGAACAGCTTTTTCGGGGGATTCGAGCGGGAACGAGCTGC 2642
 DB 217 ATTTGTGTTACGACACATGAGAAAGCCCTGTCGAAAGACATCCGTTAAAGAGGGTGT 216
 QY 2643 TCCGTGCTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCACCACGCGAAACCT 2702
 DB 277 TGAATGAGGCTGATGATGATTTTGTGTCTCATCTCTCATCTGATGATGAAAGCAGAG 336
 QY 2703 TCTTCAGACCTCTGTCCAGAGTGTCCCTGATGATGATGCTGCGTGTGAACCTGGGAA 2762
 DB 337 TTCTGACACCTCTGTGTGTGAGTTCAGATTACGCTTCCAGATTAACTCCACAGAG 396
 QY 2763 CAGTGTGACCTTCCCTGTGAAAGACGAGGCGCTGGGTCAGGCTTTTGTTCAGATGC 2822
 DB 397 TGGCGGTGAACCTTCCCGT---GTGTGTCTCTGGGTAACCTGGGCGCTCTGTGTGC 453
 QY 2823 CGGCCCCAGCGCTATTCCTCTGTGTGCGGCTGTGTGTGATACCGAGCCCTGAGAGTGC 2882
 DB 454 CGTCCAGCTGCTGTCTTCCCTGTGTGCGGCTGTGTGATACACACACAGCTGAGCTGT 513
 QY 2883 AGAGCGACTTCTCCAGCTAT 2902
 DB 514 ATAAAGACTACTACGCTAT 533

RESULT 44
 BG198331/c 813 bp mRNA linear EST 21-APR-2001
 LOCUS RST11589 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG198331
 ACCESSION BG198331
 VERSION BG198331.1 GI:13720018
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Bozzer,S., Mays,R., Smith,E., Veloso,N., Kliska,A., Hess,J., Cochran,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE JOURNAL MEDLINE 21227151
 PUBMED 11329013
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 533.
 location/Qualifiers

FEATURES
 source 1..813
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HT1080"
 /note="See 'Athersys RAGE Library'
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation

ORIGIN method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

Query Match 3.1%; Score 123.8; DB 4; Length 813;
 Best Local Similarity 94.1%; Pred. No. 4,9e-15;
 Matches 128; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3083 TACAGTTTACGACATGTGTGCTGAGCTCCATTTTCATCAGCAAGTTGGAAGACCCC 3142

DB 749 TTCAGTTTACGACATGTGTGCTGAGCTCCATTTTCATCAGCAAGTTGGAAGACCCC 690

QY 3143 ACATTTTCTGCGGCTCATCTCTGACACGCGCTTCTCTGCTACTTCATCTGAAAGCC 3202

DB 689 ACATTTTCTGCGGCTCATCTCTGACACGCGCTTCTCTGCTACTTCATCTGAAAGCC 630

QY 3203 AAGAACGCGAGATGT 3218
 DB 629 AAGAACGCGAGATTT 614

RESULT 45
 CA353864 632 bp mRNA linear EST 05-NOV-2002
 LOCUS 625469 NCCGWA 1RT Oncorhynchus mykiss cDNA clone 1RT74012_C_H06 5',
 DEFINITION mRNA sequence.
 ACCESSION CA353864
 VERSION CA353864.1 GI:24599035
 KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss

REFERENCE Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Bozzer,S., Mays,R., Smith,E., Veloso,N., Kliska,A., Hess,J., Cochran,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE JOURNAL MEDLINE 21227151
 PUBMED 11329013
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccgwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_aln option. Vector identified by
 cross_match v0.990329.
 Seg primer: AGCGATTAACAATTTTCACACAGGA.
 location/Qualifiers

FEATURES
 source 1..632
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="1RT74012_C_H06"
 /issue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="NCCGWA 1RT"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from brain, gill, liver,
 spleen, muscle, and kidney."

ORIGIN

Query Match 2.9%; Score 116.8; DB 6; Length 632;
 Best Local Similarity 59.2%; Pred. No. 1.4e-13;
 Matches 218; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

QY 2417 GATGCGGTGATATGAGAGAGGCTCTCCGTAATGAGAGCCAGAGTGAGCTCTTCAGC 2476

DB 62 GATGCGCATCTCTGGGGAGAGGATTTCTCAGAGATTCATTCAGGCAAGAGCTTTGGAG 121

QY 2477 GTCTTCTACGCTTCATGTGACACACAGCGCGTGGCATTACGAGGAGCAAGTCTTACGTCAG 2536

```

Db      122 GCTTGAACCCAGATGCTCTAGCTGATGTAACAGACTTGGAGAAAGAAATGTTCCGTACG 181
Qy      2537 TGCCAGGGGATCCCGCAGGGGCTCCATCCTCTCCAGCTGCTCTGCAAGCTGTGCTAACGCG 2596
Db      182 GGTCAAGGGGATCTCTCAGGGGCTCCGAGAGTGTCTGTGCTGGCTCTGTGTTAACGGG 241
Qy      2597 GACATGAGAAACAAGCTGTTTGC---GGGATTCGGCGGGAAGGGGCTGCTCCGCTTGG 2653
Db      242 CACATGAGAACTTCTGTTCTTCTTAACGTCAAGCGCGAGAGGGGTGTGATGAGACTG 301
Qy      2654 GTGATGATTTCTTGTGTGTAACCTCACTCACTCAAGCCAGCGAAGAACTTCTCTCAGAGC 2713
Db      302 GATGACGATTTCTCTCTCACTCTCACTGAGCAGGCAAGACTTCTCTCAAGACC 361
Qy      2714 CTGCTCCAGAGTGTCTCTGATGATGCTGCTGCTGTAATTTGGGAAAGCACTGTGTAAC 2773
Db      362 CTGATGAGCGGGGTTACACGATACGGGTGTGTGAGAAACCCCAAGAGGTGCTGTTAAC 421
Qy      2774 TTCCCTGT 2781
Db      422 TTCCCTTT 429

```

RESULT 46
BX889962 724 bp mRNA linear EST 27-JUL-2004
LOCUS BX889962 cdbk Oncorhynchus mykiss cdna clone tcdk0041c.i.20 5prim,
DEFINITION mRNA sequence.
ACCESSION BX889962
VERSION BX889962.2 GI:43411444
KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 724)
GOVERNOR, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Dec 18, 2003 this sequence version replaced gi:40140362.
CONTACT: Guiguen Y

JOURNAL INRA - SCRIB
AUTHORS Campus de Beaulieu, RENNES cedex, 35042, France
TITLE Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signaasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0041 row: 1 column: 20
Seq primer: M13R.

FEATURES
Location/Qualifiers
1..724
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcdk0041c.i.20"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="tcdk"
/lab_host="DH10B"
/note="Vector: pT7T3D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution: AGENAE Resource centre, Francois PIUMI,
Francois Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 2.9%; Score 115.8; DB 5; Length 724;
Best Local Similarity 52.9%; Pred. No. 2.2e-13;
Matches 370; Conservative 0; Mismatches 287; Indels 42; Gaps 4;

```

Qy      1528 CAAAGATTATCTCTCCCTGGGAGACATGACCAGCTCTGCTGACAGAGCTGACGTGAA 1587
Db      19 CAGGAATCTTCTGCTCATGAGGCAAGTTGAGAGGATGTCATTGAGCTGACCTATATGGAA 78
Qy      1588 GATGACCGGGGGAAGCTGGCTGGCTGGCGAGAGCCAGGGGTGGTGTGTTCCGAC 1647
Db      79 GATGAAGGTAATGACTGATGATGCTGTAAGATCGCAAGACAGGCGCTG---CCGCGC 135
Qy      1648 CGCAGAGACCCGTCTGCGTGAAGAGATCCGTGCAAGTTCTGCACTGCTGATGATGT 1707
Db      136 CAGTAGAGCTGTGTAATCGGACGGGTGTAGCCAGGCTCCGCTTGGCTGTGGATGG 195
Qy      1708 GTAGCTGCTGAGCTGCTCAGGCTCTTTCTTTATGTACAGAGACCACTTTCAAAAGAA 1767
Db      196 CTATGTGTAGGCTCGGTGAGAGCTATGTCTACGTCACAGAGACATGGACAGAAAGAA 255
Qy      1768 CAGGCTCTTTTCTACCGGAAAGTGTCTGAGCAAGTTGCAAGGATTGATGATGACAGA 1827
Db      256 CGCACTGGGCTTCTACAGATACAGAGTCTGGGCCAAGCTGCAAGAGCTGCTTTCAAGTG 315
Qy      1828 GCATTTGAAGAGGTGACAGCTGCGGAGCTGTGGAAGCAGAGTCTAGCAGCATCGGGA 1887
Db      316 TCACCTCTTAAGGTCAAGATGTCAAGATGTGACCCGTGGCCAGGTGAGCTGCTCCCAA 375
Qy      1888 AGCCAGAGCCCGCTGCTGACGTCACAGTCCGCTTATCCCAAGCTGACGGCTGGG 1947
Db      376 AACCACTGTCCCC-----TCCGCTCCGCTTCATCCCAAGACCAAGAGGAGTAGG 426
Qy      1948 GCGGATTGGAACATGACTAGTGTGGGAGCCGAAGCTGCCGAGAAAGAGAGGCG 2007
Db      427 ACCCATACACAGGGTATAGGGGCTGAGCGCCAAACAAAGTT----- 468
Qy      2008 CGAGGCTCACTCGAGGGTGAAGGCACTGTTACAGCTGCTCAACTACAGAGCGGCGG 2067
Db      469 -----GTTCCAGAACCGGTGAAGAGCTGTTAGATGTGATGATGTGTGTACAGT 522
Qy      2068 GGGCCCGGCGCTCTGGGCGCTCTGTGTGGGCTGTGACGATATTCACAGAGGCTGGGG 2127
Db      523 CTCTCCCTCTCTCTGGGCTTACAGTGTGGGGTTGACCGCAATCCACAGAGCTCTTC 582
Qy      2128 CACCTTGTGTCGCTGTGCGGGGCCCAAGCCCGGCTGAGCTGACTTTGTCAAGGT 2187
Db      583 TTCCATACCCCTGTCTCAG-----AAAGACAAACCAAGCGCTCTACTTTGTCAAGGT 636
Qy      2188 GGATGAGCGGCGGTACGACACCATCCCGCAGGACAG 2226
Db      637 GGATGAGTGGGGCTATGACAGTCTACCACTCAG 675

```

RESULT 47
BX882610 646 bp mRNA linear EST 20-JUL-2004
LOCUS BX882610 cdbk Oncorhynchus mykiss cdna clone tcdk0060c.h.01 5prim,
DEFINITION mRNA sequence.
ACCESSION BX882610
VERSION BX882610.2 GI:42815406
KEYWORDS EST.
SOURCES Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 646)
GOVERNOR, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
JOURNAL On Dec 18, 2003 this sequence version replaced gi:40127495.
COMMENT Contact: Guiguen Y

INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0060 row: h column: 1
Seq primer: M13R.

FEATURES

source
Location/Qualifiers
1. 646
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcba0060c.h.01"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="cldb"
/note="Vector: pTT73D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution: AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 2.9%; Score 114.8; DB 5; Length 646;
Best Local Similarity 55.2%; Pred. No. 3.6e-13;
Matches 224; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
QY 3052 CAACATCTAACAAGATCCCTCGCTGCGAGGGGTACAGATTTCACGATGTCGTGACGCT 3111
DB 2 CAACATCTAATAGTATAGTGTCTGCAAGGCTTCAAGTTCATGCTGTCACAGAGTTT 61
QY 3112 CCCATTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGTCATCTTGACAC 3171
DB 62 GCGTTTGGTCAAGAAAGTGGCGGAACCACTGTAATCTCATCTGATCTGGGACTT 121
QY 3172 GGGCTCCCTGTGATCTCATCTCTGAAAGCGAAGAGGATGTCGTCGGGGCCCA 3231
DB 122 GCGGAGTACACCAACATCTAGTACACTGCAACAAAGGTGTCTCTAGGCTGTAA 181
QY 3232 GGGCGCCGCGCCCTCTGCTCCCTCCGAGGCGGTGAGTGGCTGTGCAACAAGATTCT 3291
DB 182 GGGTTTAAACAGTAGGCTTCAATATGAGGAGTAACTGATATATCTGTCTGCTTCT 241
QY 3292 GCTCAAGCTGACTGACACCGGTGTACCTTACGTGCACTCTGGGGTCACTCAGACAGC 3351
DB 242 GTTGGTTCTGTCCCGTCACTGCGCCCTCTACTACATCACTCTGCTCCGCTACGCA 301
QY 3352 CCAGACGAGCTGAGTCGGAAGCTCCCGGGAGAGAGCTGACGCTCCCTGGAAGCCGACG 3411
DB 302 TAAAGAGAGAGCTGAGAGGAGAGCTGAGAGGATTTGAGATTGGCCGATACAGAGGCTGC 361
QY 3412 CAACCCGCACTGCCCTCCTCAGACTTCAAGACCAATCTCTGAGTGTAGG 3457
DB 362 CACACCCAAATGCTTGAAGAGCTTCAAGGCGCATCCAGGCTTAGAGG 407

RESULT 48
BX315053 731 bp mRNA linear EST 14-MAY-2004
LOCUS BX315053 tcaay Oncorhynchus mykiss cdna clone tcaay0029b.n.21 5prim,
DEFINITION mRNA sequence.
ACCESSION BX315053
VERSION BX315053.2 GI:42620226
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 731)
AUTHORS Govoroun,M., Guiguen,Y. and Le Gac,F.
TITLE Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
JOURNAL Unpublished (2003)
COMMENT On Apr 7, 2003 this sequence version replaced gi:29595698.
Contact: Guiguen Y

INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0029 row: n column: 21
Seq primer: M13R.

FEATURES

source
Location/Qualifiers
1. 731
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcaay0029b.n.21"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="cay"
/note="Vector: pTT73D-pac; Rainbow trout multi-tissues -
normalized + 1 subtraction (tcaay); Clone distribution:
AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 2.9%; Score 114.8; DB 5; Length 731;
Best Local Similarity 55.2%; Pred. No. 3.6e-13;
Matches 224; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
QY 3052 CAACATCTAACAAGATCCCTCGCTGCGAGGGGTACAGATTTCACGATGTCGTGACGCT 3111
DB 2 CAACATCTAATAGTATAGTGTCTGCAAGGCTTCAAGTTCATGCTGTCACAGAGTTT 61
QY 3112 CCCATTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGTCATCTTGACAC 3171
DB 62 GCGTTTGGTCAAGAAAGTGGCGGAACCACTGTAATCTCATCTGATCTGGGACTT 121
QY 3172 GGGCTCCCTGTGATCTCATCTCTGAAAGCGAAGAGGATGTCGTCGGGGCCCA 3231
DB 122 GCGGAGTACACCAACATCTAGTACACTGCAACAAAGGTGTCTCTAGGCTGTAA 181
QY 3232 GGGCGCCGCGCCCTCTGCTCCCTCCGAGGCGGTGAGTGGCTGTGCAACAAGATTCT 3291
DB 182 GGGTTTAAACAGTAGGCTTCAATATGAGGAGTAACTGATATATCTGTGCTTCT 241
QY 3292 GCTCAAGCTGACTGACACCGGTGTACCTTACGTGCACTCTGGGGTCACTCAGACAGC 3351
DB 242 GTTGGTTCTGTCCCGTCACTGCGCCCTCTACTACATCTCTGCTCCGCTACGACAGC 301
QY 3352 CCAGACGAGCTGAGTCGGAAGCTCCCGGGAGAGAGCTGACGCTCCCTGGAAGCCGACG 3411
DB 302 TAAAGAGAGAGCTGAGAGGAGAGCTGAGAGGATTTGAGATTGGCCGAAACAGAGGCTGC 361
QY 3412 CAACCCGCACTGCCCTCCTCAGACTTCAAGACCAATCTCTGAGTGTAGG 3457
DB 362 CACACCCAAATGCTTGAAGAGCTTCAAGGCGCATCCAGGCTTAGAGG 407


```

RESULT 49
BX521269          568 bp      mRNA      linear      EST 27-JUN-2003
LOCUS             BX521269          Sugano mouse kidney mKia Mus musculus cDNA clone
DEFINITION        BX521269 Sugano mouse kidney mKia Mus musculus cDNA clone
IMAGE             IMAGP98M035892 ; IMAGE:2373290, mRNA sequence.
ACCESSION         BX521269
VERSION           BX521269.1  GI:32295739
KEYWORDS          EST.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 568)
Hell,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
and Korn,B.
Mouse Unigeneset - RZPD2
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP98M035892.
RZPDLIB; I.M.A.G.E. cDNA clone Collection;
Mouse Unigeneset - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD.
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
Bngf, primer sequence: CTCTGCTCTAAAGCTGCG.
Location/Qualifiers
1..568
/organism="Mus musculus"
/mo_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGP98M035892 ; IMAGE:2373290"
/sex="female"
/lab_storage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mKia"
/notes="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACTGCTG); Site 2: DraIII (CAGCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [GTGTCGCTTACTG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGCTG, 3' site CAGCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
primer CGACTGTGAGCTCGAGACA."
ORIGIN
Query Match      2.8%; Score 113.4; DB 5; Length 568;
Beet Local Similarity 69.9%; Pred. No. 6.8e-13;
Matches 153; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
3236  GCCGCCGCCCTCTGCGCCCTCGAGGCGGTGCGAGTGTGCGACACGATTCCTGCTC 3295S
Db 143  GCTCTGGCTCTTCTCTCTCTGTAAGCCGACATTTGGCTCTGTACAGACCCCTTCTGCTC 202
Qy 3296  AAGCTGACTCGACACCGTGTCACTTACGTGCGCACTCTGGGGGTCACTCGAGACAGCCGAG 3355S
Db 203  AAGCTGGCTGCTCATTTCTGTATCTACAATAATGTCTCTGGGACCTCTGAGGACAGCCCAA 262
Qy 3356  ACGACGTGAGTCCGAAGCTCCCGGAGCAGACGTGACTGCCCTTGGAGACCGGACGCAAC 3415S

```

Db		263	AAATGCTGTGGCCGGAAGTCCCGACAGGCACAATGACATCCTTTAAAGTCGACAGTGACC	322
Oy		3416	CCGGCACTGCCCTTCAGACTTCAGACCATCTGTGACTGCA	3454
Db		323	CCAGCCCTTAAGCACAGCTTTCAGACCATTTTGGACTPA	361
RESULT_50				
LOCUS		AG363333		
DEFINITION		Mus musculus molossinus DNA, clone:MSMg01-165A22.TJ, genomic survey sequence.		
ACCESSION		AG363333		
VERSION		AG363333.1		
KEYWORDS		GSS.		
SOURCE		Mus musculus molossinus		
ORGANISM		Mus musculus molossinus		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS		Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.		
TITLE		BAC end Sequences of Library MSMg01		
JOURNAL		Unpublished		
AUTHORS		2 (bases 1 to 2332)		
REFERENCE		Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.		
SEQUENCE		Direct Submission		
COMMENT		Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://ngp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)		
		Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).		
		The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan		
		phone: 81-298-36-9189, fax: 81-298-36-9199		
		e-mail: abe@rtc.riken.jp		
		PRIMERS		
		Sequencing : TV		
		LIBRARY		
		Rector : pBACe3.6		
		R.Site 1 : EcoRI		
		R.Site 2 : EcoRI		
FEATURES		Location/Qualifiers		
source		1..2332		
		/organism="Mus musculus molossinus"		
		/mol_type="genomic DNA"		
		/sub_species="molossinus"		
		/db_xref="taxon:57486"		
		/clone="MSMg01-165A22.TJ"		
		/sex="male"		
		/tissue type="mixture of kidney and spleen"		
		/clone_lib="MSMg01 Mouse Male BAC Library"		
ORIGIN				
		Query Match 2.8%; Score 112.4; DB 9; Length 2332;		
		Best Local Similarity 43.7%; Pred.No.1.4e-12;		
		Matches 679; Conservative 0; Mismatches 864; Indels 10; Gaps 4;		
Oy		7	CTGCGTCTGCTGCGCAGTGGAGAAGCCCTTGCCCCCGGACCCCGCGATCCGCGCGC	66
Db		695	CCGGCGGATGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	754
Oy		67	TCCCGCGTCCGCGAGCCGTGCGCTCCCTGCGTGGCGAGCAGCAGCGGAGTGTGCGCGT	126
Db		755	CCTCCGT	814
Oy		127	GAGCAGCTTGTGCGCGCGCGCTTGAGGCCCAAGAGCGCTGCGCTGTGTGAGCGCGGAGACC	186
Db		815	GCGCGGCG	874
Oy		187	GAGCGGCTTTCCGCGCGCGCTGTGAGCCCAAGTGTGTGTGCTGCTGCCCTTGAGACGACGCGC	246

[illegible][illegible]

Search completed: October 28, 2004, 18:35:29
Job time : 11555 secs

1629 CCGGCTGGCCGAGGACCGTTCCTGGCCAGGTTC 1688

Db 721 CCTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTCACCTGCAGAGACCAGCC 780

AUTHORS
Clark, A.G., Głanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Feld, M., ...

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

QY 3360 AGCTGAGTGGAGAGCTCCCGGGGAGCGAGCTGACCTCGAGGCGCGAGCAACCCG 3419
DB 1741 TGCTGTGCGGAGAGCTCCCGAGGAGGAGCAATGACCTTAACTGTGAGTGCAGC 1800
QY 3420 CACTGCGCTCAGACTTCAAGACCATCTGACTGA 3454
DB 1801 CCTAAGCAGAGACTTTCAGACATTTTGGACTAA 1835

RESULT 4
BM453198 925 bp mRNA linear EST 05-FEB-2002
LOCUS DEFINITION AGENCOURT 6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840
5', mRNA sequence.
BM453198
ACCESSION BM453198.1 GI:18502238
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 925)
NIH-MGC http://mgi.mgi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2208 row: p column: 01
High quality sequence stop: 646.
Location/Qualifiers
1..925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5529840"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1: Not;
Site_2: Salt; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN
Query Match 20.1%; Score 806; DB 4; Length 925;
Best Local Similarity 99.2%; Pred. No. 1.7e-157;
Matches 821; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 2149 GGGCCAGAGCCCGCGCTGACTGACTTGTCAAGTGTGAGCGGCGGTACGA 2208
DB 2 GGGCCAGAGCCCGCGCTGACTGACTTGTCAAGTGTGAGCGGCGGTACGA 61
QY 2209 CACCATCCCCAGAGCAGGCTCAGCGAGGTGATCGGACATCATCAACCCAGAAC 2268
DB 62 CACCATCCCCAGAGCAGGCTCAGCGAGGTGATCGGACATCATCAACCCAGAAC 121
QY 2269 GAACTGCGGTGCTGATGCGGTGCTGCAAGAGCGCGCTGAGGACAGTCCGAGAGC 2328
DB 122 GAACTGCGGTGCTGATGCGGTGCTGCAAGAGCGCGCTGAGGACAGTCCGAGAGC 181
QY 2329 CTTCAAGAGCCAGTCTTACCTTGACAGACTCCAGCGTACATGCGAGTGTGTC 2388
DB 182 CTTCAAGAGCCAGTCTTACCTTGACAGACTCCAGCGTACATGCGAGTGTGTC 241
QY 2389 TCACCTGAGAGAGACAGCCCGCTGAGGAGTGGTGTGATCGAGAGAGTCTCTCT 2448
DB 242 TCACCTGAGAGAGACAGCCCGCTGAGGAGTGGTGTGATCGAGAGAGTCTCTCTCT 301

QY 2449 GAATGAGCCAGAGAGTGCCTCTTGAAGTCTTCTTACGCTTATGATGACAGCCGT 2508
DB 302 GAATGAGCCAGAGAGTGCCTCTTGAAGTCTTCTTACGCTTATGATGACAGCCGT 361
QY 2509 GCGCATCAGAGGAGCAAGTCTTACAGTGCAGGAGATCCCGAGGCTTCATCTCTC 2568
DB 362 GCGCATCAGAGGAGCAAGTCTTACAGTGCAGGAGATCCCGAGGCTTCATCTCTC 421
QY 2569 CACGCTGCTTGCAGCCTGTGCTAGGAGCATGAGAACAGCTGTTGGGGATTCG 2628
DB 422 CACGCTGCTTGCAGCCTGTGCTAGGAGCATGAGAACAGCTGTTGGGGATTCG 481
QY 2629 GCGGAGCAGGAGTGCCTCTGCTGTTGGTGGATGATTTCTTGTGGAGACCTCACCTGAC 2688
DB 482 GCGGAGCAGGAGTGCCTCTGCTGTTGGTGGATGATTTCTTGTGGAGACCTCACCTGAC 541
QY 2689 CCAGCGAAGAACTTCTCAGAGACCTGCTGCTGAGTCTCCCTGATGCTGCTGCT 2748
DB 542 CCAGCGAAGAACTTCTCAGAGACCTGCTGCTGAGTCTCCCTGATGCTGCTGCTGCT 601
QY 2749 GAACCTTGGGAGAGAGAGTGTGAATCTTCCCTGTAGAGAGAGGCTGAGGAGAGCC 2808
DB 602 GAACCTTGGGAGAGAGAGTGTGAATCTTCCCTGTAGAGAGAGGCTGAGGAGAGCC 661
QY 2809 TTTTGTGAGATGCGGCGCCAGAGGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2868
DB 662 TTTTGTGAGATGCGGCGCCAGAGGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
QY 2869 GACCTTGAAGTGCAGAGCAGTACTGACAGTATGCGGAGCTTCATCAGAGCAGTCT 2928
DB 722 GACCTTGAAGTGCAGAGCAGTACTGACAGTATGCGGAGCTTCATCAGAGCAGTCT 781
QY 2929 CACCTTCAACCGCGCTTCAA--GGCTGGAGAGAACATGCGTGGGAAA 2974
DB 782 CACCTTCAACCGCGCTTCAAAGGCTGGAGAGAACATGCGTGGGAAA 829

RESULT 5
BU702370 851 bp mRNA linear EST 15-JUL-2003
LOCUS DEFINITION UI-M-F10-byx-f-12-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
IMAGE:6400523 5', mRNA sequence.
BU702370
ACCESSION BU702370.1 GI:23627105
VERSION
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 851)
NIH-MGC http://mgi.mgi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1..851
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6400523"

Db 288 GCCACCTTTCTTCACAGAGACCCGGCTTTCACCTCCACATAGGAATGTCATCCCC 229
Oy 3783 AGATTGCGCATTTGTCACCCCTGCGCCCTCCCTTCCTTCCATCCCAACATCCAG 3842
Db 228 AGATTGCGCATTTGTCACCCCTGCGCCCTCCCTTCCTTCCATCCCAACATCCAG 169
Oy 3843 GTGAGACCCCTGAGAGACCCCTGAGAGCTCTGGGAATTTGAGTAGACCAAGCTGTGCC 3902
Db 168 GTGAGACCCCTGAGAGACCCCTGAGAGCTCTGGGAATTTGAGTAGACCAAGCTGTGCC 109
Oy 3903 CTGTAACAGAGCGAGAGACCCCTGAGAGCTCTGGGAATTTGAGTAGACCAAGCTGTGCC 3962
Db 108 CTGTAACAGAGCGAGAGACCCCTGAGAGCTCTGGGAATTTGAGTAGACCAAGCTGTGCC 49
Oy 3963 GGTGCTGTGGAGTAAATATCTGAATATTTGAGTTTTCAGTTTGA 4010
Db 48 GGTGCTGTGGAGTAAATATCTGAATATTTGAGTTTTCAGTTTGA 1

RESULT 7

LOCUS BM824748 492 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0096335 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-99-E07
5', mRNA sequence.

ACCESSION BM824748
KEYWORDS EST.
SOURCE Homo sapiens (human)

REFERENCE
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, U.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 99 row: E column: 07
High quality sequence stop: 492.
Location/Qualifiers

FEATURES

source 1..492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNUI6n1-99-E07"
/sex="F"
/tissue_type="Asclites"
/cell_type="Lymphoblast-like"
/cell_line="SNV-16"
/lab_host="DH10B"
/clone_lib="S22SNUI6n1"
/note="Organ: Stomach; Vector: pT73-Pac; Site 1: EcorI; Site 2: NotI; The S22SNUI6 library was contributed by the Soars laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNV-16 culture. SNV-16 cell was obtained from Korean Cell Line Bank (KCLB). SNV-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 11.1%; Score 445; DB 4; Length 492;
Best Local Similarity 100.0%; Pred. No. 3.7e-82;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2768 GGAACCTTCCCTGTAAGAGAGAGCCCTGGGTGACAGGCTTTTGTTCAGATGCCGCC 2827
Db 1 GGAACCTTCCCTGTAAGAGAGAGCCCTGGGTGACAGGCTTTTGTTCAGATGCCGCC 60
Oy 2828 CAGGCGCTATTTCCCTGTGTGGCGGCTGTCTGTGATATCCCGAGCCCTGAGAGTGCAGAGC 2887
Db 61 CAGGCGCTATTTCCCTGTGTGGCGGCTGTCTGTGATATCCCGAGCCCTGAGAGTGCAGAGC 120
Oy 2888 GACTACTCCAGTATAGCCCGGACCTCCATCAGAGGCACTTCACCTTCAACCGGGCTTC 2947
Db 121 GACTACTCCAGTATAGCCCGGACCTCCATCAGAGGCACTTCACCTTCAACCGGGCTTC 180
Oy 2948 AAGCGTGGAGAGAGATCGGTGCAAACTTTGGGGCTTTGCGGCTGAAGTGCAGAGC 3007
Db 181 AAGCGTGGAGAGAGATCGGTGCAAACTTTGGGGCTTTGCGGCTGAAGTGCAGAGC 240
Oy 3008 CTGTTTCTGATTTTTCAGGTGAACAGCTCCAGAGCGGTGTGACCAACATCTACAGAGATC 3067
Db 241 CTGTTTCTGATTTTTCAGGTGAACAGCTCCAGAGCGGTGTGACCAACATCTACAGAGATC 300
Oy 3068 CTCTGCTGTCAGAGCTTACAGGTTTTCAGGATGTGTGTCAGCTCCCATTTTCATCAGCA 3127
Db 301 CTCTGCTGTCAGAGCTTACAGGTTTTCAGGATGTGTGTCAGCTCCCATTTTCATCAGCA 360
Oy 3128 GTTGGAGAGAACCCCAATTTTCTGCGCGGCTATCTGTGACAGGAGGCTCCTGTGCTAC 3187
Db 361 GTTGGAGAGAACCCCAATTTTCTGCGCGGCTATCTGTGACAGGAGGCTCCTGTGCTAC 420
Oy 3188 TCCATCTCGAAGGCCAGAGCGAG 3212
Db 421 TCCATCTCGAAGGCCAGAGCGAG 445

RESULT 8
LOCUS BG917907 851 bp mRNA linear EST 05-JUN-2001
DEFINITION 602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
mRNA sequence.

ACCESSION BG917907
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10903 row: K column: 08
High quality sequence stop: 753.
Location/Qualifiers

FEATURES

source 1..851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4949887"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"

/note="Organ: mammary; Vector: pCMV-SPORTS; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

10.4%; Score 419; DB 4; Length 851.

Query Match	10.4%;	Score 419;	DB 4;	Length 831;
Best Local Similarity	71.9%;	Pred. No. 1.1e-76;		
Matches 579; Conservative	0;	Mismatches 215;	Indels 11;	Gaps 2

[illegible]

RESULT 9					
AM276315/c					
LOCUS	AM276315	416 bp	mRNA	linear	EST 03-JAN-2000
DEFINITION	xrl0b12.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3'				
ACCESSION	mRNA sequence.				
	AM276315				

VERSION	AW276315.1	GI:666334
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

FEATURES

acinos

High quality sequence stop: 413

High quality sequence stop: 413

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2759711"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/clone_1b="NCI CGAP Lu28"
/name="Organ: lung; Vector: pCMV-Sport6; Site: 1: SalI;
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

```

RESULT 10			
AA281296			
LOCUS	389 bp	mRNA	linear
AA281296			EST 14-AUG-1997

DEFINITION	z080902.t1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5', mRNA sequence.
ACCESSION	AA281296
VERSION	AA281296.1
KEYWORDS	EST.
SOURCE	GI:1924194
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 389) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LML ; contact the IMGE Consortium (info@image.llnl.gov) for further information. Insert length: 2187 Std Error: 0.00 Seq primer: -28ml3 rev2 ER from Amerham High quality sequence stop: 385. Location/Qualifiers 1..389
FEATURES	

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:712562"
/tissue_type="germinal center B cell"
/lab_host="MDH10B"
/clone_lib="NCI CGAP GCBI1"
/notes="vector: pT7TD-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I, Site.2: Eco RI, 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, Ig-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marcu (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCTAGATGGAGGCGCGCTCATTTTTTTTTTTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7TS vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Ronaldo."

```

ORIGIN

Query Match	Best Local Match	Similarity	Score	DB 1	Length	Matches	Conservative	Mismatches	Indels	Gaps
		99.5%	385.8	DB 1	389	387	0	2	0	0
Qy	1679	GCCAAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGCTCTTCTTT	1738							
Db	1	GCCAAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGCTCTTCTTT	60							
Qy	1739	TATGTACGGAAGACCAGCTTTCAAAAAGAACAGGCTCTTTTCTACGGAAGAGTGTCTGG	1798							
Db	61	TATGTACGGAAGACCAGCTTTCAAAAAGAACAGGCTCTTTTCTACGGAAGAGTGTCTGG	120							
Qy	1799	AGCAAGTTGCAAAAGATTGGAATCGAACAAGCACTTGAAGAGGTGCACTCGGAGCTG	1855							
Db	121	AGCAAGTTGCAAAAGATTGGAATCGAACAAGCACTTGAAGAGGTGCACTCGGAGAGCTG	180							
Qy	1859	TCGGAGCAGAGGTGAGCAGCATTCGGAGAGCCAGCCCGCTCTGACGTCCAGATC	1918							
Db	181	TCGGAGCAGAGGTGAGCAGCATTCGGAGAGCCAGCCCGCTCTGACGTCCAGATC	240							
Qy	1919	CGCTTCATCCCCAGCCTGACGGGCTGGCGGATTTGTGAACATGAACATGCTGTGGGA	1978							
Db	241	CGCTTCATCCCCAGCCTGACGGGCTGGCGGATTTGTGAACATGAACATGCTGTGGGA	300							
Qy	1979	GCCGAAGAGTTCCGAGAGAAAAGAGGGCCGAGCGCTCACTCGAGGGTGAAGGCACTG	2038							
Db	301	GCCGAAGAGTTCCGAGAGAAAAGAGGGCCGAGCGCTCACTCGAGGGTGAAGGCACTG	360							

```

QY      2039 TTACGCGTGTCACTACGAGCGGGCGC 2067
        |||||
Db       361 TTCAGCGTGCTCACTACGAGCGGGCGC 389

```

RESULT	11
CN274427	
LOCUS	CN274427 409 bp mRNA linear EST 16-MAY-2004
DEFINITION	U70005J31226763 GRN_ES Homo sapiens CDNA 5' , mRNA sequence
ACCESSION	CN274427
VERSION	CN274427.1 GI:47290841
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (Pages 1 to 409)
Brandenberger R., Wei H., Zhang S., Lei S., Muraige J., Flisk G J ,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam R ,
Lebkowskij, J and Stanton, J. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R

```

Geeron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel.: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geeron.com
Insert Length: 409 Std Error: 0.00.
Location/Qualifiers
1. 409

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref=
/tissue="
H9"
/clone_id="
/notes="
from und
and H9

```

Query Match	Best Local Similarity	Matches	382; Conservat
QY	1	GCAGCGCTGGCT	9
Db	27	GCAGCGCTGGCG	
QY	61	GGCGGCTGGCC	
Db	87	GGCGGCTGGCC	
QY	121	GGCGGCTGGC	
Db	147	GGCGGCTGG	
QY	181	GGACCCGG	
Db	207	GGACCCG	
QY	241	ACGGCG	
Db	267	ACGGCT	
QY	301	CCGAG	
Db	327	CCG	
QY	361	GCTT	

Page

GGACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCCT 241

CGCCCCCGCGCGCCCCCTCCTTCGGCCAGGTGTG 279

CACCTGGCCGACCTTTCCTTCACCAAGGTGTG 302

GAGGCTGTGCGAGCGCGGCGCAAGAA 339

CTGCGAGCGCAACGAGAGAAA 362

GGGCCCCCCCCGAGGCCCTT 399

CCTCCCATGGCCTT 422

GGGGGAGCGG 459

CAGTGG 482

CG 519

42

Db 387 GCTGTCGACGCGGCCCGCGG 409

RESULT 12
LOCUS CF531121 688 bp mRNA linear EST 12-SEP-2003
DEFINITION UI-M-FY0-cgp-m-21-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:30355988 5', mRNA sequence.
ACCESSION CF531121
VERSION CF531121.1 GI:34583085
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 688)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
Seq primer: PYX-5.
Location/Qualifiers
1..688
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355988"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN
Query Match 8.6%; Score 346.2; DB 7; Length 688;
Best Local Similarity 73.9%; Pred. No. 1.7e-61;
Matches 438; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

40 CCGGCGACCCCGGATGCGGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGTCG 99
63 CCGGCGCTTGAGACAAATACCCGCGCTCTGTTGCCCGCGGTCCTCTCTCG 122
100 CAGCCACTACCCGAGGTCGTCGCGTGCACAGTTGTCGCGCCGCTTGCGGCCAGG 159
123 CAGCCGATACCGGAGAGTGTGCGCGCACTTTGTGCGCGCGCTGCGGCCGAGAG 182
160 CTGGCGGCTGTGTCACCGCGGCGGCGCTTCCGCGCGCTGTGCGCCAGTGCT 219

Db 183 CAGCGGCTGTGCAACCCG 220
GATGTGCGTCCTCTGGACGACG 243
AGTGTGATGACATCGGGGCTCACAGCCTC 280
CTGCTTAAGAGTGTGTGCCCCGAGTGTGCA 303
ATCCCTAAGAGTGTGTGCGCAGGTTGTGCA 340
CGTGTGCGCTTGGCTTCCGCTGTCGACGCGG 363
CTGTGCTTTTGTGCTTTGAGTCTTAAGAGG 400
CAGCAGCGCTGCGCAGCTACTCTGCCCAAC 423
CACTAGTAGCGTGTGCTACTTGTCCCAAC 460
GGCGTGGGGGTGCTGCTGCGCGCGCTGGG 483
TGCAATGATGCTACTGTGAGCCGAGTGAG 520
CTGCGCGCTCTTGTGCTGTGCTGCCAGCT 543
CTGTGCTTTTATCTTCTGCGGCCCGAGCT 580
GTACCACTGCGCGCTGCACTCAGGCCCGCC 602
GCTAAACCCCTCATTTCTACTCAGCANCCT 632
GCTAAACCCCTCATTTCTACTCAGCANCCT 655

RESULT 13
LOCUS CF531069 649 bp mRNA linear EST 12-SEP-2003
DEFINITION UI-M-FY0-cgp-c-19-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:30355746 5', mRNA sequence.
ACCESSION CF531069
VERSION CF531069.1 GI:34583033
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 649)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
Seq primer: PYX-5.
Location/Qualifiers
1..649
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose

1996. Denatured RNA was size fractionated on a 1% agarose

QY 62 CGCGCTCCCGGCGGAGCCGTCGCTCCCTGTCGCGAGCACTACCGCGAGCTGCTG 121
 DB 121 CGCGCTCCCGGCGGAGCCGTCGCTCCCTGTCGCGAGCACTACCGCGAGCTGCTG 180
 QY 122 CGCGCTCCCGGCGGAGCCGTCGCTCCCTGTCGCGAGCACTACCGCGAGCTGCTG 181
 DB 181 CGCGCTCCCGGCGGAGCCGTCGCTCCCTGTCGCGAGCACTACCGCGAGCTGCTG 240
 QY 182 GACCCGCGGCTTTCGCGCGGCTGTCGCGAGCACTACCGCGAGCTGCTG 241
 DB 241 GACCCGCGGCTTTCGCGCGGCTGTCGCGAGCACTACCGCGAGCTGCTG 300
 QY 242 CGCGCGGCTTTCGCGCGGCTGTCGCGAGCACTACCGCGAGCTGCTG 301
 DB 301 CGCGCGGCTTTCGCGCGGCTGTCGCGAGCACTACCGCGAGCTGCTG 360
 QY 302 CGAGTGTGCAAGAGCTGTCGCGAGCACTACCGCGAGCTGCTG 361
 DB 361 AGGGTGTGCAAGAGCTGTCGCGAGCACTACCGCGAGCTGCTG 420
 QY 362 CTGCTGAGCGGCGGCGGCGGCTTTCGCGAGCTTTCACACAGCTGCGAGCTAC 421
 DB 421 CTGCTGAGCGGCGGCGGCGGCTTTCGCGAGCTTTCACACAGCTGCGAGCTAC 480
 QY 422 CTGCTGAGCGGCGGCGGCGGCTTTCGCGAGCTTTCACACAGCTGCGAGCTAC 481
 DB 481 TTGCCCAACTGTATTTGAGACCTTCTGCGAGCTTTCACACAGCTGCGAGCTAC 540
 QY 482 CGCGTGGCGGCGGCGGCGGCTTTCGCGAGCTTTCACACAGCTGCGAGCTAC 539
 DB 541 CGAGTGGCGGCGGCGGCGGCTTTCGCGAGCTTTCACACAGCTGCGAGCTAC 598

RESULT 15
 LOCUS BQ258274 664 bp mRNA linear EST 06-MAY-2002
 DEFINITION NISC_Kp11904.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone
 IMAGE:5409222, mRNA sequence.
 ACCESSION BQ258274
 VERSION BQ258274.1 GI:20459030
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 664)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strauberg, Ph.D.
 EMAIL: cga@bbs-rmail.nih.gov
 CDNA Library Preparation: J. Baker (Stanford University)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/ILNLS
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLS at: info@image.llnl.gov
 MGI:1845958
 Plate: ILNLS2043 row: N column: 7
 Seq primer: Sp6 primer.
 Location/Qualifiers
 1..664
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:5409222"
 /tissue_type="embryo", late gastrula"
 /dev_stage="embryo", 7.5 dpc"
 /lab_host="XLI-Blue"

ORIGIN
 Query Match 7.9%; Score 317.8; DB 5; Length 664;
 Best Local Similarity 68.3%; Pred. No. 1.4e-55;
 Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;
 /clone.lib="Baker mouse embryo e7.5"
 /note="Vector: PCS105; Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned into SalI/NotI sites using the following 5' adaptor: 5'-TCACCCAGGCTCC-3'. Size-selected for average insert size 1.8-1.9 kb. Library constructed by J. Baker (Stanford University)."
 1108 GCCAGCCTGACTGCGGCTCGAGGCTGAGACATCTTCTGAGTTCCAGGCTTG 1167
 DB 9 GCTTACCTGACCTGGGCGAGAGACTGAGATCATCTTCTGAGCTCAAGGCTAG 68
 QY 1168 GATGCGAGGACTCCCGCAGCTTGGCCCGCCGAGGCTACCTGCAATGCGGCC 1227
 DB 69 GACATCAAGACCACTGCGAGGACACCGCTATGCGCTGATCTGCGAGATGCGGCC 128
 QY 1228 CCGTCTTCTGAGCTGCTGAGAACCAAGCGCAGTGCCTTACGAGGCTCTCAAGAC 1287
 DB 129 CCGTCTTCAAGCTGCTGCTGAGAACCAAGCGCAGTGCCTTACGAGATGCTCAAGGCTC 188
 QY 1288 GCACTGCGGCTGCGAGCTGCGTCAACCCAGACCGGCTGCTGCTGCGGAGAACCC 1347
 DB 189 ACATTGAGGTTTGAGACAGCAACCAAGTGCAGATGCTC----- 232
 QY 1348 CCAAGGCTCTGAGGCGGCGGCGGAGGAGAGACAGACAGCCCGCTGCTGAGACT 1407
 DB 233 -----TGAAACAGGCCACCGACCTCAAGATTT 263
 QY 1408 GCTCCGAGCAGACAGACCCCTGCGAGTACGCTTCTGCGGCTGCTGCGCGC 1467
 DB 264 GCTCCGCTGACACAGACCTCTGCGAGTATGATGTTCTTGGGCTGCTTCTGCA 323
 QY 1468 GCTGTCGCGGCGGCTGCTGAGGCTCCAGGACCAAGAGCGGCTTCTCAGGAACAC 1527
 DB 324 GGTGTCGCTGCTGCTGCTGAGGCTCCAGGACCAATAGCGCTTCTTAAAGACTT 383
 QY 1528 CAAGAAGTTCATCTCCGAGGAGACATGCAAGCTCTGCTGAGAGCTGACGTGAA 1587
 DB 384 AAGAGATTCATCTCTGAGGAAATAGGCAAGCTATCAGTCAGGAATGATGGA 443
 QY 1588 GATGAGCGTGCAGGACTGCTGCTGCTGCGAGGAGCCAGGAGGCTGCTGCTGCGGC 1647
 DB 444 GATGAAGTGAAGGATGCTGCTGCTGCTGCGAGGAGCCAGGAGGAGCCGCTGCTGCG 503
 QY 1648 CGAGAGCAACCGTGCAGGAGGAGATCTGAGCAAGTCTGCACTGCTGATGATGT 1707
 DB 504 TGCAGAGCACCGTGCAGGAGGAGATCTGCTGATGCTGCTGCTGATGAGAC 563
 QY 1708 GTAGCTGCTGAGCTGCTGAGTCTTCTTATGTACGAGACCACTTCAAAAGAA 1767
 DB 564 ATACGTCGTCAGCTGCTTATGATCTTCTTATCAACAGAGACCACTTCAAGAGAA 623
 QY 1768 CAGGCTCTTCTTACCGGAGAGTCTGAGGACAAAGTTGC 1808
 DB 624 CAGGCTCTTCTTACCGGAGAGTGTGAGCAAGCTGC 664

Search completed: October 30, 2004, 03:12:56
 Job time : 1157 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 08:05:49 : Search time 1764 Seconds

(without alignments)
11948.087 Million cell updates/sec

Title: US-10-044-692-1

Perfect score: 4015
Sequence: 1 GCAGCGCGCGCCGCTGTC.....TTTTCAGTTTGAAGAAAA 4015

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001s:*
- 5: geneseqn2002s:*
- 6: geneseqn2002bs:*
- 7: geneseqn2003s:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2003ds:*
- 11: geneseqn2004s:*
- 12: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4015	100.0	4015	2	AAZ00724 Human tel
2	4015	100.0	4015	2	AAZ020279 Human tel
3	4015	100.0	4015	2	AAZ30154 enco
4	4015	100.0	4015	4	AAH45901 Human htr
5	4015	100.0	4015	6	AAH46821 Human tel
6	4015	100.0	4015	6	ABH97534 Cancer ce
7	4015	100.0	4015	8	ABH97552 Human tel
8	4015	100.0	4015	8	ABZ22474 Human tel
9	4015	100.0	4015	9	ACC54482 Human tel
10	4015	100.0	4015	10	ACC58039 Human tel
11	4015	100.0	4015	12	ADG85223 Human tel
12	4015	100.0	4015	12	ADH82171 Human CDN
13	4015	100.0	4015	12	AAV72117 Human cat
14	4015	100.0	4015	6	ABH53711 Human tel
15	4015	100.0	4015	8	AAZ08150 Human tel
16	4015	100.0	4015	8	ABZ18391 Group III
17	4015	100.0	4015	2	AAV60320 Human tel
18	4015	100.0	4015	2	AAV22428 Human tel
19	4015	100.0	4015	2	AAH89424 Human EST
20	4015	100.0	4015	3	AAA29388 HEST2, a
21	4015	100.0	4015	10	ADC47060 Human TER

22	4002	99.7	4027	10	ADH40481	Adh40481 Human tel
23	3956.8	98.6	3964	2	AAH18254	AAH18254 Human tel
24	3885	96.8	3955	2	AAV22379	AAV22379 Human tel
25	3872	96.4	3918	2	AAH18269	AAH18269 Telomeras
26	3872	96.4	3918	2	AAH18278	AAH18278 Telomeras
27	3782.8	94.2	3798	2	AAV27876	AAV27876 Human tel
28	3641	90.7	3855	2	AAV22382	AAV22382 Human tel
29	3400	84.7	3453	8	ABZ76217	ABZ76217 Human TER
30	3400	84.7	13766	6	AAH46790	AAH46790 pGRN145 p
31	3399	84.7	3399	6	ABV78144	ABV78144 Human tel
32	3399	84.7	3399	6	ABZ35720	ABZ35720 Human eio
33	3399	84.7	3399	6	ABX09963	ABX09963 Human tel
34	3399	84.7	3399	6	ABH191685	ABH191685 Human pol
35	3399	84.7	3399	12	ADG90598	ADG90598 Human TER
36	3396	84.6	3396	4	AAH48235	AAH48235 Heart mus
37	3396	84.6	3396	4	AAH49601	AAH49601 Human cod
38	3396	84.6	3396	4	AAH44366	AAH44366 Human tel
39	3396	84.6	3396	12	ADG70113	ADG70113 hTERT cod
40	3392.8	84.5	3396	2	AAH18266	AAH18266 Telomeras
41	3388	84.4	8742	6	AAH46793	AAH46793 pWGB5a pl
42	3307.8	82.4	3543	8	ABZ69628	ABZ69628 Plasmid c
43	3278.8	81.7	3500	2	AAH18275	AAH18275 Telomeras
44	3201.4	79.7	3203	2	AAH18268	AAH18268 Altered c
45	3121	77.7	3167	2	AAH18271	AAH18271 Altered c

ALIGNMENTS

RESULT 1
AAZ00724
ID AAZ00724 strandcd: DNA; 4015 BP.

XX AC AAZ00724;
XX DT 06-OCT-1999 (first entry)
XX DE Human telomerase catalytic domain DNA.

XX KM Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
XX KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
XX KM acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
XX KW breast cancer; ss.

XX OS Homo sapiens.
XX PN DE19804372-A1.
XX PD 05-AUG-1999.
XX PF 04-FEB-1998; 98DE-01004372.
XX PR 04-FEB-1998; 98DE-01004372.
XX PA (DAHM/) DAHM M W.
XX PI Dahm MW;
XX DR WPI; 1999-431408/37.
XX PT Quantifying tumor cells by amplifying mRNA encoding the catalytic subunit
XX of telomerase.
XX PS Example; Fig 1A-B; 26pp; German.

This invention describes a novel method for the quantitation of tumour cells in a body fluid which comprises (1) enrichment or isolation of tumour cells in the sample, (2) amplification of mRNA from these cells that encodes the catalytic subunit of telomerase and (3) quantifying the amount of amplified mRNA. The method is applied to tumour cells derived from (micro)metastases, e.g. associated with a wide range of tumours such as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia, melanoma, pulmonary carcinoma, cancer of colon or breast etc. This

Db 2041 CAGCGTGTCTAATCTAGACGGGCGCGCGCCCGGCTCTGTGGCGCTCTGTGTGG 2100
Qy 2101 CTTGACGATATTCACAGGGGCTTGGCGCACTTCTGCTGCGTGTGGCGGAGGAGCC 2160
Db 2101 CTTGACGATATTCACAGGGGCTTGGCGCACTTCTGCTGCGTGTGGCGGAGGAGCC 2160
Qy 2161 GCGGCTGTAGCTGTCTTGTGTCAAGGTGATGACGAGGCGGTGACACCATCCCA 2220
Db 2161 GCGGCTGTAGCTGTCTTGTGTCAAGGTGATGACGAGGCGGTGACACCATCCCA 2220
Qy 2221 GAGACGGCTACGAGGAGTATGCGCAGCATCAAAACCCAGAAACAGTACTGTGCG 2280
Db 2221 GAGACGGCTACGAGGAGTATGCGCAGCATCAAAACCCAGAAACAGTACTGTGCG 2280
Qy 2281 TCGGATGCGCGTGTCTCAAGAGCGCGCCCATGGGACGTCGCCAAGGCTTTCAAGCCA 2340
Db 2281 TCGGATGCGCGTGTCTCAAGAGCGCGCCCATGGGACGTCGCCAAGGCTTTCAAGCCA 2340
Qy 2341 GGTCTTACTTGAAGACCTTCAGCGGTCATGCGACAGTTCGTGGCTCACCTGAGGA 2400
Db 2341 GGTCTTACTTGAAGACCTTCAGCGGTCATGCGACAGTTCGTGGCTCACCTGAGGA 2400
Qy 2401 GACGACCCGCTGAGGAGTCCGTGTCTATGAGACAGAGCTCTCTGTAATGAGCCAG 2460
Db 2401 GACGACCCGCTGAGGAGTCCGTGTCTATGAGACAGAGCTCTCTGTAATGAGCCAG 2460
Qy 2461 CAGTGGCTCTTGTGACGCTTCTTCAAGTTCATGTGACCAAGCGGTGCGATCAAGGG 2520
Db 2461 CAGTGGCTCTTGTGACGCTTCTTCAAGTTCATGTGACCAAGCGGTGCGATCAAGGG 2520
Qy 2521 CAAGTCTTACGTCAGAGTCAGAGGATCCCGAGGGCTCATCTCTCCAGCTGTCTG 2580
Db 2521 CAAGTCTTACGTCAGAGTCAGAGGATCCCGAGGGCTCATCTCTCCAGCTGTCTG 2580
Qy 2581 CAGCTGTGTCTAAGCGGACATGAGAAAGAGCTGTTGCGGAGATTGCGCGAGCGGCT 2640
Db 2581 CAGCTGTGTCTAAGCGGACATGAGAAAGAGCTGTTGCGGAGATTGCGCGAGCGGCT 2640
Qy 2641 GGTCTGTGCTTGTGGAGATTTCTTGTGTGACACTTCACTTCAACCCAGCGGAAAC 2700
Db 2641 GGTCTGTGCTTGTGGAGATTTCTTGTGTGACACTTCACTTCAACCCAGCGGAAAC 2700
Qy 2701 CTTCTCAGAGACCTTGTGTCAGAGTGTCCCTGAGTGTGCTGCTGTAACCTTGGGAA 2760
Db 2701 CTTCTCAGAGACCTTGTGTCAGAGTGTCCCTGAGTGTGCTGCTGTAACCTTGGGAA 2760
Qy 2761 GACAGTGTGAACTTCCCTGTAGAAAGACGAGCCCTGAGTGTGCAAGCTTTTGTTCAGT 2820
Db 2761 GACAGTGTGAACTTCCCTGTAGAAAGACGAGCCCTGAGTGTGCAAGCTTTTGTTCAGT 2820
Qy 2821 GCGGCGCCACCGGCTTATTCCTGTGTGCGGCTGTGTGTGATCCCGAACCTTGAAGT 2880
Db 2821 GCGGCGCCACCGGCTTATTCCTGTGTGCGGCTGTGTGTGATCCCGAACCTTGAAGT 2880
Qy 2881 GAGAGCGCATCTACAGCTATGCGCGACCTTCATCAGAGCAGTCTACCTTCAACCG 2940
Db 2881 GAGAGCGCATCTACAGCTATGCGCGACCTTCATCAGAGCAGTCTACCTTCAACCG 2940
Qy 2941 CCGCTTCAAGGCTGGAGGACATGCTGTGCAAACTTTTGGGCTTTTGGCTGAAGT 3000
Db 2941 CCGCTTCAAGGCTGGAGGACATGCTGTGCAAACTTTTGGGCTTTTGGCTGAAGT 3000
Qy 3001 TACAGAGCTGTTTGTGATTTTGAAGTGAACAGCTTCCAGAGGCTGTGACCAACTCTA 3060
Db 3001 TACAGAGCTGTTTGTGATTTTGAAGTGAACAGCTTCCAGAGGCTGTGACCAACTCTA 3060
Qy 3061 CAAGATCTCTGTGTCAGAGGTCAGGTTTCAAGATGTGTCTCAAGCTTCCATTTCA 3120
Db 3061 CAAGATCTCTGTGTCAGAGGTCAGGTTTCAAGATGTGTCTCAAGCTTCCATTTCA 3120
Qy 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGTGCGGTCTCTGACAGCGGCTCCCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGTGCGGTCTCTGACAGCGGCTCCCT 3180

Qy 3181 CTGCTACTTCATCTGAAAGCCAAAGACGACAGGATGTGTGTGGGGCCAAAGGCGCGC 3240
Db 3181 CTGCTACTTCATCTGAAAGCCAAAGACGACAGGATGTGTGTGGGGCCAAAGGCGCGC 3240
Qy 3241 CCGGCTCTGCGCTTCGAGGCGGTGAGTGTGTGCAACCAAGATTCCTGCTCAAGT 3300
Db 3241 CCGGCTCTGCGCTTCGAGGCGGTGAGTGTGTGCAACCAAGATTCCTGCTCAAGT 3300
Qy 3301 GACTGACACCGTGTACCTTACAGTGTGCTCTGTGGGTCTCTCAGACAGGCCAAGCA 3360
Db 3301 GACTGACACCGTGTACCTTACAGTGTGCTCTGTGGGTCTCTCAGACAGGCCAAGCA 3360
Qy 3361 GCTGAGTGTGAAGCTCCCGGAGACGACGCTGACTGCTGAGGCGGAGCCACCGGC 3420
Db 3361 GCTGAGTGTGAAGCTCCCGGAGACGACGCTGACTGCTGAGGCGGAGCCACCGGC 3420
Qy 3421 ACTGCTCTCAGACTTCAAGACCATCTGACTGATGACCAAGCCAGCCAGGCTGA 3480
Db 3421 ACTGCTCTCAGACTTCAAGACCATCTGACTGATGACCAAGCCAGGCTGA 3480
Qy 3481 GAGCAGACACGACGACCTGTACAGCGGCTTACAGTCCAGGAGGAGGCGGCGC 3540
Db 3481 GAGCAGACACGACGACCTGTACAGCGGCTTACAGTCCAGGAGGAGGCGGCGC 3540
Qy 3541 CACACCGAGGCGCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCGAGGCTG 3600
Db 3541 CACACCGAGGCGCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCGAGGCTG 3600
Qy 3601 CATGTCCGCTGAAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTG 3660
Db 3601 CATGTCCGCTGAAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTG 3660
Qy 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCTG 3720
Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCTG 3720
Qy 3721 GGGCCAGCTTTTCTCACCAGAGGCGGCTTCCACTGCCCAATAGAAATGTCCATC 3780
Db 3721 GGGCCAGCTTTTCTCACCAGAGGCGGCTTCCACTGCCCAATAGAAATGTCCATC 3780
Qy 3781 CCAGATTCGCAATGTTTCAACCTTGCCTGCTCTTGTGCTTCAACCCCAATC 3840
Db 3781 CCAGATTCGCAATGTTTCAACCTTGCCTGCTCTTGTGCTTCAACCCCAATC 3840
Qy 3841 AGTGGAGACCTTGAAGAGACCTTGGAGCTTGGGAATTTGAGTGAACCAAGTGTG 3900
Db 3841 AGTGGAGACCTTGAAGAGACCTTGGAGCTTGGGAATTTGAGTGAACCAAGTGTG 3900
Qy 3901 CCTGTACACAGGCGAGGACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTT 3960
Db 3901 CCTGTACACAGGCGAGGACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTT 3960
Qy 3961 GAGTGTCTGTGAGTAAATTAATGATATATGATTTTCAAGTTTGAAGAAAAA 4015
Db 3961 GAGTGTCTGTGAGTAAATTAATGATATATGATTTTCAAGTTTGAAGAAAAA 4015

RESULT 2
AA220279
ID AA220279 standard; cDNA; 4015 BP.
XX
XX AA220279;
AC 17-JAN-2000 (first entry)
XX
XX
DT 17-JAN-2000 (first entry)
XX
XX
DE Human telomerase reverse transcriptase (hTERT) cDNA.
XX
XX Telomerase reverse transcriptase; human; hTERT; cell proliferation;
KW cancer; ss.
XX
XX Homo sapiens.
OS
XX

	Key	Location/Qualifiers
FT	CDS	56..3454
FT		/*tag= a
XX		
PN	WO950386-A2.	
XX		
PD	07-OCT-1999.	
XX		
PF	31-MAR-1999;	99WO-US007097.
PR	31-MAR-1998;	98US-00052864.
PR	03-AUG-1998;	98US-00128354.
XX	(GERO-) GERON CORP.	
XX	Morin GB;	
PI	WI; 1999-610842/52.	
DR	P-PSDB; AAY32090.	
XX	New catalytic polypeptide and polynucleotide, useful for increasing catalytic activity in a cell.	
PT		
PS	Disclosure; Fig 2; 24pp; English.	
XX	This is the nucleotide sequence of cDNA encoding human telomerase reverse transcriptase (hTERT, see AAY32090). Human telomerase is a target for diagnosing and treating diseases relating to cell proliferation and senescence, such as cancer, or for increasing the proliferative capacity of of a cell. A claimed method for increasing the proliferative capacity of a vertebrate cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTERT polynucleotide encoding an hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222- 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A claimed method for reducing telomerase activity in a cell involves introducing a recombinant polynucleotide encoding an hTERT variant having a deletion of amino acids 192-450, 560-565, 637-660, 748-764 or 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT coding sequence	
CC		
CC		
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 4015; DB 2; Length 4015;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GCAGCGCTGCGTCGTCTGCTGGACGACGTCGAGAGCCTTGCCCCGCCAATCCCCTGCATGTC	60
Db	1 GCAGCGCTGCGTCGTCTGCTGGACGACGTCGAGAGCCTTGCCCCGCCAATCCCCTGCATGTC	60
OY	61 GGGCGCTCCCCGCTGCGCCGAGCCGTCGCGTCCCTGTCGGGACGACTACCGAGAGTGCT	120
Db	61 GGGCGCTCCCCGCTGCGCCGAGCCGTCGCGTCCCTGTCGGGACGACTACCGAGAGTGCT	120
OY	121 GCCGCTGACGACGTTCTGTCGCGGCTCTGGAGGCCCAAGGACTGAGCTGTCACGCGG	180
Db	121 GCCGCTGACGACGTTCTGTCGCGGCTCTGGAGGCCCAAGGACTGAGCTGTCACGCGG	180
OY	181 GGAACCCGCGCGCTTTCGCGCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	240
Db	181 GGAACCCGCGCGCTTTCGCGCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	240
OY	241 AGGAGCGCGCCCGCGCGCGCCCTTTCGCGCAGAGTCTCTGCTGTAAGAAGTGGTGCG	300
Db	241 AGGAGCGCGCCCGCGCGCGCCCTTTCGCGCAGAGTCTCTGCTGTAAGAAGTGGTGCG	300
OY	301 CCAGAGTCTGCAAGAGCTGTGCGAGCGCGCGCGGAAAGAACGTGCTGAGCTTGGCTTGGC	360
Db	301 CCAGAGTCTGCAAGAGCTGTGCGAGCGCGCGCGGAAAGAACGTGCTGAGCTTGGCTTGGC	360
OY	361 GCTGCTGCGACGCGGCGCCCGCGGGGCGCCCGCAGAGGCTTTCACACAGAGGTCGACGCTA	420
Db	361 GCTGCTGCGACGCGGCGCCCGCGGGGCGCCCGCAGAGGCTTTCACACAGAGGTCGACGCTA	420

[illegible]

Db 3661 GAATGTCAGACACCTGCGCTTTCATCTCCCAAGGCTGCGCTCCACCCCA 3720
 QY 3721 GGCCGAGCTTTTCTTCCACAGAGCCCGCTTTCATCTCCCAATGATGCTTC 3780
 Db 3721 GGCCGAGCTTTTCTTCCACAGAGCCCGCTTTCATCTCCCAATGATGCTTC 3780
 QY 3781 CCAGATTCGCAATGTTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 3840
 Db 3781 CCAGATTCGCAATGTTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 3840
 QY 3841 AGGTGAGACCTTGAAGAGACCTTGAAGACCTTGAAGATTTGAGTGAACCAAGGTG 3900
 Db 3841 AGGTGAGACCTTGAAGAGACCTTGAAGACCTTGAAGATTTGAGTGAACCAAGGTG 3900
 QY 3901 CCTGTACACAGAGAGACCTTGAAGACCTTGAAGATTTGAGTGAACCAAGGTG 3960
 Db 3901 CCTGTACACAGAGAGACCTTGAAGACCTTGAAGATTTGAGTGAACCAAGGTG 3960
 QY 3961 GAGGTGCTGAGGAGTAAATACGAATATATGATGATTTTCACTTTGAAAAA 4015
 Db 3961 GAGGTGCTGAGGAGTAAATACGAATATATGATGATTTTCACTTTGAAAAA 4015

RESULT 3

AAZ30154
 ID AAZ30154 standard; cDNA; 4015 BP.

AAZ30154;

26-JAN-2000 (first entry)

cDNA encoding a human telomerase reverse transcriptase (TRT).

Human; telomerase reverse transcriptase; TRT; T lymphocyte activation; dendritic cell; telomerase activity; cancer cell; proliferating cell; immunological destruction; telomerase; cancer; proliferation disease; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 56..3454

FT /tag= a

FT /product= "telomerase reverse transcriptase"

XX MO9950392-A1.

XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US006898.

XX 31-MAR-1998; 98US-0112006P.

XX (GERO-) GERON CORP.

XX Gaeta FCA;

XX MPI; 1999-610845/52.

XX P-PSDB; AAY43621.

XX Eliciting an in vivo immune response for prevention and treatment of

XX cancer.

XX Disclosure; Fig 2; 26pp; English.

XX The present sequence encodes a human telomerase reverse transcriptase

XX (TRT) polypeptide. The protein is used in the method of the invention.

XX The specification describes a method for activating a T lymphocyte,

XX comprising contacting the T lymphocyte with a dendritic cell that

XX expresses a TRT peptide in the context of a MHC class I or MHC class II

XX molecule. The protein causes induction of an in vivo immunological

XX response to telomerase activity. Cancer cells are characterized by

XX expression of endogenous TRT gene and the presence of detectable

XX telomerase activity. Therefore, by eliciting a specific immune response

CC to TRT or to TRT-expressing cells, it is possible to selectively target
 CC proliferating cells for immunological destruction. The method is used for
 CC eliciting an in vivo immune response to telomerase by activating a T
 CC lymphocyte, and is useful for prevention and treatment of cancers and
 CC other proliferation diseases/conditions

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 4015; DB 2; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGCGCTCTGCTGCGACGCTGGAAGCCCTGCGCCACCTCCGAGTCC 60
 Db 1 GCAGCGCTGCGCTCTGCTGCGACGCTGGAAGCCCTGCGCCACCTCCGAGTCC 60
 QY 61 GCGCGCTCCCGCTGCGCGACGCTGCGCTCTGCTGCGACGCTGCGAGTCT 120
 Db 61 GCGCGCTCCCGCTGCGCGACGCTGCGCTCTGCTGCGACGCTGCGAGTCT 120
 QY 121 GCGCGCTGCGACGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 180
 Db 121 GCGCGCTGCGACGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 180
 QY 181 GGAACCTCGCGCTTCCCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 240
 Db 181 GGAACCTCGCGCTTCCCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 240
 QY 241 AGGCG 300
 Db 241 AGGCG 300
 QY 301 CCGAGTCTGCAAGAGCTGTCAGACGCGCGCGCGCGCGCGCGCGCGCGCTT 360
 Db 301 CCGAGTCTGCAAGAGCTGTCAGACGCGCGCGCGCGCGCGCGCGCGCGCTT 360
 QY 361 GCTGCTGGAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 420
 Db 361 GCTGCTGGAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 420
 QY 421 CCG 480
 Db 421 CCG 480
 QY 481 CCG 540
 Db 481 CCG 540
 QY 541 GCGTCCAGCTGCGCTTCAAGAGTGTGCGCGCGCGCGCGCGCGCGCGCG 600
 Db 541 GCGTCCAGCTGCGCTTCAAGAGTGTGCGCGCGCGCGCGCGCGCGCGCG 600
 QY 601 TCAAGCG 660
 Db 601 TCAAGCG 660
 QY 661 CTGGAACCAATAGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCG 720
 Db 661 CTGGAACCAATAGCTGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCG 720
 QY 721 GAGGCG 780
 Db 721 GAGGCG 780
 QY 781 TGCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
 Db 781 TGCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
 QY 841 GCGTGAACGAGTGAACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 900
 Db 841 GCGTGAACGAGTGAACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 900
 QY 901 CACTCTTTGGAAGGTGCGCTCTGCGACGCGCGCGCGCGCGCGCGCGCG 960

```
Db 901 CACCTCTTGGAGGGGCGCTCTCTGGCAACGCGCACTCCACCACTCCGTGGGCGCGCA 960
Qy 961 GACCAACGCGGGGCCCCCACTCCATCCGGGGCCACACAGCTCCCTGGGACACGCTTGTCC 1020
Db 961 GACCAACGCGGGGCCCCCACTCCATCCGGGGCCACACAGCTCCCTGGGACACGCTTGTCC 1020
Qy 1021 CCCGGGTATCGCGGACCAAGACACTTCTCTACTCTCAGGCGACAAAGAGAGCTGCG 1080
Db 1021 CCCGGGTATCGCGGACCAAGACACTTCTCTACTCTCAGGCGACAAAGAGAGCTGCG 1080
Qy 1081 GCGCTCTCTTCTACTAGCTCTCTGAGGCCCAAGCTGACTGCGGCTCGAGAGCTGTGGA 1140
Db 1081 GCGCTCTCTTCTACTAGCTCTCTGAGGCCCAAGCTGACTGCGGCTCGAGAGCTGTGGA 1140
Qy 1141 GACCAATCTTCTGCGGTTCAGAGCCCTGAGATGCGAGGAACTCCCGGAGTGGCCCGCT 1200
Db 1141 GACCAATCTTCTGCGGTTCAGAGCCCTGAGATGCGAGGAACTCCCGGAGTGGCCCGCT 1200
Qy 1201 GCGCCAGCGCTACTGGCAATGCGGCGCTGTTTCTGAGCTGCTTGGGAAACAAGCGCA 1260
Db 1201 GCGCCAGCGCTACTGGCAATGCGGCGCTGTTTCTGAGCTGCTTGGGAAACAAGCGCA 1260
Qy 1261 GTGCGCTTACGCGGAGTCTCTCAAGACGACCTGCGGCTGCGAGCTGCGGTCAACCGAC 1320
Db 1261 GTGCGCGCTTACGCGGAGTCTCTCAAGACGACCTGCGGCTGCGAGCTGCGGTCAACCGAC 1320
Qy 1321 AGCGCGTCTGCTGCGCGGAGAAAGCCCAAGGCTTGTGGCGGCGCCCGGAGAGAGGA 1380
Db 1321 AGCGCGTCTGCTGCGCGGAGAAAGCCCAAGGCTTGTGGCGGCGCCCGGAGAGAGGA 1380
Qy 1381 CACAGACCCCGCTGCGCTGCTGAGCTGCTCCGCGAGCAAGAGCGCCCTGGAGGTTGA 1440
Db 1381 CACAGACCCCGCTGCGCTGCTGAGCTGCTCCGCGAGCAAGAGCGCCCTGGAGGTTGA 1440
Qy 1441 CGGCTTCTGCGCGGCGCTGCGCTGCGCGGCTGCTGCGCGGCTTGGGAGCTCCAGCA 1500
Db 1441 CGGCTTCTGCGCGGCGCTGCGCTGCGCGGCTGCTGCGCGGCTTGGGAGCTCCAGCA 1500
Qy 1501 CAACGAAACCGCTTCTCTCAGGAAACAAGAAATTCATCTCCCTGGGAGAGATGCCAA 1560
Db 1501 CAACGAAACCGCTTCTCTCAGGAAACAAGAAATTCATCTCCCTGGGAGAGATGCCAA 1560
Qy 1561 GCTCTGCGCTGAGGAGCTGAGCTGAGGAGATGAGCGTGGGAGCTGCGCTTGGCTGCGAG 1620
Db 1561 GCTCTGCGCTGAGGAGCTGAGCTGAGGAGATGAGCGTGGGAGCTGCGCTTGGCTGCGAG 1620
Qy 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGCGCAGAGCAACGCTGCGTGAAGATCTGCGC 1680
Db 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGCGCAGAGCAACGCTGCGTGAAGATCTGCGC 1680
Qy 1681 CAACTTCTGCGCTGAGCTGATGATGTGTAAGTCTGAGCTGCTCAGGTCTTTCTTTTA 1740
Db 1681 CAACTTCTGCGCTGAGCTGATGATGTGTAAGTCTGAGCTGCTCAGGTCTTTCTTTTA 1740
Qy 1741 TGTCAAGGAGACAGTTCCTTCAAAAGAACAGGCTCTTTCTACCGGAAAGTGTGAG 1800
Db 1741 TGTCAAGGAGACAGTTCCTTCAAAAGAACAGGCTCTTTCTACCGGAAAGTGTGAG 1800
Qy 1801 CAACTTTCAGAAACATTTGAATGACAGACCTTGAAGAGGTTGCAAGCTGAGAGCTGTC 1860
Db 1801 CAACTTTCAGAAACATTTGAATGACAGACCTTGAAGAGGTTGCAAGCTGAGAGCTGTC 1860
Qy 1861 GGAAGAGAGGTTGAGGACATCGGGAAGCAGGCGCGCTGCTGACCTTCAAGCTCCG 1920
Db 1861 GGAAGAGAGGTTGAGGACATCGGGAAGCAGGCGCGCTGCTGACCTTCAAGCTCCG 1920
Qy 1921 CTTTCACTCCCAAGCCTGAGAGGCTGCGGCGATTTGAACTAGACTTACGTGGGAGC 1980
Db 1921 CTTTCACTCCCAAGCCTGAGAGGCTGCGGCGATTTGAACTAGACTTACGTGGGAGC 1980
Qy 1981 CAGAAAGTTCCGAGAGAAAGAGGCGTCTCACTCGAGGTTGAAGCACTGTT 2040
Db 1981 CAGAAAGTTCCGAGAGAAAGAGGCGTCTCACTCGAGGTTGAAGCACTGTT 2040

Db 1981 CAGAAAGTTCCGAGAGAAAGAGGCGGAGGCTCTCACTCGAGGTTGAAGCACTGTT 2040
Qy 2041 CAGCGGCTCAACTAGCGCGGGGCGCGGCGCCCTGAGGAGCTCTGTGCTGGG 2100
Db 2041 CAGCGGCTCAACTAGCGCGGGGCGCGGCGCCCTGAGGAGCTCTGTGCTGGG 2100
Qy 2101 CCTGAGCATATTCAGAGGCGCTGCGGCACTTCTGTGCTGCTGTGCGGCGCAGAGCC 2160
Db 2101 CCTGAGCATATTCAGAGGCGCTGCGGCACTTCTGTGCTGCTGTGCGGCGCAGAGCC 2160
Qy 2161 GCGCGCTGAGCTGTACTTGTCAAGTGTGATGTGACGCGCGCTGACAGACATCCCA 2220
Db 2161 GCGCGCTGAGCTGTACTTGTCAAGTGTGATGTGACGCGCGCTGACAGACATCCCA 2220
Qy 2221 GGAAGAGGCTCAGGAGGTCATGCGAGATCTCAAAACCCAGAACAGTACTGGGTGG 2280
Db 2221 GGAAGAGGCTCAGGAGGTCATGCGAGATCTCAAAACCCAGAACAGTACTGGGTGG 2280
Qy 2281 TCGGTATGCGGCTGTCCAGAAAGCGCCCATGCGGACGTCGCAAGGCTTCAAGAGCA 2340
Db 2281 TCGGTATGCGGCTGTGTCCAGAAAGCGCCCATGCGGACGTCGCGCAAGGCTTCAAGAGCA 2340
Qy 2341 CGTCTTACTTTCAGACACTTCAGCGCTGATGCGACATGCGAGATTTGCTGCTGAGGA 2400
Db 2341 CGTCTTACTTTCAGACACTTCAGCGCTGATGCGACATGCGAGATTTGCTGCTGAGGA 2400
Qy 2401 GACCAAGCGCGCTGAGAGGATCCGCTGTGATGAGAGAGCTCCTCTGAATGAGGCGAG 2460
Db 2401 GACCAAGCGCGCTGAGAGGATCCGCTGTGATGAGAGAGCTCCTCTGAATGAGGCGAG 2460
Qy 2461 CAGTGGCTCTTTCAGAGCTTCTCTAGCTTCTCATGTGTGCAACAGCGCGTGCATCAGGG 2520
Db 2461 CAGTGGCTCTTTCAGAGCTTCTCTAGCTTCTCATGTGTGCAACAGCGCGTGCATCAGGG 2520
Qy 2521 CAACTCTTACGTCAGTGCAGAGGATCCCGAGGCTTCATCTCTTCCACCTGCTGTG 2580
Db 2521 CAACTCTTACGTCAGTGCAGAGGATCCCGAGGCTTCATCTCTTCCACCTGCTGTG 2580
Qy 2581 CAGCGTGTCTACGCGCGACATGGAACAAGCTGTTGCGGAGATTCGCGGAGAGCGGCT 2640
Db 2581 CAGCGTGTCTACGCGCGACATGGAACAAGCTGTTGCGGAGATTCGCGGAGAGCGGCT 2640
Qy 2641 GCTCTGCGTGTGAGATGATTTCTGTTGTGACACTCACTCAACGAGCGGAAAC 2700
Db 2641 GCTCTGCGTGTGAGATGATTTCTGTTGTGACACTCACTCAACGAGCGGAAAC 2700
Qy 2701 CTTCTCAGAGACCTGCTCCAGGTTGCCCTGAGTATGAGCTGCTGAGAACTTGCAGAA 2760
Db 2701 CTTCTCAGAGACCTGCTCCAGGTTGCCCTGAGTATGAGCTGCTGAGAACTTGCAGAA 2760
Qy 2761 GACAGTGTGAACTTCCCTGTATGAAGAAGAGCCCTGGGTGGCAAGGCTTTTGTTCAGAT 2820
Db 2761 GACAGTGTGAACTTCCCTGTATGAAGAAGAGCCCTGGGTGGCAAGGCTTTTGTTCAGAT 2820
Qy 2821 GCGGCGCCACGCGCTATTCCCTGGTGGCGGCTGCTGCTGATACCCGGAACCTGAGGT 2880
Db 2821 GCGGCGCCACGCGCTATTCCCTGGTGGCGGCTGCTGCTGATACCCGGAACCTGAGGT 2880
Qy 2881 GCAGAGCGACTTACTCAGCTATGCGCGGACCTTCATCAGAGGCAATCTTCAACCG 2940
Db 2881 GCAGAGCGACTTACTCAGCTATGCGCGGACCTTCATCAGAGGCAATCTTCAACCG 2940
Qy 2941 CGGCTTCAAGGCTGGAAGAAATGCGTGCAGAACTCTTGGGGTCTTGGCGCTGAAGTG 3000
Db 2941 CGGCTTCAAGGCTGGAAGAAATGCGTGCAGAACTCTTGGGGTCTTGGCGCTGAAGTG 3000
Qy 3001 TCACAGCCTGTTTCTGATTTGACATGAAAGCTTCCAGAGCGTGTGCAACAATCTTA 3060
Db 3001 TCACAGCCTGTTTCTGATTTGACATGAAAGCTTCCAGAGCGTGTGCAACAATCTTA 3060
Qy 3061 CAAAGTCTCTCTGCTGAGAGGCTACAGATTTCAAGCATGTGTGCTGCAAGCTTCA 3120
Db 3061 CAAAGTCTCTCTGCTGAGAGGCTACAGATTTCAAGCATGTGTGCTGCAAGCTTCA 3120
```


FT exon /number= 15
 3351. .4015
 /*tag= w
 /number= 16
 EP1108789-A2.
 PD 20-JUN-2001.
 XX 15-DEC-2000; 2000EP-00127226.
 XX 16-DEC-1999; 99US-00465491.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Chang SP, Santini CD;
 XX WPI; 2001-376930/40.
 DR Quantitating expression of mRNA encoding hTERT, the catalytic subunit of
 XX telomerase, as an indicator of cancer, by amplifying RNA using primers
 XX complementary to hTERT gene sequence and quantitating amplified products.
 XX Claim 1; Page 5-7; 29pp; English.
 XX The present sequence is that of the hTERT gene encoding the catalytic
 CC subunit of the human telomerase, comprising 16 exons, which is useful in
 CC a method for quantitating hTERT mRNA. The method is useful for detecting
 CC the presence of beta-region (a 182 nucleotide region consisting of exons
 CC 7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
 CC of cancer. The method provides an accurate measure of telomerase activity
 CC by selectively measuring mRNA that encodes an active hTERT protein
 XX
 SO Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 4015; DB 4; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGCTGCTCTCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCCCGCATGCGC 60
 DB 1 GGAGCGCTGCTGCTCTCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 60
 QY 61 GCGCGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 120
 DB 61 GCGCGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 120
 QY 121 GCGCGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 180
 DB 121 GCGCGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 180
 QY 181 GGAACCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 240
 DB 181 GGAACCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 240
 QY 241 AGGCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 300
 DB 241 AGGCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 300
 QY 301 CCGAGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 360
 DB 301 CCGAGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 360
 QY 361 GCTGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 420
 DB 361 GCTGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 420
 QY 421 CCGAGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 480
 DB 421 CCGAGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 480
 QY 481 CCGAGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 540
 DB 481 CCGAGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 540

DB 481 CCGAGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 540
 QY 541 GCTGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 600
 DB 541 GCTGTGTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 600
 QY 601 TCAGGCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 660
 DB 601 TCAGGCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 660
 QY 661 CTGGAACCATGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 720
 DB 661 CTGGAACCATGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 720
 QY 721 GAGGCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 780
 DB 721 GAGGCGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 780
 QY 781 TGCCCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 840
 DB 781 TGCCCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 840
 QY 841 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 900
 DB 841 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 900
 QY 901 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 960
 DB 901 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 960
 QY 961 GCAACAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1020
 DB 961 GCAACAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1020
 QY 1021 CCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1080
 DB 1021 CCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1080
 QY 1081 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1140
 DB 1081 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1140
 QY 1141 GACCATCTTCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1200
 DB 1141 GACCATCTTCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1200
 QY 1201 GCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1260
 DB 1201 GCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1260
 QY 1261 GTCGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1320
 DB 1261 GTCGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1320
 QY 1321 AGCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1380
 DB 1321 AGCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1380
 QY 1381 CACAGACCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1440
 DB 1381 CACAGACCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1440
 QY 1441 CCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1500
 DB 1441 CCGGCTGAGCGGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1500
 QY 1501 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1560
 DB 1501 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1560
 QY 1561 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1620
 DB 1561 GCTGTGCTGCTGCTGCTGCGACGCTGGGAAAGCCCTGGCCCGCCAGCATGCGC 1620

QY 1621 GAGCCGAGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTAGAGAGATCCCTGGC 1680
DB 1621 GAGCCGAGGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTAGAGAGATCCCTGGC 1680
QY 1681 CAAGTTCCTGCACTGGCTGATGAGTGTGATCGTGTGAGCTGTGCTAGGTCTTTCTTTA 1740
DB 1681 CAAGTTCCTGCACTGGCTGATGAGTGTGATCGTGTGAGCTGTGCTAGGTCTTTCTTTA 1740
QY 1741 TGTGACGAGAACACCGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCTGGAG 1800
DB 1741 TGTGACGAGAACACCGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCTGGAG 1800
QY 1801 CAAGTTCGAAAGATTGGAATCAGACAGCACTTGAAGAGGTGACAGTGGGAGCTGTC 1860
DB 1801 CAAGTTCGAAAGATTGGAATCAGACAGCACTTGAAGAGGTGACAGTGGGAGCTGTC 1860
QY 1861 GGAAGCAGAGGTGACGAGCATGGGAGACCAAGGCCCGCTGTGACGTCCAGACTCCG 1920
DB 1861 GGAAGCAGAGGTGACGAGCATGGGAGACCAAGGCCCGCTGTGACGTCCAGACTCCG 1920
QY 1921 CTTCATCCCAAGCTGACGAGCGGCGCGCGATTTGGAATGAGACTGACGTGGGAGC 1980
DB 1921 CTTCATCCCAAGCTGACGAGCGGCGCGCGATTTGGAATGAGACTGACGTGGGAGC 1980
QY 1981 CAGAACTTCGAGAGAGAGAGAGGCGAGCGCTCACTCGAGGAGTGAAGCACTGTT 2040
DB 1981 CAGAACTTCGAGAGAGAGAGAGGCGAGCGCTCACTCGAGGAGTGAAGCACTGTT 2040
QY 2041 CAGGCTGCTCACTACGAGCGGCGCGCGCGCTTCCTGAGCGCTCTGTGTGG 2100
DB 2041 CAGGCTGCTCACTACGAGCGGCGCGCGCGCTTCCTGAGCGCTCTGTGTGG 2100
QY 2101 CTGGAAGATATCAGAGGCGCTGGGCACTTCGTGTGCTGATGGGCGGCGAGAGCCC 2160
DB 2101 CTGGAAGATATCAGAGGCGCTGGGCACTTCGTGTGCTGATGGGCGGCGAGAGCCC 2160
QY 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGAGCGCGCTGACAGACCAATCCCA 2220
DB 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGAGCGCGCTGACAGACCAATCCCA 2220
QY 2221 GGAAGGCTCAAGAGGTCACTGCGCAGCATCATCAAACTCCAGAGACAGTGTGGCG 2280
DB 2221 GGAAGGCTCAAGAGGTCACTGCGCAGCATCATCAAACTCCAGAGACAGTGTGGCG 2280
QY 2281 TCGGTAGCGGTGTCCAGAGGCGCGCAGTGGCAAGTCCGAGGCGCTTCAAGAGCCA 2340
DB 2281 TCGGTAGCGGTGTCCAGAGGCGCGCAGTGGCAAGTCCGAGGCGCTTCAAGAGCCA 2340
QY 2341 CGTCTTACCTTGAAGAGCTCCAGCGGTATGATGAGCAGTGTGCTGACCTGAGAG 2400
DB 2341 CGTCTTACCTTGAAGAGCTCCAGCGGTATGATGAGCAGTGTGCTGACCTGAGAG 2400
QY 2401 GACGAGCGGCTGAGAGGTGCGGTGATGAGCAGAGCTCTCTGTAATGAGGCGAG 2460
DB 2401 GACGAGCGGCTGAGAGGTGCGGTGATGAGCAGAGCTCTCTGTAATGAGGCGAG 2460
QY 2461 GACGAGCGGCTGAGAGGTGCGGTGATGAGCAGAGCTCTCTGTAATGAGGCGAG 2520
DB 2461 GACGAGCGGCTGAGAGGTGCGGTGATGAGCAGAGCTCTCTGTAATGAGGCGAG 2520
QY 2521 CAAGTCTTACGTCAGAGGAGATCCGAGAGGCTCCATCTCTCCAGCTGCTG 2580
DB 2521 CAAGTCTTACGTCAGAGGAGATCCGAGAGGCTCCATCTCTCTCCAGCTGCTG 2580
QY 2581 CAGCTGTGTGCTAGGAGCATGAGAACAGCTGTTTGGGAGGATTTGGGAGGAGCGGCT 2640
DB 2581 CAGCTGTGTGCTAGGAGCATGAGAACAGCTGTTTGGGAGGATTTGGGAGGAGCGGCT 2640
QY 2641 GCTCTGCGGTTTGGTGTGATGATTTCTGTGTGTGAGCAGCTCACTCAAGCGGAAAC 2700
DB 2641 GCTCTGCGGTTTGGTGTGATGATTTCTGTGTGTGAGCAGCTCACTCAAGCGGAAAC 2700

QY 2701 CTTCCTCAGAGACCTGTGTCCAGGTGTCTCTGATATGAGCTGCTGTGAATCTTGGGAA 2760
DB 2701 CTTCCTCAGAGACCTGTGTCCAGGTGTCTCTGATATGAGCTGCTGTGAATCTTGGGAA 2760
QY 2761 GACAGTGTGAATCTTCCCTGTGTGAAGACAGAGGCTCTGGGTGTGACAGGCTTTTGTCAAT 2820
DB 2761 GACAGTGTGAATCTTCCCTGTGTGAAGACAGAGGCTCTGGGTGTGACAGGCTTTTGTCAAT 2820
QY 2821 GCGGCGGCAAGGCGCTATTTCCCTGAGGCGGCTGTGCTGATATACCGGAGCTGTAGGT 2880
DB 2821 GCGGCGGCAAGGCGCTATTTCCCTGAGGCGGCTGTGCTGATATACCGGAGCTGTAGGT 2880
QY 2881 GGAAGCGACTATCTCCAGCTATGCGGACCTTCATAGAGCCAGTCTCACTTCAACCG 2940
DB 2881 GGAAGCGACTATCTCCAGCTATGCGGACCTTCATAGAGCCAGTCTCACTTCAACCG 2940
QY 2941 CCGCTTCAAGGCTGGAGAGAACATGGTGTGCAAACTTTTGGGAGTTTGGGCTGTGAAGT 3000
DB 2941 CCGCTTCAAGGCTGGAGAGAACATGGTGTGCAAACTTTTGGGAGTTTGGGCTGTGAAGT 3000
QY 3001 TCACAGCTGTTTCTGATTTTGAGGTGAACAGGCTCCAGACGAGTGTGACCAACTTA 3060
DB 3001 TCACAGCTGTTTCTGATTTTGAGGTGAACAGGCTCCAGACGAGTGTGACCAACTTA 3060
QY 3061 CAAGATCTCTGTGTGACAGCGGTACAGGTTTACAGCATGTGTGTGACAGCTCCATTTCA 3120
DB 3061 CAAGATCTCTGTGTGACAGCGGTACAGGTTTACAGCATGTGTGTGACAGCTCCATTTCA 3120
QY 3121 TCGAAGATTTTGAAGAACCCCACTTTTCTGTGCGGTGATCTGTGACAGGCTCTCT 3180
DB 3121 TCGAAGATTTTGAAGAACCCCACTTTTCTGTGCGGTGATCTGTGACAGGCTCTCT 3180
QY 3181 CTGCTACTCATCTCTGAAAGCAAGAACGAGGAGTGTGCTGGGAGGCGCAAGGCGCGC 3240
DB 3181 CTGCTACTCATCTCTGAAAGCAAGAACGAGGAGTGTGCTGGGAGGCGCAAGGCGCGC 3240
QY 3241 CCGGCTCTGCTCCGAGGCGGTGTGAGTGTGTGCAACAAGCTTCTGTCAAGCT 3300
DB 3241 CCGGCTCTGCTCCGAGGCGGTGTGAGTGTGTGCAACAAGCTTCTGTCAAGCT 3300
QY 3301 GACTGCAACCGGTGTACTTACGTGTGCACTTCTGGGAGTACTGAGGAGCGCCAGAGCA 3360
DB 3301 GACTGCAACCGGTGTACTTACGTGTGCACTTCTGGGAGTACTGAGGAGCGCCAGAGCA 3360
QY 3361 GCTGAGTGTGAGAGCTCCGAGGAGCAAGCGGTGACTGAGGCGCTGAGAGGCGGAGCCG 3420
DB 3361 GCTGAGTGTGAGAGCTCCGAGGAGCAAGCGGTGACTGAGGCGCTGAGAGGCGGAGCCG 3420
QY 3421 ACTGCCCTGAGACTTCAAGACCATCTGTGATGTATGAGCCAGCGGCTCAGAGGCGCA 3480
DB 3421 ACTGCCCTGAGACTTCAAGACCATCTGTGATGTATGAGCCAGCGGCTCAGAGGCGCA 3480
QY 3481 GAGCAGACACAGAGAGCTGTGTACGCGCGGCTGTACGTGTCCAGAGGAGGAGGCGGCG 3540
DB 3481 GAGCAGACACAGAGAGCTGTGTACGCGCGGCTGTACGTGTCCAGAGGAGGAGGCGGCG 3540
QY 3541 CACACCCAGGCGCGAGCGGTGAGTGTGAGGCGTGTGAGTGTGTGAGGCGAGGCTG 3600
DB 3541 CACACCCAGGCGCGAGCGGTGAGTGTGAGGCGTGTGAGTGTGTGAGGCGAGGCTG 3600
QY 3601 CATGTCCGCTGAGAGCTGATGTTCGAGTGTGAGGCTGTGAGGAGTGTGAGGCGAGGCT 3660
DB 3601 CATGTCCGCTGAGAGCTGATGTTCGAGTGTGAGGCTGTGAGGAGTGTGAGGCGAGGCT 3660
QY 3661 GAGTGTGACAGACACTGCGGTCTTCACTTCCACAGGCTGTGCGCTGTGAGGCTCA 3720
DB 3661 GAGTGTGACAGACACTGCGGTCTTCACTTCCACAGGCTGTGCGCTGTGAGGCTCA 3720
QY 3721 GGGCAGGCTTTTCTACAGAGAGGCGGCTTCACTTCCACATATGAAATGTCCATCC 3780
DB 3721 GGGCAGGCTTTTCTACAGAGAGGCGGCTTCACTTCCACATATGAAATGTCCATCC 3780
QY 3781 CCAGATTCGCATTTGTACACCCCTCGCCTGTGCTCTTGTGCTTCAACCCCAACATCC 3840

Db	3781	CCAAGTTGCGCATTTGTTACCCCTTGCCCTGCTCTTTGCTTCCACCCCAACATCC	3840
QY	3841	AGGTGAGAACCCCTGAGAAAGACCCCTGGAGCTTGGGAATTTGGAGTACCAAAAGTGTG	3900
Db	3841	AGGTGAGAGACCCCTGAGAAAGACCCCTGGAGCTTGGGAATTTGGAGTACCAAAAGTGTG	3900
QY	3901	CCCTGTACACAGGGGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
Db	3901	CCCTGTACACAGGGGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
QY	3961	GAGGTGCTGTGGAGTAAATATCTGAATATATGATTTTTCAGTTTGAATAAAAA	4015
Db	3961	GAGGTGCTGTGGAGTAAATATCTGAATATATGATTTTTCAGTTTGAATAAAAA	4015
RESULT 5			
AAd46821			
ID	AAd46821	standard; cDNA, 4015 BP.	
XX	AAd46821;		
AC			
XX			
DT	27-JAN-2003	(first entry)	
XX			
DE	Human telomerase reverse transcriptase (TERT) cDNA.		
KW	Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;		
KW	transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;		
OS	telomerase reverse transcriptase; gene; ss.		
XX	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	56..3454	
FT		/*tag= a	
FT		/product= "Human telomerase reverse transcriptase"	
XX	WO200274948-A2.		
PN			
XX			
PD	26-SEP-2002.		
XX			
PE	21-MAR-2002; 2002WO-CA000378.		
XX			
PR	21-MAR-2001; 2001US-0277811P.		
XX			
PA	(GERO-) GERON CORP.		
XX			
PI	Denning C, Clark AJ, Schiffe JM;		
XX			
DR	WPI; 2002-759895/82.		
DR	P-PSDB; NAE29226.		
PT	Mammalian cells, useful for producing animal tissues with carbohydrate		
XX	antigens that are compatible for transplantation into human patients.		
XX			
PS	Disclosure; Page 33-34; 71pp; English.		
XX			
CC	The invention relates to animal tissues with carbohydrate antigens that		
CC	are compatible for transplantation into human patients. The mammalian		
CC	cell is inactivated homoygously for expression of alpha(1,3)galactosyl-		
CC	transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-		
CC	fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue		
CC	with carbohydrate antigens that are compatible for transplantation into		
CC	human patients. The present sequence is human telomerase reverse		
CC	transcriptase (TERT) cDNA used in the invention		
XX			
Sequence	4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;		
Query Match	100.0%; Score 4015; DB 6; Length 4015;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 4015; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		

[illegible]

Db 1081 GCCCTCTTCTACTAGCTCTCTGAGGCCAGCCTGACTGAGGCGCTGGAGGCTCGTGA 1140
Qy 1141 GACCATCTTTCTGAGTTCCAGGCCCTGATGCGAGGACTCCCGCAGGTTGCCCCCT 1200
Db 1141 GACCATCTTTCTGAGTTCCAGGCCCTGATGCGAGGACTCCCGCAGGTTGCCCCCT 1200
Qy 1201 GCCCCAGCGTACTGCGAATGCGGCCCTGTTCTGAGCTGCTTGAGGAAACAGCGGCA 1260
Db 1201 GCCCCAGCGTACTGCGAATGCGGCCCTGTTCTGAGCTGCTTGAGGAAACAGCGGCA 1260
Qy 1261 GTCGCCCTACGAGGAGTGTCTTCAAGAGCAGCTCCCGCTGCGAGTGCAGTCAACCCAGC 1320
Db 1261 GTCGCCCTACGAGGAGTGTCTTCAAGAGCAGCTCCCGCTGCGAGTGCAGTCAACCCAGC 1320
Qy 1321 AGCCGAGTGTGTGCCCCGAGGAAAGCCCGAGGCTCTGTGCGCGCCCGCAGAGAGAGA 1380
Db 1321 AGCCGAGTGTGTGCCCCGAGGAAAGCCCGAGGCTCTGTGCGCGCCCGCAGAGAGAGA 1380
Qy 1381 CACAGACCCCGCTGCGCTGAGCTGCTCCGCAAGCAGGAGCCCTGCGAGGTGA 1440
Db 1381 CACAGACCCCGCTGCGCTGAGCTGCTCCGCAAGCAGGAGCCCTGCGAGGTGA 1440
Qy 1441 CGGCTTGTGCGGCTGCTGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1441 CGGCTTGTGCGGCTGCTGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Qy 1501 CAACGAAAGCGCGCTTCTCTAGGAAACCAAGAAATATCTCTCTGAGGAAAGCATGCGAA 1560
Db 1501 CAACGAAAGCGCGCTTCTCTAGGAAACCAAGAAATATCTCTCTGAGGAAAGCATGCGAA 1560
Qy 1561 GCTCTGCTGAGAGAGCTGAGCTGAGAGATGAGGCTGCGGAGCTGCTGCTGCTGCTGCTG 1620
Db 1561 GCTCTGCTGAGAGAGCTGAGCTGAGAGATGAGGCTGCGGAGCTGCTGCTGCTGCTGCTG 1620
Qy 1621 GAGCCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 GAGCCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 1681 CAATTTCTGACCTGAGCTGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 CAATTTCTGACCTGAGCTGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1741 TGTCAAGGAGACAGCTTTCAAAAGAAAGAGCTTTTCTAACCGAAGAGTGTCTGAG 1800
Db 1741 TGTCAAGGAGACAGCTTTCAAAAGAAAGAGCTTTTCTAACCGAAGAGTGTCTGAG 1800
Qy 1801 CAAGTTGCAAGCATTTGATCAAGACACTTGAAGAGGTGACCTGCGGAGCTGTC 1860
Db 1801 CAAGTTGCAAGCATTTGATCAAGACACTTGAAGAGGTGACCTGCGGAGCTGTC 1860
Qy 1861 CAAGTTGCAAGCATTTGATCAAGACACTTGAAGAGGTGACCTGCGGAGCTGTC 1920
Db 1861 CAAGTTGCAAGCATTTGATCAAGACACTTGAAGAGGTGACCTGCGGAGCTGTC 1920
Qy 1921 CTTGATCCCAAGCTGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1980
Db 1921 CTTGATCCCAAGCTGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1980
Qy 1981 CAGAACTTTCCGCGAGAGAAAGAGGCGGAGCTGCTGAGAGGTGAAAGGAGCTGTT 2040
Db 1981 CAGAACTTTCCGCGAGAGAAAGAGGCGGAGCTGCTGAGAGGTGAAAGGAGCTGTT 2040
Qy 2041 CAGAGTGTCAACTAGAGCGGAGCGGCGGCGGCGGCTCTGAGGCGCTGCTGCTGCTG 2100
Db 2041 CAGAGTGTCAACTAGAGCGGAGCGGCGGCGGCGGCTCTGAGGCGCTGCTGCTGCTG 2100
Qy 2101 CTTGACGATATCCAGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 2160
Db 2101 CTTGACGATATCCAGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 2160
Qy 2161 GCGGCTTGAAGCTGATCTTTGTCAGAGTGTGACGCGGCGGCTGACGACCATCCCA 2220
Db 2161 GCGGCTTGAAGCTGATCTTTGTCAGAGTGTGACGCGGCGGCTGACGACCATCCCA 2220

Qy 2221 GGAAGAGCTCAAGAGGCTATGCGAGCATGATCAAAACCCAGAGACGTAAGTCTGTCG 2280
Db 2221 GGAAGAGCTCAAGAGGCTATGCGAGCATGATCAAAACCCAGAGACGTAAGTCTGTCG 2280
Qy 2281 TCGATATCCGCTGCTCAAGAGGCGGCTGAGGCTGCGGCTGCGGCTGCGGCTGCGGCT 2340
Db 2281 TCGATATCCGCTGCTCAAGAGGCGGCTGAGGCTGCGGCTGCGGCTGCGGCTGCGGCT 2340
Qy 2341 CGTCTTACTTGAAGACCTTCAAGGCTGATGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 2400
Db 2341 CGTCTTACTTGAAGACCTTCAAGGCTGATGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 2400
Qy 2401 GACAGCGCGCTGAGAGATGCGCTGCTGATGAGAGAGCTCTCTGAAATGAGGCGAG 2460
Db 2401 GACAGCGCGCTGAGAGATGCGCTGCTGATGAGAGAGCTCTCTGAAATGAGGCGAG 2460
Qy 2461 CAGTGGCTCTTGAAGCTTCTTCAAGCTTCAATGTCACACGCGCTGCGCATGAGGG 2520
Db 2461 CAGTGGCTCTTGAAGCTTCTTCAAGCTTCAATGTCACACGCGCTGCGCATGAGGG 2520
Qy 2521 CAACTTCTTACCTGCAAGCTGCGAGGAGATCCCGAGGCTTCAATCTTCAAGCTTCTG 2580
Db 2521 CAACTTCTTACCTGCAAGCTGCGAGGAGATCCCGAGGCTTCAATCTTCAAGCTTCTG 2580
Qy 2581 CAGCTGTGCTGAGGAGATGAGAAAGAGCTGTTGCGGAGATTCGAGGAGCGGCT 2640
Db 2581 CAGCTGTGCTGAGGAGATGAGAAAGAGCTGTTGCGGAGATTCGAGGAGCGGCT 2640
Qy 2641 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
Db 2641 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
Qy 2701 CTTCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Db 2701 CTTCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Qy 2761 GACAGTGTGAACTTCTCTGTAAGAAAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTG 2820
Db 2761 GACAGTGTGAACTTCTCTGTAAGAAAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTG 2820
Qy 2821 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 2821 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Qy 2881 GCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Db 2881 GCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Qy 2941 CCGCTTCAAGGCTGAGGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
Db 2941 CCGCTTCAAGGCTGAGGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
Qy 3001 TCAACGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
Db 3001 TCAACGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
Qy 3061 CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
Db 3061 CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3120
Qy 3121 TCAAGAGTTTGAAGAAACCCCATTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 3180
Db 3121 TCAAGAGTTTGAAGAAACCCCATTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 3180
Qy 3181 CTCTACTCTCATCTGTAAGAGCAAGAGAGTGTGCTGAGGAGGCTGCTGCTGCTGCTG 3240
Db 3181 CTCTACTCTCATCTGTAAGAGCAAGAGAGTGTGCTGAGGAGGCTGCTGCTGCTGCTG 3240
Qy 3241 CCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
Db 3241 CCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300

QY	721	GAGGCGGGGGGCAGTGCCAGCCGAAGTCTGCCCTTGCCCAAGAGGCCACGGCTGTGGC	780
Db	721	GAGGCGGGGGGGAGTGTCACGCCGAAGTCTGCGGTGGCCCAAGAGGCCACGGCTGTGGC	780
QY	781	TGCCCCGTGAGCCGAGAGCGAGCGCCCGTGGGACAGAGGATCTGTAGGCCCAACCCGGAGAGAC	840
Db	781	TGCCCCGTGAGCCGAGAGCGAGCGCCCGTGGGACAGAGGATCTGTAGGCCCAACCCGGAGAGAC	840
QY	841	GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTCACTGTCCAGACCCGCGGAGAAAC	900
Db	841	GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTCACTGTCCAGACCCGCGGAGAAAC	900
QY	901	CACCTCTTGGAGGGGTGCGCTCTGTGGCAAGCGCACTCCCAACCCATCCGTTGGACGCGCA	960
Db	901	CACCTCTTGGAGGGGTGCGCTCTGTGGCAAGCGCACTCCCAACCCATCCGTTGGACGCGCA	960
QY	961	GCAACACGCGGGCCCCCATTCACATGTGGGCGCACACGTCTCGTGGACACGCTTGTTC	1020
Db	961	GCAACACGCGGGCCCCCATTCACATGTGGGCGCACACGTCTCGTGGACACGCTTGTTC	1020
QY	1021	CCCGGTGATGCCCGAAGCAAAAGCACTTCCCTACTCCCTCAGAGGGACAAAGAGCAGCTGGG	1080
Db	1021	CCCGGTGATGCCCGAAGCAAAAGCACTTCCCTACTCCCTCAGAGGGACAAAGAGCAGCTGGG	1080
QY	1081	GCCCTCTCTTCACTCAAGCTCTCTGAGAGCCACGCTTGAATGGCGCTTCGAGGCTGTGGA	1140
Db	1081	GCCCTCTCTTCACTCAAGCTCTCTGAGAGCCACGCTTGAATGGCGCTTCGAGGCTGTGGA	1140
QY	1141	GACCACTCTTCTGGGTTCCAGGCTTCAGGCTTCGATGACAGAGGACCTCCCGAGAGTTGGCCGCGCT	1200
Db	1141	GACCACTCTTCTGGGTTCCAGGCTTCAGGCTTCGATGACAGAGGACCTCCCGAGAGTTGGCCGCGCT	1200
QY	1201	GCCCCAGCGCTACTGTGGCAAAATGCGGAGCCCTGTGTTCTGTGAGCTGTGGGAAACAACGCGCA	1260
Db	1201	GCCCCAGCGCTACTGTGGCAAAATGCGGAGCCCTGTGTTCTGTGAGCTGTGGGAAACAACGCGCA	1260
QY	1261	GTGCCCCCTTACGGGGGTGCTCTCAAGACGCACTGCCCGCTGTGAGCTGTGGATCGGTACCCAGC	1320
Db	1261	GTGCCCCCTTACGGGGGTGCTCTCAAGACGCACTGCCCGCTGTGAGCTGTGGATCGGTACCCAGC	1320
QY	1321	AGCGGATGTCTGTGCGCCGAGAGAAAGCCCAAGGCTCTGTGTGCGGAGCCCGAGAGAGGA	1380
Db	1321	AGCGGATGTCTGTGCGCCGAGAGAAAGCCCAAGGCTCTGTGTGCGGAGCCCGAGAGAGGA	1380
QY	1381	CACAGAACCCCGGTGCTGT	1440
Db	1381	CACAGAACCCCGGTGCTGT	1440
QY	1441	CGGCTTCTGTGCGGGGCTGTGCGCGCGGCTGTGTGCCCCAGGCTCTGTGGGCTCCAGGCA	1500
Db	1441	CGGCTTCTGTGCGGGGCTGTGCGCGCGGCTGTGTGCCCCAGGCTCTGTGGGCTCCAGGCA	1500
QY	1501	CAACGAAACGCGCTTCTCAAGAAACAACAAGAAATTCATCTCCCTGGGAAAGCATGCCAA	1560
Db	1501	CAACGAAACGCGCTTCTCAAGAAACAACAAGAAATTCATCTCCCTGGGAAAGCATGCCAA	1560
QY	1561	GCTTCTGTGTGCAAGAGCTGACGTGAAAGATGAGCGTGTGGGAGCTGCGCTTGTGGCGAG	1620
Db	1561	GCTTCTGTGTGCAAGAGCTGACGTGAAAGATGAGCGTGTGGGAGCTGCGCTTGTGGCGAG	1620
QY	1621	GAGCCACAGGGGTTGT	1680
Db	1621	GAGCCACAGGGGTTGT	1680
QY	1681	CAAGTTCCTGTGCACTGGCTGTGATGAGTGTGACGTGTCCAGAGCTGTCAAGTCTTCTTTTA	1740
Db	1681	CAAGTTCCTGTGCACTGGCTGTGATGAGTGTGACGTGTCCAGAGCTGTCAAGTCTTCTTTTA	1740
QY	1741	TGTGACGAGAACCAAGCTTCAAAAAGAACAGGCTCTTTTCTACCGGAAAGATGTGTGAG	1800
Db	1741	TGTGACGAGAACCAAGCTTCTCAAAAAGAACAGGCTCTTTTCTACCGGAAAGATGTGTGAG	1800
QY	1801	CAAGTTCAAAACGATTGGAATCAGACACTTGAAGAGGGTGTGACGTGCGGAGACTGTG	1860

Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGGTGCGAGCTGCGGAGACTCTGC	1860
Qy	1861	GGAAGCAGAGGTCAAGCAGACATTCGGGAACCGAGGCCCGCCCTGCTGAAGTCCAGACTCG	1920
Db	1861	GGAAGCAGAGGTCAAGCAGACATTCGGGAACCGAGGCCCGCCCTGCTGAAGTCCAGACTCG	1920
Qy	1921	CTTCATCCCAAGCCTGACAGGGCTGCGGCCGATTTGTGAACATGACCTACGTCGTGGAAC	1980
Db	1921	CTTCATCCCAAGCCTGACAGGGCTGCGGCCGATTTGTGAACATGACCTACGTCGTGGAAC	1980
Qy	1981	CAGAACCTTCCGACAGAAAAGAGGGCCGAGAGCTCTACCTGAGGGGTGAAGCACTGTT	2040
Db	1981	CAGAACCTTCCGACAGAAAAGAGGGCCGAGAGCTCTACCTGAGGGGTGAAGCACTGTT	2040
Qy	2041	CAGAGTCTCAACATACAGAGGGGACGAGGCGCCCGAGCTCTTGAGGCGCTCTGTGTGAG	2100
Db	2041	CAGAGTCTCAACATACAGAGGGGACGAGGCGCCCGAGCTCTTGAGGCGCTCTGTGTGAG	2100
Qy	2101	CCTGAGCAGATATCCAGAGGGGCTTGAGGCGACCTTTCGTGCTGCTGTGTGAGGCCCAAGAAC	2160
Db	2101	CCTGAGCAGATATCCAGAGGGGCTTGAGGCGACCTTTCGTGCTGCTGTGTGAGGCCCAAGAAC	2160
Qy	2161	GCCGCTCAGCTGTACCTTGTCAAGGTGATGAGCGGGCGCTGACAGACATCCCGCA	2220
Db	2161	GCCGCTCAGCTGTACCTTGTCAAGGTGATGAGCGGGCGCTGACAGACATCCCGCA	2220
Qy	2221	GGACAGGCTCAGAGAGGTCAATCGCCAGCATCATCAACCCAGAACACGTACTGCTGCG	2280
Db	2221	GGACAGGCTCAGAGAGGTCAATCGCCAGCATCATCAACCCAGAACACGTACTGCTGCG	2280
Qy	2281	TGCGTATGCGCTGGTCCAGAAAGCGCCCATGAGCGACCTGCGGAAAGGCTTCAAGAGCCA	2340
Db	2281	TGCGTATGCGCTGGTCCAGAAAGCGCCCATGAGCGAGTCCGAAAGGCTTCAAGAGCCA	2340
Qy	2341	CGTCTCACTTGAACAAGCCTCAGACGCTCATGCGACAGTTCGTGAGCTCACCTGCAGGA	2400
Db	2341	CGTCTCACTTGAACAAGCCTCAGACGCTCATGCGACAGTTCGTGAGCTCACCTGCAGGA	2400
Qy	2401	GACACAGCCGCTGAGAGGATGCGCTGCTCATGAGCAGAGCTCCTCCCTGAAATGAGGCCAG	2460
Db	2401	GACACAGCCGCTGAGAGGATGCGCTGCTCATGAGCAGAGCTCCTCCCTGAAATGAGGCCAG	2460
Qy	2461	CAGTGGCCTTCCAGACGTCCTCTCAACGCTTCAATGTCACACAGCGCTGAGCAATCAGGG	2520
Db	2461	CAGTGGCCTTCCAGACGTCCTCTCTCAACGCTTCAATGTCACACAGCGCTGAGCAATCAGGG	2520
Qy	2521	CAAGTCTTACGTCAGATGCGAGGGGATCCGCGAGGCTCOATCCTCTTCCAGCTGCTCTG	2580
Db	2521	CAAGTCTTACGTCAGATGCGAGGGGATCCGCGAGGCTCOATCCTCTTCCAGCTGCTCTG	2580
Qy	2581	CAGCCTGTGCTACCGGCGACATGAGAAACAAAGCTTTTGGCGGAGTTGAGCGGACGAGCT	2640
Db	2581	CAGCCTGTGCTACCGGCGACATGAGAAACAAAGCTTTTGGCGGAGTTGAGCGGACGAGCT	2640
Qy	2641	GCTCCGAGTGTGGTGAATGATTTCTTGTGTGTGACACTCACTCAACCCACGGAAGAC	2700
Db	2641	GCTCCGAGTGTGGTGAATGATTTCTTGTGTGTGACACTCACTCAACCCACGGAAGAC	2700
Qy	2701	CTTCTCAGAGACCTTGTGTCGAGGTCTCCCTGAATATGAGCTGCGAGGTGAACCTTGCGGAA	2760
Db	2701	CTTCTCAGAGACCTTGTGTCGAGGTCTCCCTGAATATGAGCTGCGAGGTGAACCTTGCGGAA	2760
Qy	2761	GACAGTGTGAACCTTCCCTGTGAAAGACAGAGCCCTGGGTGGCAAGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGAACCTTCCCTGTGAAAGACAGAGCCCTGGGTGGCAAGGCTTTTGTTCAGAT	2820
Qy	2821	GCGGCGCCACGAGCTATTCCTCCGTGTGCGGCTGTCTGATACCCGGAACCTTGAGGT	2880
Db	2821	GCGGCGCCACGAGCTATTCCTCCGTGTGCGGCTGTCTGATACCCGGAACCTTGAGGT	2880
Qy	2881	GCAAGCGACTACTCCAGTATGCCCCGACCTTCATTCAGACAGTCTCACTTCAACCG	2940
Db	2881	GCAAGCGACTACTCCAGTATGCCCCGACCTTCATTCAGACAGTCTCACTTCAACCG	2940

```

Db      2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGAGTCCACCTTCAACCG 2940
Qy      2941 CGGCTTGAAGGCTGGAGAGAAATGCCCTCGAAATCTTTGGGGCTTGGCGGTGAAGTG 3000
Db      2941 CGGCTTGAAGGCTGGAGAGAAATGCCCTCGAAATCTTTGGGGCTTGGCGGTGAAGTG 3000
Qy      3001 TCACAGCTGTTTTCGAGATTGGAGAGTGAACAGCTCCAGAGCGGTGTGACCAACATCTA 3060
Db      3001 TCACAGCTGTTTTCGAGATTGGAGAGTGAACAGCTCCAGAGCGGTGTGACCAACATCTA 3060
Qy      3061 CAAGATCTCTGCTGAGCGGTACAGGTTTTCAGCATGTGTGCTGACAGCTCCATTTCA 3120
Db      3061 CAAGATCTCTGCTGAGCGGTACAGGTTTTCAGCATGTGTGCTGACAGCTCCATTTCA 3120
Qy      3121 TCAGAAATTGGAGAAACCCCACTTTTCTGGCGGTGATCTGTGACAGGCTCCCT 3180
Db      3121 TCAGAAATTGGAGAAACCCCACTTTTCTGGCGGTGATCTGTGACAGGCTCCCT 3180
Qy      3181 CTGCTACTCCATCTCGAAGCGGTACAGGATGTGCTGGGGGCAAGGGGCGCG 3240
Db      3181 CTGCTACTCCATCTCGAAGCGGTACAGGATGTGCTGGGGGCAAGGGGCGCG 3240
Qy      3241 CGGCGCTCTGCTCGAGCGGTGAGAGCTGTGTGCAACAGGATTTCTGCTCAAGCT 3300
Db      3241 CGGCGCTCTGCTCGAGCGGTGAGAGCTGTGTGCAACAGGATTTCTGCTCAAGCT 3300
Qy      3301 GACTTGAAACCGGTGCTACCTAATGTGCCACTCTGGGGGTCACTCAGAGACGCCAAGCGA 3360
Db      3301 GACTTGAAACCGGTGCTACCTAATGTGCCACTCTGGGGGTCACTCAGAGACGCCAAGCGA 3360
Qy      3361 GCTGAGTGGAAAGCTCCCGGGGAGCAGCGTGACTGCTCGAGGCGCAGCAACCCGCG 3420
Db      3361 GCTGAGTGGAAAGCTCCCGGGGAGCAGCGTGACTGCTCGAGGCGCAGCAACCCGCG 3420
Qy      3421 ACTGCGCTCAGACTTCAAGACCATCTGTGAGTGTGACCCGCGCAAGCGAGCGCGA 3480
Db      3421 ACTGCGCTCAGACTTCAAGACCATCTGTGAGTGTGACCCGCGCAAGCGAGCGCGA 3480
Qy      3481 GAGCGAAGAACGAGCGCTCTGTCAAGCGCGGCTTACGTCCCAAGGAGAGAGGGCGCGC 3540
Db      3481 GAGCGAAGAACGAGCGCTCTGTCAAGCGCGGCTTACGTCCCAAGGAGAGAGGGCGCGC 3540
Qy      3541 CACACCCAGGCGCGCAGCGCTGTGAGAGCTGTGAGTGTGCTTTGGCGAGGCGCTG 3600
Db      3541 CACACCCAGGCGCGCAGCGCTGTGAGAGCTGTGAGTGTGCTTTGGCGAGGCGCTG 3600
Qy      3601 CATGTCCGCGTGAAGGCTGAGTGTCCGCGTGAAGCGCTGAGCGAGTGTCCAGCGAGGCT 3660
Db      3601 CATGTCCGCGTGAAGGCTGAGTGTCCGCGTGAAGCGCTGAGCGAGTGTCCAGCGAGGCT 3660
Qy      3661 GAGTGTCCAGACACCTGCGCTTTCATCTTCCCAAGGCTGTGGCGTCCACCCCA 3720
Db      3661 GAGTGTCCAGACACCTGCGCTTTCATCTTCCCAAGGCTGTGGCGTCCACCCCA 3720
Qy      3721 GGGCGAGCTTTTCCACAGAGAGCGCGCTTCCATCCCAATGAGAAATGTGCATCC 3780
Db      3721 GGGCGAGCTTTTCCACAGAGAGCGCGCTTCCATCCCAATGAGAAATGTGCATCC 3780
Qy      3781 CCAGATTGCCATTGTTCACCCCTCGCCCTGCTTGTGCTTCCACCCCAACATCC 3840
Db      3781 CCAGATTGCCATTGTTCACCCCTCGCCCTGCTTGTGCTTCCACCCCAACATCC 3840
Qy      3841 AGGTGGAAGACCTTGAGAGAGACCTTGAGAGCTTGGGAAATTTGAGTGAACCAAGTGTG 3900
Db      3841 AGGTGGAAGACCTTGAGAGAGACCTTGAGAGCTTGGGAAATTTGAGTGAACCAAGTGTG 3900
Qy      3901 CCCTGTACACAGGCGAGGACCTTGACCTGATGGGAGGCTCTGTGGGTCAATTTGGGG 3960
Db      3901 CCCTGTACACAGGCGAGGACCTTGACCTGATGGGAGGCTCTGTGGGTCAATTTGGGG 3960
Qy      3961 GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAAAA 4015
Db      3961 GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAAAA 4015

```

```

RESULT 7
ACCS7552
ID ACCS7552 standard; cDNA; 4015 BP.
XX
AC ACCS7552;
XX
DT 28-JUL-2003 (first entry)
XX
DE Human telomerase reverse transcriptase cDNA.
XX
KW Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antifertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT FT /*tag= a
FT FT /product= "TERT"
XX
PD WO2003034985-A2.
XX
PF 01-MAY-2003.
XX
PR 16-OCT-2002; 2002WO-US033146.
XX
PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
PA (UVRP ) UNIV ROCHESTER.
XX
PI Rowley PT;
XX
DR MPI: 2003-403289/38.
DR P-PSDB; ABR42063.
XX
PT Novel nucleic acid encoding or comprising interfering RNAs which target
PT telomerase RNA, useful for inhibiting telomerase activity for treating
PT cancer, infertility and disorders of the immune system.
XX
PS Disclosure; Fig 3; 52pp; English.
XX
SS The present sequence is that of human telomerase reverse transcriptase
CC (TERT) cDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germ-line cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 100.0%; Score 4015; DB 8; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAGCGCTGCGCTGCGAGCGTGGAGAGCCCTGAGCGCGGACCCCGGAGATGCC 60
Db 1 GCAGCGCTGCGCTGCGAGCGTGGAGAGCCCTGAGCGCGGACCCCGGAGATGCC 60
Qy 61 GCGCGCTCCCGCTGCGAGCGTGGCGCTCCCTGTGCGAGCCACTACCGGAGTGTCT 120
Db 61 GCGCGCTCCCGCTGCGAGCGTGGCGCTCCCTGTGCGAGCCACTACCGGAGTGTCT 120

```


Dh 61 GCGCGCTCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGGAGCACTACCGGAGTGTCT 120
Qy 121 GCGCGTGGGCAAGTTGCTGCGGAGCCGCTGGGAGCCGAGGAGCTGGGAGTGTGCAAGCGCG 180
Dh 121 GCGCGTGGGCAAGTTGCTGCGGAGCCGCTGGGAGCCGAGGAGCTGGGAGTGTGCAAGCGCG 180
Qy 181 GGAAGCGGAGGCTTTTCCGCGCGCTGGTGGCCCAAGTGTCTGTGTGTGTGCTGTGGAGCGC 240
Dh 181 GGAAGCGGAGGCTTTTCCGCGCGCTGGTGGCCCAAGTGTCTGTGTGTGTGCTGTGGAGCGC 240
Qy 241 AGGCG 300
Dh 241 AGGCG 300
Qy 301 CCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Dh 301 CCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy 361 GCTGTGTGAGCGGAGCG 420
Dh 361 GCTGTGTGAGCGGAGCG 420
Qy 421 CCGGCGCAACAGAGGTGACCGAGCGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Dh 421 CCGGCGCAACAGAGGTGACCGAGCGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 481 CCGGCGTGGGCGACGACGCTGTGTGCTTACCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCG 540
Dh 481 CCGGCGTGGGCGACGACGCTGTGTGCTTACCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCG 540
Qy 541 GCGCTCCAGAGCTGGCGCTTACAGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Dh 541 GCGCTCCAGAGCTGGCGCTTACAGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Qy 601 TCAGAGCCGAGCG 660
Dh 601 TCAGAGCCGAGCG 660
Qy 661 CTGGAACCAATAGCGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Dh 661 CTGGAACCAATAGCGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Qy 721 GAGGCGGCGGAGGAGTGTGCGAGCGCGAGTGTGCGCGTGTGCGCGCGCGCGCGCGCGCGCG 780
Dh 721 GAGGCGGCGGAGGAGTGTGCGAGCGCGAGTGTGCGCGTGTGCGCGCGCGCGCGCGCGCGCG 780
Qy 781 TGCCCTGAGCGCGAGCG 840
Dh 781 TGCCCTGAGCGCGAGCG 840
Qy 841 GCGTGTGAGCGAGTGTGCGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Dh 841 GCGTGTGAGCGAGTGTGCGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Qy 901 CACCTCTTTGAGGAGTGTGCGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Dh 901 CACCTCTTTGAGGAGTGTGCGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Qy 961 GCAACGCGGAGCG 1020
Dh 961 GCAACGCGGAGCG 1020
Qy 1021 CCGGCGTGTGAGCGCGAGCAAGCACTTCTCTACTCTCTAGCGCGCAAGAGGAGCTTGTGCG 1080
Dh 1021 CCGGCGTGTGAGCGCGAGCAAGCACTTCTCTACTCTCTAGCGCGCAAGAGGAGCTTGTGCG 1080
Qy 1081 GCGCTCTCTTCTACTAGCTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Dh 1081 GCGCTCTCTTCTACTAGCTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Qy 1141 GACCATCTTTCTGT 1200
Dh 1141 GACCATCTTTCTGT 1200

Qy 1201 GCGCGAGCGCTACTGTGCAATGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
Dh 1201 GCGCGAGCGCTACTGTGCAATGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
Qy 1261 GTGCGCGCTTACGAGGAGTGTCTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Dh 1261 GTGCGCGCTTACGAGGAGTGTCTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Qy 1321 AGCGGAGT 1380
Dh 1321 AGCGGAGT 1380
Qy 1381 CAGAGACCGCGCGCTGT 1440
Dh 1381 CAGAGACCGCGCGCTGT 1440
Qy 1441 CCGCTGT 1500
Dh 1441 CCGCTGT 1500
Qy 1501 CAGCGAAGCGCGCTTCTCTCAAGAGCACCAAGAGTGTCTCTCTGTGTGTGTGTGTGTGTGT 1560
Dh 1501 CAGCGAAGCGCGCTTCTCTCAAGAGCACCAAGAGTGTCTCTCTGTGTGTGTGTGTGTGTGT 1560
Qy 1561 GCTCTGT 1620
Dh 1561 GCTCTGT 1620
Qy 1621 GAGCCGAGGAGGTTGT 1680
Dh 1621 GAGCCGAGGAGGTTGT 1680
Qy 1681 CAAGTTCCTGACGCTGT 1740
Dh 1681 CAAGTTCCTGACGCTGT 1740
Qy 1741 TGTCAAGAGAGCACGCTTCAAGAGACAGGCTCTTTTCTTCAAGAGAGAGTGTGTGTGT 1800
Dh 1741 TGTCAAGAGAGCACGCTTCAAGAGACAGGCTCTTTTCTTCAAGAGAGAGTGTGTGTGT 1800
Qy 1801 CAAGTTCCTGACGCTGT 1860
Dh 1801 CAAGTTCCTGACGCTGT 1860
Qy 1861 GGAAGCAGAGGTCAAGCAGCATGTGGAAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
Dh 1861 GGAAGCAGAGGTCAAGCAGCATGTGGAAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
Qy 1921 CTTTCAATCCCAAGCTGT 1980
Dh 1921 CTTTCAATCCCAAGCTGT 1980
Qy 1981 CAGAGGTTCCGCGAGAGAAAGAGGCGCGAGGCTCTCACTTGTGTGTGTGTGTGTGTGTGT 2040
Dh 1981 CAGAGGTTCCGCGAGAGAAAGAGGCGCGAGGCTCTCACTTGTGTGTGTGTGTGTGTGTGT 2040
Qy 2041 CAGCGTGTCTCACTAGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
Dh 2041 CAGCGTGTCTCACTAGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
Qy 2101 CTTGTGAGAGATCAAGAGGCG 2160
Dh 2101 CTTGTGAGAGATCAAGAGGCG 2160
Qy 2161 GCGCGTGTGAGCTGT 2220
Dh 2161 GCGCGTGTGAGCTGT 2220
Qy 2221 GCGCGTGTGAGCTGT 2280
Dh 2221 GCGCGTGTGAGCTGT 2280

XX (GERO-) GERON CORP.
XX Jiang X, Chiu C, Harley CB;
PI WPI, 2003-120591/11.
XX P-PSDB; ABP56676.
XX
XX Composition for treating wounds and enhancing epithelialization of a skin
PT surface, comprises vector encoding telomerase reverse transcriptase or
PT telomerized epithelial cells on a microparticle or a matrix.
XX
XX Disclosure, Page 31-32; 68pp; English.
XX
XX The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomerized epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnerary and anti-ulcer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelialization of a skin surface. The wound is especially skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment. The also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence encodes human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 100.0%; Score 4015; DB 8; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACGCGCTCCCTGCTGCGGAGAGCCCTGAGCCCGGCGGATGCC 60
DB 1 GCACGCGCTCCCTGCTGCGGAGAGCCCTGAGCCCGGCGGATGCC 60
QY 61 GCGGCTCCCGCTGCGGAGCGCTGCTCCCTGCTGCGGAGAGCTGCT 120
DB 61 GCGGCTCCCGCTGCGGAGCGCTGCTCCCTGCTGCGGAGAGCTGCT 120
QY 121 GCGGCTGCGGAGCGCTGCTGCGGAGCGCTGCGGAGAGCTGCT 180
DB 121 GCGGCTGCGGAGCGCTGCTGCGGAGCGCTGCGGAGAGCTGCT 180
QY 181 GGAACCGGCGGCTTCCGCGGAGCGCTGCGGAGAGCTGCTGCT 240
DB 181 GGAACCGGCGGCTTCCGCGGAGCGCTGCGGAGAGCTGCTGCT 240
QY 241 AGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
DB 241 AGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 301 CGGAGTGTGCGGAGAGCTGCTGCGGAGCGGCGGAGAGAGCTGCT 360
DB 301 CGGAGTGTGCGGAGAGCTGCTGCGGAGCGGCGGAGAGAGCTGCT 360
QY 361 GCTGCTGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
DB 361 GCTGCTGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 421 CCTGCCCAACACGCTGACCGACGCACTGCGGAGGAGCGGAGCT 480

DB 421 CCTGCCCAACACGCTGACCGACGCACTGCGGAGGAGCGGAGCT 480
QY 481 CCGGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCTGCT 540
DB 481 CCGGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCTGCT 540
QY 541 GAGTCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCTGCT 600
DB 541 GAGTCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCTGCT 600
QY 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
DB 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 CTGGAACCATAGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCTG 720
DB 661 CTGGAACCATAGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCTG 720
QY 721 GAGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCT 780
DB 721 GAGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCT 780
QY 781 TCCCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 840
DB 781 TCCCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 840
QY 841 GCGTGGACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 900
DB 841 GCGTGGACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 900
QY 901 CACTCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 CACTCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 GAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
DB 961 GAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
QY 1021 CCGGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1080
DB 1021 CCGGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1080
QY 1081 GCGCTCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 GCGCTCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GACCATCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
DB 1141 GACCATCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1201 GCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1260
DB 1201 GCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1260
QY 1261 GTCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1320
DB 1261 GTCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1320
QY 1321 AGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGGAG 1380
DB 1321 AGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGGAG 1380
QY 1381 CACAGACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGGAG 1440
DB 1381 CACAGACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGGAG 1440
QY 1441 GCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
DB 1441 GCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
QY 1501 CACAGACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGGAG 1560

Db 1501 CAACGAAGCGCGCTTCTTCAGAGAACCAAGAAATTCTCTCCGTGGGAGACATGCGCA 1560
Qy 1561 GCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGCGGAGACTGGCTTGGCTGGCGAG 1620
Db 1561 GCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGCGGAGACTGGCTTGGCTGGCGAG 1620
Qy 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGAGCACGCTGCGTGAAGAGATCTTGGC 1680
Db 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGAGCACGCTGCGTGAAGAGATCTTGGC 1680
Qy 1681 CAAGTTCCTGCACTGGCTGATGAGTGTGATCGTCCGAGCTGCTCAGGTCTTTCTTTTA 1740
Db 1681 CAAGTTCCTGCACTGGCTGATGAGTGTGATCGTCCGAGCTGCTCAGGTCTTTCTTTTA 1740
Qy 1741 TGTCAAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTGAG 1800
Db 1741 TGTCAAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTGAG 1800
Qy 1801 CAAGTTGCAAAAGCATTTGGAATCAGACAGCATTTGAAGAGGTGCAAGCTGCGGAGCTGTC 1860
Db 1801 CAAGTTGCAAAAGCATTTGGAATCAGACAGCATTTGAAGAGGTGCAAGCTGCGGAGCTGTC 1860
Qy 1861 GGAAGCAGAGGTCAAGGAGCATCGGGAAGCCAGGCCCCGCTGCTGACGTTCCAGACTCCG 1920
Db 1861 GGAAGCAGAGGTCAAGGAGCATCGGGAAGCCAGGCCCCGCTGCTGACGTTCCAGACTCCG 1920
Qy 1921 CTTTCACTCCCAAGCCTGACGGGCTGCGGCGAATTGGAACTAGGACTAGTGTGGAGC 1980
Db 1921 CTTTCACTCCCAAGCCTGACGGGCTGCGGCGAATTGGAACTAGGACTAGTGTGGAGC 1980
Qy 1981 CAGAAGCTTCCGACAGAAAGAGGCGCGAGGCTCTCACTCGAGGGTGAAGGCACTGTT 2040
Db 1981 CAGAAGCTTCCGACAGAAAGAGGCGCGAGGCTCTCACTCGAGGGTGAAGGCACTGTT 2040
Qy 2041 CAGCGTCTCAACTACGAGCGGGGCGCGGCGCCGCGCTCTGCGGCGCTCTGTGTGG 2100
Db 2041 CAGCGTCTCAACTACGAGCGGGGCGCGGCGCCGCGCTCTGCGGCGCTCTGTGTGG 2100
Qy 2101 CCGTGAACATATTCACAGGGGCTGCGGCACTTCCGTGCTGCGTGGCCGAGAGACC 2160
Db 2101 CCGTGAACATATTCACAGGGGCTGCGGCACTTCCGTGCTGCGTGGCCGAGAGACC 2160
Qy 2161 GCGGCTGAGCTGATCTTGTCAAGGTGATGACGAGGCGGTACACACCATCCCCA 2220
Db 2161 GCGGCTGAGCTGATCTTGTCAAGGTGATGACGAGGCGGTACACACCATCCCCA 2220
Qy 2221 GGAACAGGCTCAAGGAGGTGATGCGCATCAAAACCCAGAAACGCTACTGCGTGG 2280
Db 2221 GGAACAGGCTCAAGGAGGTGATGCGCATCAAAACCCAGAAACGCTACTGCGTGG 2280
Qy 2281 TCGGTATGCGGTGTCAGAAAGCGCCCATAGGCGACGTCCGCAAGGCTTTCAAGGCCA 2340
Db 2281 TCGGTATGCGGTGTCAGAAAGCGCCCATAGGCGACGTCCGCAAGGCTTTCAAGGCCA 2340
Qy 2341 CGTCTCTACCTTGACAGACCTCAGCGGTACATGAGACAGTTGTTGGGCTCACCTGAGGA 2400
Db 2341 CGTCTCTACCTTGACAGACCTCAGCGGTACATGAGACAGTTGTTGGGCTCACCTGAGGA 2400
Qy 2401 GACCAAGCCGCTGAGGAGATGCGTGTCTATCGAGCAGAGACTCTCTCTGAATGAGGCCAG 2460
Db 2401 GACCAAGCCGCTGAGGAGATGCGTGTCTATCGAGCAGAGACTCTCTCTGAATGAGGCCAG 2460
Qy 2461 CAGTGGCTCTTTCAGAGCTTCTCTAGGCTTCAATGTCACACAGCCGTGCGATCAGGGG 2520
Db 2461 CAGTGGCTCTTTCAGAGCTTCTCTAGGCTTCAATGTCACACAGCCGTGCGATCAGGGG 2520
Qy 2521 CAAGTCTTAAGTCAAGTCAAGTCAAGGAGATCCGCAAGGCTCATCTCTCAAGCTGTCTG 2580
Db 2521 CAAGTCTTAAGTCAAGTCAAGTCAAGGAGATCCGCAAGGCTCATCTCTCAAGCTGTCTG 2580
Qy 2581 CAGCTGTGCTACGAGGAGCATGGAAGACAAAGCTGTTTGGGGGATTCCGCGGAGCGGCT 2640
Db 2581 CAGCTGTGCTACGAGGAGCATGGAAGACAAAGCTGTTTGGGGGATTCCGCGGAGCGGCT 2640

Qy 2641 GCTCTGCGGTTTGGATGATTTCTGTGGTGAACACTCACTCACCCACGCGAAAC 2700
Db 2641 GCTCTGCGGTTTGGATGATTTCTGTGGTGAACACTCACTCACCCACGCGAAAC 2700
Qy 2701 CTTTCTCAGAGACCTTGTGTCAGAGGTGTCCTGAGTATGCTGCTGCTGAACCTTGGGAA 2760
Db 2701 CTTTCTCAGAGACCTTGTGTCAGAGGTGTCCTGAGTATGCTGCTGCTGAACCTTGGGAA 2760
Qy 2761 GACAGTGTGAACCTTCCCTGTAAGAGAGGCGCTGGGTGGCAAGGCTTTTGTTCAGAT 2820
Db 2761 GACAGTGTGAACCTTCCCTGTAAGAGAGGCGCTGGGTGGCAAGGCTTTTGTTCAGAT 2820
Qy 2821 GCCGCGCCACGCGCTATTCCCTGGTGGGCTGTGCTGCTGATACCCGAGCTGAGGT 2880
Db 2821 GCCGCGCCACGCGCTATTCCCTGGTGGGCTGTGCTGCTGATACCCGAGCTGAGGT 2880
Qy 2881 GCAGAGCACTATCTCAGCTATGCCGGAACCTTCATCAGAGCAAGTCTTCACTTCAACCG 2940
Db 2881 GCAGAGCACTATCTCAGCTATGCCGGAACCTTCATCAGAGCAAGTCTTCACTTCAACCG 2940
Qy 2941 CCGCTTCAAGGCTGGAGAGAAATGCTGCAAACTTTTGGGGTCTTGGGCTGAAGT 3000
Db 2941 CCGCTTCAAGGCTGGAGAGAAATGCTGCAAACTTTTGGGGTCTTGGGCTGAAGT 3000
Qy 3001 TCACAGCCTGTTCTGGAATTGCAAGTGAACAGCTCCAGAGAGTGTGACCAACTTA 3060
Db 3001 TCACAGCCTGTTCTGGAATTGCAAGTGAACAGCTCCAGAGAGTGTGACCAACTTA 3060
Qy 3061 CAAAGTCTCTCTGCTGACAGGCGCTACAGGTTTCAAGCATGTGTGCTGACACTTCAATTTCA 3120
Db 3061 CAAAGTCTCTCTGCTGACAGGCGCTACAGGTTTCAAGCATGTGTGCTGACACTTCAATTTCA 3120
Qy 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACAGGCTCTCCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACAGGCTCTCCT 3180
Qy 3181 CTGCTACTCCATCCGAAAGCCCAAGAACGAGGAGTGTGCTGGGGGCCAAGGCGCGC 3240
Db 3181 CTGCTACTCCATCCGAAAGCCCAAGAACGAGGAGTGTGCTGGGGGCCAAGGCGCGC 3240
Qy 3241 CCGGCTCTGCGCTCCGAGGCGGTGAGTGTGCTGAGGCTGCTGAGGCTCTGAGGCT 3300
Db 3241 CCGGCTCTGCGCTCCGAGGCGGTGAGTGTGCTGAGGCTGCTGAGGCTCTGAGGCT 3300
Qy 3301 GACTGACACCGTGTCACTACGTGCACTCTGGGGTCACTCAGGACAGCCAGACGCA 3360
Db 3301 GACTGACACCGTGTCACTACGTGCACTCTGGGGTCACTCAGGACAGCCAGACGCA 3360
Qy 3361 GGTGAGTGGGAAGCTCCGCGGAGACGCTGACGTGACCTGGAGGCGCGACCCCGC 3420
Db 3361 GGTGAGTGGGAAGCTCCGCGGAGACGCTGACGTGACCTGGAGGCGCGACCCCGC 3420
Qy 3421 ACTGCGCTCAGACTTCAAGAACATCTGAGATGAGGCAACCGGCCACAGGCGAGCGA 3480
Db 3421 ACTGCGCTCAGACTTCAAGAACATCTGAGATGAGGCAACCGGCCACAGGCGAGCGA 3480
Qy 3481 GAGCAGACACAGAGCCCTGTACGCGCGGCTTACGTCCAGGAGGAGGAGCGCGC 3540
Db 3481 GAGCAGACACAGAGCCCTGTACGCGCGGCTTACGTCCAGGAGGAGGAGCGCGC 3540
Qy 3541 CACACCCAGGCGCGGACCGCTGGAGTCTGAGGCGTGAAGTGTGTTGGCCGAGGCGCTG 3600
Db 3541 CACACCCAGGCGCGGACCGCTGGAGTCTGAGGCGTGAAGTGTGTTGGCCGAGGCGCTG 3600
Qy 3601 CATGTCCGAGTGAAGGCTGAGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Db 3601 CATGTCCGAGTGAAGGCTGAGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Qy 3661 GAGTGTCAAGCACCTGCGCTTCACTTCCCAAGGCTGCGCTCGCTTCAACCCCA 3720
Db 3661 GAGTGTCAAGCACCTGCGCTTCACTTCCCAAGGCTGCGCTCGCTTCAACCCCA 3720

Db 901 CACCTCTTGGAGGGGCGCTCTTGCA CGGCCCACTCCCA CCACTCCGCGCGCA 960
Qy 961 GACACAGCGGGGCCCCCATCCACATCGGGGCA CCAAGTCCCTGGGACACCCCTTGTCC 1020
Db 961 GACACAGCGGGGCCCCCATCCACATCGGGGCA CCAAGTCCCTGGGACACCCCTTGTCC 1020
Qy 1021 CCGGGTGTACGGCGAGAACCAACTTCTCTTACTCTCAGAGGACAAAGAGACAGCTGCG 1080
Db 1021 CCGGGTGTACGGCGAGAACCAACTTCTCTTACTCTCAGAGGACAAAGAGACAGCTGCG 1080
Qy 1081 GCGCTCTCTTCTACTACTAGCTCTTGAAGG CCAAGCTGAGCTGCGAGCTGCTGGA 1140
Db 1081 GCGCTCTCTTCTACTACTAGCTCTTGAAGG CCAAGCTGAGCTGCGAGCTGCTGGA 1140
Qy 1141 GACCACTTTTCTGGGTTCAGAGCCCTGATGTC CAGGGAATCCCCGAGGTTCGCCGCT 1200
Db 1141 GACCACTTTTCTGGGTTCAGAGCCCTGATGTC CAGGGAATCCCCGAGGTTCGCCGCT 1200
Qy 1201 GCGCCAGCGCTACTGGCAAAATGCGGCCCTGT TTTCTGAGCTGCTTGGGAA CCAAGCGCA 1260
Db 1201 GCGCCAGCGCTACTGGCAAAATGCGGCCCTGT TTTCTGAGCTGCTTGGGAA CCAAGCGCA 1260
Qy 1261 GTGCCCTTACGGGGGTCTCTCAAGACGCA CTGCGCGTGCAGCTGCGGTCA CCGCAGC 1320
Db 1261 GTGCCCTTACGGGGGTCTCTCAAGACGCA CTGCGCGTGCAGCTGCGGTCA CCGCAGC 1320
Qy 1321 AGCGGTGTCTGTGCCCCGGGAAAGCCCAAGG GTTGTGCGGGCCCCCGAGAGAGAGA 1380
Db 1321 AGCGGTGTCTGTGCCCCGGGAAAGCCCAAGG GTTGTGCGGGCCCCCGAGAGAGAGA 1380
Qy 1321 AGCGGTGTCTGTGCCCCGGGAAAGCCCAAGG GTTGTGCGGGCCCCCGAGAGAGAGA 1380
Db 1321 AGCGGTGTCTGTGCCCCGGGAAAGCCCAAGG GTTGTGCGGGCCCCCGAGAGAGAGA 1380
Qy 1381 CACAGACCCCGCTGCGCTGCTGAGCTGCTCG CCGCAGCA CAGAGCCCTGAGAGGTGA 1440
Db 1381 CACAGACCCCGCTGCGCTGCTGAGCTGCTCG CCGCAGCA CAGAGCCCTGAGAGGTGA 1440
Qy 1441 CGGCTTCTGTCGGGCGCTGCTGCGCGAGCTG TGGTCCCGAGGCTTCTGAGGA 1500
Db 1441 CGGCTTCTGTCGGGCGCTGCTGCGCGAGCTG TGGTCCCGAGGCTTCTGAGGA 1500
Qy 1501 CAAAGGACCGCGCTTCTCTAGAGAACCAAG AAGTTCATCTCCCTGGGGAACATGCCAA 1560
Db 1501 CAAAGGACCGCGCTTCTCTAGAGAACCAAG AAGTTCATCTCCCTGGGGAACATGCCAA 1560
Qy 1561 GCTCTGCGCTGAGGAGCTGACGTGGAAGATG ACGTGGGGA CTGCGCTTGGCTGCGAG 1620
Db 1561 GCTCTGCGCTGAGGAGCTGACGTGGAAGATG ACGTGGGGA CTGCGCTTGGCTGCGAG 1620
Qy 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGGCCG CAGAGCACCGTCTGCGTGAAGATCTGGC 1680
Db 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGGCCG CAGAGCACCGTCTGCGTGAAGATCTGGC 1680
Qy 1681 CAAAGTTCCTGCACTGCGCTGATGATGTGTA CGTCTGAGCTGCTAGGTCTTTCTTTTA 1740
Db 1681 CAAAGTTCCTGCACTGCGCTGATGATGTGTA CGTCTGAGCTGCTAGGTCTTTCTTTTA 1740
Qy 1741 TGTCAAGGAGCA CAGTTTCAAAGAAAGGCTC TTTTCTTACCGGAGAGTGTGAG 1800
Db 1741 TGTCAAGGAGCA CAGTTTCAAAGAAAGGCTC TTTTCTTACCGGAGAGTGTGAG 1800
Qy 1801 CAAAGTTCAAAGCATTTGAATCAGACAGCA CTTTGAAGAGGTGCACTGCGGAGCTGTC 1860
Db 1801 CAAAGTTCAAAGCATTTGAATCAGACAGCA CTTTGAAGAGGTGCACTGCGGAGCTGTC 1860
Qy 1861 GGAAGGAGAGTTCAGGCAAGATTCGGGAAAC CAGGCCCCGCTGCTGAAGTTCAGACTGTCG 1920
Db 1861 GGAAGGAGAGTTCAGGCAAGATTCGGGAAAC CAGGCCCCGCTGCTGAAGTTCAGACTGTCG 1920
Qy 1921 CTTTCATCCCCAAGCTGACGGGCTGCGGCGAT TTTGAACATGACTGACTGAGGAGC 1980
Db 1921 CTTTCATCCCCAAGCTGACGGGCTGCGGCGAT TTTGAACATGACTGACTGAGGAGC 1980
Qy 1981 CAGAAAGTTCGCGAGAGAAAAGAGGCGCAGC GTCTCACCTCGAGGGGTGAAGGCACTGTT 2040
Db 1981 CAGAAAGTTCGCGAGAGAAAAGAGGCGCAGC GTCTCACCTCGAGGGGTGAAGGCACTGTT 2040

Qy 2041 CAGCGTGTCAA CTACGAGCGGGGCGGGGCGCC GCGGCTCTGAGGCGCTGTGTGCGG 2100
Db 2041 CAGCGTGTCAA CTACGAGCGGGGCGGGGCGCC GCGGCTCTGAGGCGCTGTGTGCGG 2100
Qy 2101 CTTGAGCAATATCA CAGGGCTGAGCGCACTT GCTGTGCTGTGTGCGGGCCAGAGACC 2160
Db 2101 CTTGAGCAATATCA CAGGGCTGAGCGCACTT GCTGTGCTGTGTGCGGGCCAGAGACC 2160
Qy 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTG ACGGGCGGTGACACATATCCCCA 2220
Db 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTG ACGGGCGGTGACACATATCCCCA 2220
Qy 2221 GGAAGGGCTCACGGAGGTATGCGCAGAGTCA TCAAA CCGCAGAA CAGCTACTGCGTGG 2280
Db 2221 GGAAGGGCTCACGGAGGTATGCGCAGAGTCA TCAAA CCGCAGAA CAGCTACTGCGTGG 2280
Qy 2281 TCGGTATGCGGTGTCTCAAGAGCGGCCCAT GGGGCAAGTCCGCAAGGCTTTGAAGGCCA 2340
Db 2281 TCGGTATGCGGTGTCTCAAGAGCGGCCCAT GGGGCAAGTCCGCAAGGCTTTGAAGGCCA 2340
Qy 2341 GGTCTTCTACTTGA CAGACCTTCAGACCTGTA CATGCGACAGTTCTGTGCTCACCTGACAGA 2400
Db 2341 GGTCTTCTACTTGA CAGACCTTCAGACCTGTA CATGCGACAGTTCTGTGCTCACCTGACAGA 2400
Qy 2401 GACAGCGCGCTGAGGGATGCGGTGTCATGAG AAGAGAGCTCTCCCTGAATGAGGCGAG 2460
Db 2401 GACAGCGCGCTGAGGGATGCGGTGTCATGAG AAGAGAGAGCTCTCCCTGAATGAGGCGAG 2460
Qy 2461 CAGTGGCGCTTCTGAGAGCTTCTCTACGTCTA TGTGCCAACAGCGCGTGCATAGGGG 2520
Db 2461 CAGTGGCGCTTCTGAGAGCTTCTCTACGTCTA TGTGTGCCAACAGCGCGTGCATAGGGG 2520
Qy 2521 CAAAGTCTACGTTCAGCTGCGCAGGGGATCC CGAGGGCTTCATCTCTCCAGCTGTCTG 2580
Db 2521 CAAAGTCTACGTTCAGCTGCGCAGGGGATCC CGAGGGCTTCATCTCTCCAGCTGTCTG 2580
Qy 2581 CAGCGTGTGCTACGGCGACATGGAAGAACAG CTTGTTGCGGGGATTTCCGCGGAGCGGCT 2640
Db 2581 CAGCGTGTGCTACGGCGACATGGAAGAACAG CTTGTTGCGGGGATTTCCGCGGAGCGGCT 2640
Qy 2641 GCTCTGCGTGTGTGATGATTTCTTGTGTGTA CACTCACTCA CCGCAGCAAAAC 2700
Db 2641 GCTCTGCGTGTGTGATGATTTCTTGTGTGTA CACTCACTCA CCGCAGCAAAAC 2700
Qy 2701 CTTCTCAGAGACCTTGTGTCAGAGTGTCTC TGAAGTGTGCTGCTGTGTGA 2760
Db 2701 CTTCTCAGAGACCTTGTGTCAGAGTGTCTC TGAAGTGTGCTGCTGTGTGA 2760
Qy 2761 GACAGTGTGGA CTTCCCTGTGTAAGACAGAG CCGTGGGTGSCAGGCGTTTGTTCAGAT 2820
Db 2761 GACAGTGTGGA CTTCCCTGTGTAAGACAGAG CCGTGGGTGSCAGGCGTTTGTTCAGAT 2820
Qy 2821 GCGGCGCCAGCGCTATTCCTCTGTCGGGCTG TGTGATGATACCGGACCTTGAGGT 2880
Db 2821 GCGGCGCCAGCGCTATTCCTCTGTCGGGCTG TGTGATGATACCGGACCTTGAGGT 2880
Qy 2881 GCAAGAGCGACTTACTCAGCTATGCCCCGAG CTTCCATCAGAGCAGTCTCACTTCAACG 2940
Db 2881 GCAAGAGCGACTTACTCAGCTATGCCCCGAG CTTCCATCAGAGCAGTCTCACTTCAACG 2940
Qy 2941 CCGCTTCAAGGCTGGAAGGAAATGCTGTGCA AACTTTTGGGGCTTGGCGGCTGAAGT 3000
Db 2941 CCGCTTCAAGGCTGGAAGGAAATGCTGTGCA AACTTTTGGGGCTTGGCGGCTGAAGT 3000
Qy 3001 TCACAGCGCTGTTCTGATTTGACAGGTGAAC GCTTCCAGAGCGGTGTGCAACATCTA 3060
Db 3001 TCACAGCGCTGTTCTGATTTGACAGGTGAAC GCTTCCAGAGCGGTGTGCAACATCTA 3060
Qy 3061 CAAAGTCTCTCTGCTGCAAGGCGTACAGTTT TACCGCATGTGTGCTGCAAGCTCCATTTCA 3120
Db 3061 CAAAGTCTCTCTGCTGCAAGGCGTACAGTTT TACCGCATGTGTGCTGCAAGCTCCATTTCA 3120


```

QY 3121 TCAGAGATTGGAGAACCCACATTTTCTGCGCGATCTCTGACACGGCTCCCT 3180
DB 3121 TCAGCAAGTTGGAGAACCCACATTTTCTGCGCGATCTCTGACACGGCTCCCT 3180
QY 3181 CTGCTACTCCATCTCTGAAAGCCAAAGAACGAGGAGATGTGCTGGGGGCCAAGGCCCCGC 3240
DB 3181 CTGCTACTCCATCTCTGAAAGCCAAAGAACGAGGAGATGTGCTGGGGGCCAAGGCCCCGC 3240
QY 3241 CGGCGCTGCGCCCTCCGAGGCGCGTGAAGTGGCTGTGACACCAAGCATTCCTGCTCAAGCT 3300
DB 3241 CGGCGCTGCGCCCTCCGAGGCGCGTGAAGTGGCTGTGACACCAAGCATTCCTGCTCAAGCT 3300
QY 3301 GACTCGACACCGTGTCACTACCTAGTGCCTCTCTGGGGTCACTGAGACAGCCCAAGCAGA 3360
DB 3301 GACTCGACACCGTGTCACTACCTAGTGCCTCTCTGGGGTCACTGAGACAGCCCAAGCAGA 3360
QY 3361 GCTGAGTGGAGAGCTCCCGGGGAGAGAGCTGATGCTGCTGAGAGCCGCAAGCCCGGC 3420
DB 3361 GCTGAGTGGAGAGCTCCCGGGGAGAGAGCTGATGCTGCTGAGAGCCGCAAGCCCGGC 3420
QY 3421 ACTGCGCTGAGACTTCAAGACCATCTCGAGCTGATGAGCCAGCCGCGCAAGCGAGCCGA 3480
DB 3421 ACTGCGCTGAGACTTCAAGACCATCTCGAGCTGATGAGCCAGCCGCGCAAGCGAGCCGA 3480
QY 3481 GAGGAGACACACGAGAGCCCTGTGACAGCCGGGCTCTACGTCCAGAGAGGAGGGCGCC 3540
DB 3481 GAGGAGACACACGAGAGCCCTGTGACAGCCGGGCTCTACGTCCAGAGAGGAGGGCGCC 3540
QY 3541 CACACCCAGGCGCGGACCTGCGGAGTCTGAGGCTGAGAGTGTGTTGGCCGAGGCTTG 3600
DB 3541 CACACCCAGGCGCGGACCTGCGGAGTCTGAGGCTGAGAGTGTGTTGGCCGAGGCTTG 3600
QY 3601 CATGTCGGGCTGAAGGCTGAGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
DB 3601 CATGTCGGGCTGAAGGCTGAGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
QY 3661 GAGTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGCGGCTCCACCCCA 3720
DB 3661 GAGTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGCGGCTCCACCCCA 3720
QY 3721 GGGCGAGCTTTTCTCTACAGAGAGCCGGCTTCCACTCCCACTAGAGATAGTCCATCC 3780
DB 3721 GGGCGAGCTTTTCTCTACAGAGAGCCGGCTTCCACTCCCACTAGAGATAGTCCATCC 3780
QY 3781 CCAGATTGCGCATTTTCAACCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 3840
DB 3781 CCAGATTGCGCATTTTCAACCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 3840
QY 3841 AGGTGAGACCCCTGAGAGAGACCTTGGAGTCTGAGAGATTTGAGAGTGCACCAAGGTGTG 3900
DB 3841 AGGTGAGACCCCTGAGAGAGACCTTGGAGTCTGAGAGATTTGAGAGTGCACCAAGGTGTG 3900
QY 3901 CCTCTGACACAGGAGAGACCCCTGACACTGAGATGGGGTCCCTGGGTCAAAATTTGGGGG 3960
DB 3901 CCTCTGACACAGGAGAGACCCCTGACACTGAGATGGGGTCCCTGGGTCAAAATTTGGGGG 3960
QY 3961 GAGTGTCTGAGAGTAAATATGAAATATGAGATTTTCAAGTTTGAAGAAAAA 4015
DB 3961 GAGTGTCTGAGAGTAAATATGAAATATGAGATTTTCAAGTTTGAAGAAAAA 4015

```

RESULT 10

ACCS8039 ID ACCS8039 standard; cDNA; 4015 BP.

ACCS8039;

11-AUG-2003 (first entry)

Human telomerase reverse transcriptase cDNA.

XX Telomerase reverse transcriptase; TERT; enzyme: RNA interference;
 KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;

```

KW immunosuppressive; antifertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy; gene; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 56..3454
XX FT /*tag= a
XX FT /product= "TERT"
PN MO2003035667-A2.
XX
XX 01-MAY-2003.
PD
XX
XX 16-OCT-2002; 2002WO-US033065.
PF
XX
XX 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196B.
PR 22-MAY-2002; 2002US-0383195P.
XX
XX (UYP) UNIV ROCHESTER.
PA
XX
XX Rowley PT;
PI
XX WPI; 2003-403336/38.
DR P-PSDB; ABR42384.
DR
XX
XX Novel double-stranded short interfering RNA having sense and antisense
PT nucleic acids which are complementary to each other and to target nucleic
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
PT transcriptase.
XX
XX Disclosure; Fig 3A-B; 37pp; English.
XX
XX The present sequence is that of human telomerase reverse transcriptase
CC (TERT) cDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germine cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
SQ

```

Query Match 100.0%; Score 4015; DB 10; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GCAGCGCTGCTGCTCTGCTGCGACCTGAGAGCGCTGCGCGCCGAGCCCGGAGATGCC 60
DB 1 GCAGCGCTGCTGCTCTGCTGCGACCTGAGAGCGCTGCGCGCCGAGCCCGGAGATGCC 60
QY 61 GCGCGCTCCCGGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCACTACCGAGAGTGCT 120
DB 61 GCGCGCTCCCGGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCACTACCGAGAGTGCT 120
QY 121 GCGGCTGCGCAGCTTGTGTGGGCGCTGAGGCGCCAGGCGCTGAGCGCTGAGCGCG 180
DB 121 GCGGCTGCGCAGCTTGTGTGGGCGCTGAGGCGCCAGGCGCTGAGCGCTGAGCGCG 180
QY 181 GAGACCGGCGGCTTTCCGCGCGCTGAGTGGCCAGTGCCTGTGTGTCCTCCCTGGGAGCG 240
DB 181 GAGACCGGCGGCTTTCCGCGCGCTGAGTGGCCAGTGCCTGTGTGTCCTCCCTGGGAGCG 240
QY 241 ACGGCGCGCCCGCGCGCGCCCTCTTCCGCGCAGGTGTCTGCTGAGAGAGTGTGGC 300
DB 241 ACGGCGCGCCCGCGCGCGCCCTCTTCCGCGCAGGTGTCTGCTGAGAGAGTGTGGC 300

```


QY 301 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGAGAAAGCTGTGCTGGCTTGGCTTGGC 360
DB 301 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGAGAAAGCTGTGCTTGGCTTGGC 360
QY 361 GCTGTGAGCGAGGCGCGCGCGCGCGCGCGAGAGCTTCAACCAAGCGTGTGAGCTA 420
DB 361 GCTGTGAGCGAGGCGCGCGCGCGCGCGCGAGAGCTTCAACCAAGCGTGTGAGCTA 420
QY 421 CTTGCGCCAAACAGGTGACCGACGCACTGTGCGAGAGCGAGCGGTGTGAGCTGTGCG 480
DB 421 CTTGCGCCAAACAGGTGACCGACGCACTGTGCGAGAGCGAGCGGTGTGAGCTGTGCG 480
QY 481 CCGCGTGGGCGAGAGAGCTGTGCTGCTTCACTGTGCGAGCGCTGTGCGAGCTTGTGCTGT 540
DB 481 CCGCGTGGGCGAGAGAGCTGTGCTGCTTCACTGTGCGAGCGCTGTGCGAGCTTGTGCTGT 540
QY 541 GCGTCCAGCTGTGCTTCAAGGTGTGCGGCGCGCGCTGTACAGCTGTGCGCTGTGCGAC 600
DB 541 GCGTCCAGCTGTGCTTCAAGGTGTGCGGCGCGCGCTGTACAGCTGTGCGCTGTGCGAC 600
QY 601 TTAGGCG 660
DB 601 TTAGGCG 660
QY 661 CTAGGCG 720
DB 661 CTAGGCG 720
QY 721 GAGGCG 780
DB 721 GAGGCG 780
QY 781 TGCCTTGTGAGCG 840
DB 781 TGCCTTGTGAGCG 840
QY 841 GGTGGAACGAGTGTGAGCG 900
DB 841 GGTGGAACGAGTGTGAGCG 900
QY 901 CACCTCTTGTGAGCG 960
DB 901 CACCTCTTGTGAGCG 960
QY 961 GCAACAACG 1020
DB 961 GCAACAACG 1020
QY 1021 CCGGCTGTGAGCG 1080
DB 1021 CCGGCTGTGAGCG 1080
QY 1081 GCGCTCTTGTGAGCG 1140
DB 1081 GCGCTCTTGTGAGCG 1140
QY 1141 GACCAATCTTGTGAGCG 1200
DB 1141 GACCAATCTTGTGAGCG 1200
QY 1201 GCGGCAACG 1260
DB 1201 GCGGCAACG 1260
QY 1261 GTGCGCTGTGAGCG 1320
DB 1261 GTGCGCTGTGAGCG 1320
QY 1321 AGCGGCTGTGAGCG 1380
DB 1321 AGCGGCTGTGAGCG 1380

QY 1381 CACAGACCCCGCTGTGAGCG 1440
DB 1381 CACAGACCCCGCTGTGAGCG 1440
QY 1441 CCGCTTGTGAGCG 1500
DB 1441 CCGCTTGTGAGCG 1500
QY 1501 CAAGCAACGCGCGCTTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1560
DB 1501 CAAGCAACGCGCGCTTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1560
QY 1561 GCTTGTGAGCG 1620
DB 1561 GCTTGTGAGCG 1620
QY 1621 GAGCCAGAGGCTGTGAGCG 1680
DB 1621 GAGCCAGAGGCTGTGAGCG 1680
QY 1681 CAAGTCTGTGAGCG 1740
DB 1681 CAAGTCTGTGAGCG 1740
QY 1741 TGTCAAGAGAGCAAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 TGTCAAGAGAGCAAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 CAAGTCTGTGAGCG 1860
DB 1801 CAAGTCTGTGAGCG 1860
QY 1861 GGAAGCAAG 1920
DB 1861 GGAAGCAAG 1920
QY 1921 CTTCAATCCCAAG 1980
DB 1921 CTTCAATCCCAAG 1980
QY 1981 CAGAAAGTTCGAG 2040
DB 1981 CAGAAAGTTCGAG 2040
QY 2041 CAGCGTGTGAGCG 2100
DB 2041 CAGCGTGTGAGCG 2100
QY 2101 CCGGCAACGAG 2160
DB 2101 CCGGCAACGAG 2160
QY 2161 GCGGCTGTGAGCG 2220
DB 2161 GCGGCTGTGAGCG 2220
QY 2221 GGAAG 2280
DB 2221 GGAAG 2280
QY 2281 TCGGATGTGAG 2340
DB 2281 TCGGATGTGAG 2340
QY 2341 CCGTCTTGTGAG 2400
DB 2341 CCGTCTTGTGAG 2400
QY 2401 GACCAAGCGCGAG 2460
DB 2401 GACCAAGCGCGAG 2460
QY 2461 CAGTGGCTTGTGAG 2520

```

Db      2461 CAGTGGCTCTTCAAGGTCTTCTTACGCTCAATGTCCACCAAGCCGTCCGATCAGGGG
Qy      2521 CAAGTCTTACGCTCAAGGTCAAGGGGATCCCGAGGGCTCATTCTCCACAGCTGTCTCG
Db      2521 CAAGTCTTACGCTCAAGGTCAAGGGGATCCCGAGGGCTCATTCTCCACAGCTGTCTCG
Qy      2581 CAGCTGTGTCTACGCGCATGTGAGAACAGAGCTGTTGCGGGATTCGCGCGGACGGGCT
Db      2581 CAGCTGTGTCTACGCGCATGTGAGAACAGAGCTGTTGCGGGATTCGCGCGGACGGGCT
Qy      2641 GCTCTGCGTTGGTGTGATGATTTCTTGTGTGACACTCACCCTACCCAGCGGAAAC
Db      2641 GCTCTGCGTTGGTGTGATGATTTCTTGTGTGACACTCACCCTACCCAGCGGAAAC
Qy      2701 CTTCCTCAGAGACCTGTGCGAGGTGCTCCCTGAGTATGCTGTGCTGTAACCTTGCGAA
Db      2701 CTTCCTCAGAGACCTGTGCGAGGTGCTCCCTGAGTATGCTGTGCTGTAACCTTGCGAA
Qy      2761 GACAGTGTGAACTTCCCTGTAGAACAGAGCCCTGCGTGGACCGGCTTTTGTGAGAT
Db      2761 GACAGTGTGAACTTCCCTGTAGAACAGAGCCCTGCGTGGACCGGCTTTTGTGAGAT
Qy      2821 GCCGCGCCACGCGCTTATCCCTGTGTGCGGCTGTGTGATATCCCGGACCTTGAGGT
Db      2821 GCCGCGCCACGCGCTTATCCCTGTGTGCGGCTGTGTGATATCCCGGACCTTGAGGT
Qy      2881 GCGAGCGACTACTCAGAGTATGCGCGGACCTCCATCAGAGCGAGTCTACCTTCAACCG
Db      2881 GCGAGCGACTACTCAGAGTATGCGCGGACCTCCATCAGAGCGAGTCTACCTTCAACCG
Qy      2941 CGGCTTCAAGGCTGGAGAGAACATGCGTCCAAACTCTTGGGCTTGGCGCTGAAGTG
Db      2941 CGGCTTCAAGGCTGGAGAGAACATGCGTCCAAACTCTTGGGCTTGGCGCTGAAGTG
Qy      3001 TCACAGCTGTTTCTGTGATTTGAGGTGAACAGCTTCCAGAGGCTGTGACCAACTTA
Db      3001 TCACAGCTGTTTCTGTGATTTGAGGTGAACAGCTTCCAGAGGCTGTGACCAACTTA
Qy      3061 CAAGATCCCTCTCTGAGGCGTACAGGTTTCAAGATGCTGTGAGCTCCCATTTTA
Db      3061 CAAGATCCCTCTCTGAGGCGTACAGGTTTCAAGATGCTGTGAGCTCCCATTTTA
Qy      3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGTATCTGACACGCGCTCCCT
Db      3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGTATCTGACACGCGCTCCCT
Qy      3181 CTGCTACTCATCTCTAAAGCCAAAGACGAGGGATGTCTGTGGGGCCAAAGGCGCGC
Db      3181 CTGCTACTCATCTCTAAAGCCAAAGACGAGGGATGTCTGTGGGGCCAAAGGCGCGC
Qy      3241 CGGCGCTCTGCGCTCCGAGGCGGAGTGTGCTGTGCAACAGCAATTCCTGCTCAAGCT
Db      3241 CGGCGCTCTGCGCTCCGAGGCGGAGTGTGCTGTGCAACAGCAATTCCTGCTCAAGCT
Qy      3301 GACTCGACACCGTGTCACTTACGTGCCACTCTTGGGGTCACTGAGCAAGCCCAAGCGCA
Db      3301 GACTCGACACCGTGTCACTTACGTGCCACTCTTGGGGTCACTGAGCAAGCCCAAGCGCA
Qy      3361 GCTGAGTCTGGAAGTCTCCCGGGAGAGAGCTGATGCTCTTGAAGGCGCAACCCGCGC
Db      3361 GCTGAGTCTGGAAGTCTCCCGGGAGAGAGCTGATGCTCTTGAAGGCGCAACCCGCGC
Qy      3421 ACTGCCCTCAGACTTCAAGACCATCTCTGACTGATGTGCGACCCGCAAGCGGCGCA
Db      3421 ACTGCCCTCAGACTTCAAGACCATCTCTGACTGATGTGCGACCCGCAAGCGGCGCA
Qy      3481 GAGCAGACACACAGAGCCCTGTCAAGCGCGGCTTCAAGTCCAGGAGGAGGCGGCGC
Db      3481 GAGCAGACACACAGAGCCCTGTCAAGCGCGGCTTCAAGTCCAGGAGGAGGCGGCGC
Qy      3541 CACACCCAGGCGGACCGCTGGAGTCTGAGGCTTGAAGTGTGCTTGGCCGAGGCTTG

```

```

Db      3541 CACACCCAGGCGGACCGCTGGAGTCTGAGGCTTGAAGTGTGCTTGGCCGAGGCTTG
Qy      3601 CATGTCCGCGTGAAGAGTGAAGTGCAGGCTGAGGCTGAGGCTGCAAGCAAGGCT
Db      3601 CATGTCCGCGTGAAGAGTGAAGTGCAGGCTGAGGCTGAGGCTGCAAGCAAGGCT
Qy      3661 GAGTGTCCAGACACCTGCGCTTCTCACTTCCCAAGGCTGAGGCTGAGGCTTCCCA
Db      3661 GAGTGTCCAGACACCTGCGCTTCTCACTTCCCAAGGCTGAGGCTGAGGCTTCCCA
Qy      3721 GGGCCAGCTTTTCTCACAGGAGCCGCGCTTCCACTCCCAATAGATATGTCATCC
Db      3721 GGGCCAGCTTTTCTCACAGGAGCCGCGCTTCCACTCCCAATAGATATGTCATCC
Qy      3781 CCAGATTGCGCAATTTGTCACCCCTGCGCTTCTTGTGCTTCAACCCCAACATCC
Db      3781 CCAGATTGCGCAATTTGTCACCCCTGCGCTTCTTGTGCTTCAACCCCAACATCC
Qy      3841 AGGTGAGACCTCTGAGAGAGACCTTGGAGCTTGGAAATTTGAGTGAACAAAGTGTG
Db      3841 AGGTGAGACCTCTGAGAGAGACCTTGGAGCTTGGAAATTTGAGTGAACAAAGTGTG
Qy      3901 CCTGTACACAGCGAGGACCTTGCACCTGAGTGGGGGCTCCGTGGGTCAATTTGGGG
Db      3901 CCTGTACACAGCGAGGACCTTGCACCTGAGTGGGGGCTCCGTGGGTCAATTTGGGG
Qy      3961 GAGTGTCTGTGGAGTAAATATGATATGATTTTCAAGTTTGAAGAAAAA
Db      3961 GAGTGTCTGTGGAGTAAATATGATATGATTTTCAAGTTTGAAGAAAAA

```

```

RESULT 11
AD85223
ID AD85223 standard; DNA; 4015 BP.
XX
AC AD85223;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human telomerase reverse transcriptase DNA.
XX
KW telomerase catalytic activity;
KW hydrogen peroxide-induced cellular senescence; proliferative disease;
KW cancer; human; telomerase reverse transcriptase; de; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2702..3454
FT FT /tag=a
FT FT /partial
FT FT /product="Telomerase reverse transcriptase"
FT FT /note="No start codon given"
XX
PN US2003225027-A1.
XX
PD 04-DEC-2003.
XX
PF 30-MAY-2003; 2003US-00449565.
XX
PR 31-MAY-2002; 2002US-0384806P.
XX
PA (HUAN/) HUANG J.
PA (HUAN/) HUANG C.
PA (LINM/) LIN M C M.
PA (KUNG/) KUNG H.
XX
PI Huang J, Huang C, Lin MCM, Kung H;
XX
XX WPI; 2004-089418/09.
XX
XX P-PDB; AD85224.
XX
XX New human telomerase reverse transcriptase polypeptide, useful in

```


QY	1921	TTTTCATCCCAAGCGCTGACGGGGCGTGGCGGCACTTGAGAACATGAGACTACGTCGTGGAGC	1980
Db	1921	CTTATATCCCAAGCTCTACCGGGCTGGCGGCGGATTTGTGAACATGAGACTACGTCGTGGAGC	1980
QY	1981	CAGAACCTTCCGACAGAAAAAGAGGGCGAGCGCTTCACCTCGAGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTCCGACAGAAAAAGAGGGCGAGCGCTTCACCTCGAGGGTGAAGGCACTGTT	2040
QY	2041	CAGCGTCTCAACTACACAGCGGGGCGCGAGCGCCCGGCTCCTGGAGCGCTCTGTGCTGGG	2100
Db	2041	CAGGTCCTCAACTACACAGCGGGGCGCGAGCGCCCGGCTCCTGGAGCGCTCTGTGCTGGG	2100
QY	2101	CTTGAGAGATATCCACAGGGGCTGGCGCACCTTCGTCTGCTGCTGTGGGCCAGAGACC	2160
Db	2101	CTTGAGAGATATCCACAGGGGCTGGCGCACCTTCGTCTGCTGCTGTGGGCCAGAGACC	2160
QY	2161	GCGCGCTGAGCTGTACTTTGTGCAGGGTGAATGTGACGGGGCGGTACGACACATCCCCCA	2220
Db	2161	GCGCGCTGAGCTGTACTTTGTGCAGGGTGAATGTGACGGGGCGGTACGACACATCCCCCA	2220
QY	2221	GGAAGAAGGTACGGAGGTCATCGCAGCATCATGAACCCCAAGAACATGATACGCGTGC	2280
Db	2221	GGAAGAAGGTACGGAGGTCATCGCAGCATCATGAACCCCAAGAACATGATACGCGTGC	2280
QY	2281	TGGTATATCCCTGTGTCCAGAAAGCGCGCCATAGGCACTCCGCAAGGCTTTCAAGACCA	2340
Db	2281	TGGTATATCCCTGTGTCCAGAAAGCGCGCCATAGGCACTCCGCAAGGCTTTCAAGACCA	2340
QY	2341	CGTCTCTTACTTTGACAGACTCTCCAGCGGTACATGCGACAGTTGCTGCTCACTCGACGA	2400
Db	2341	CGTCTCTTACTTTGACAGACTCTCCAGCGGTACATGCGACAGTTGCTGCTCACTCGACGA	2400
QY	2401	GACCAGCCCGCTGAGGGATGCGCTGTCTATCGACAGAGCTCTCCCTGATGAGGCGAG	2460
Db	2401	GACCAGCCCGCTGAGGGATGCGCTGTCTATCGACAGAGCTCTCCCTGATGAGGCGAG	2460
QY	2461	CAGTGGCTCTTTGACAGCTTCTTCTACGCTTATGTGCAACCAAGCCGTGGGCATCAGGG	2520
Db	2461	CAGTGGCTCTTTGACAGCTTCTTCTACGCTTATGTGCAACCAAGCCGTGGGCATCAGGG	2520
QY	2521	CAGGCTCAACGTCCAGTSCAGSGGATCCGCGAGGGCTCACTCCCTCTCAAGCTGCTCTG	2580
Db	2521	CAGGCTCAACGTCCAGTSCAGSGGATCCGCGAGGGCTCACTCCCTCTCAAGCTGCTCTG	2580
QY	2581	CAGCCTGTGCTACGGCGACATGAGAAACAGACTGTTTTCGGGGATTGGCGGGACGGGCT	2640
Db	2581	CAGCCTGTGCTACGGCGACATGAGAAACAGACTGTTTTCGGGGATTGGCGGGACGGGCT	2640
QY	2641	GCTCGTGGTGTGGTGAATGATTTCTGTGTGTGACACTCACTCAACCCAGCGAANAAC	2700
Db	2641	GCTCGTGGTGTGGTGAATGATTTCTGTGTGTGACACTCACTCAACCCAGCGAANAAC	2700
QY	2701	CTTCCCTCAGGACCCCTGTGCCAGGTGTCCCTGAGTATGAGCTGCGTGTGAACCTTCCGAAA	2760
Db	2701	CTTCCCTCAGGACCCCTGTGCCAGGTGTCCCTGAGTATGAGCTGCGTGTGAACCTTCCGAAA	2760
QY	2761	GACAGTGTGAACCTTCCCTGTGAGAAAGAGAGCCCTGGGTGGCAACGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGTGAACCTTCCCTGTGAGAAAGAGAGCCCTGGGTGGCAACGCTTTTGTTCAGAT	2820
QY	2821	GCGCGCCACAGCGCACTTCCCTGTGGTGGCGCTGCTGTGTGATATCCCGAACCTCGAGAGT	2880
Db	2821	GCGCGCCACAGCGCACTTCCCTGTGGTGGCGCTGCTGTGTGATATCCCGAACCTCGAGAGT	2880
QY	2881	GCGAGCGACTACTCCAGCTATGCCCGGACCTTCATCAAGCCAGCTTCACCTTCAACCG	2940
Db	2881	GCGAGCGACTACTCCAGCTATGCCCGGACCTTCATCAAGCCAGCTTCACCTTCAACCG	2940
QY	2941	CGGCTTCAAGGCTGGAGAGAAATGCGTGCAGAACTCTTTGGGGCTTTGGGGCTGGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGAGAGAAATGCGTGCAGAACTCTTTGGGGCTTTGGGGCTGGAAGTG	3000

3001	TCACAGCTGTTTCGAAATTTCAGAGTGAACAGCTCCACACGGTGTGCACCAACATCTA	3060
3001	TCACAGCTGTTTCGAAATTTCAGAGTGAACAGCTCCACACGGTGTGCACCAACATCTA	3060
3061	CACATCCTCTCTGTCGAGGGGTACAGGTTTCACGATGTGTGTGACGCTCCCATTTCA	3120
3061	CACATCCTCTCTGTCGAGGGGTACAGGTTTCACGATGTGTGTGACGCTCCCATTTCA	3120
3121	TCACCAAGTTTGGAGAAGACCCACATTTTTCCTGCGGGTATCTCTGACACGGGCTCCT	3180
3121	TCACCAAGTTTGGAGAAGACCCACATTTTTCCTGCGGGTATCTCTGACACGGGCTCCT	3180
3181	CTGTACTCCATCTCTGAAAAGCCAAAGAAACGAGGATGTCTGTGGGGGCCAAAGGCGCCG	3240
3181	CTGTACTCCATCTCTGAAAAGCCAAAGAAACGAGGATGTCTGTGGGGGCCAAAGGCGCG	3240
3241	CGGCGCTCTGCGCCCTCCGAGGCGCGTGAAGTGGCTGTGCACCAAGCATTTCTGTCAAGCT	3300
3241	CGGCGCTCTGCGCCCTCCGAGGCGCGTGAAGTGGCTGTGCACCAAGCATTTCTGTCAAGCT	3300
3301	GACTCGACCCGCTGTACCTTACGTCGCACTTCGAGGGTCACTCGAGACAGGCCAGACGCA	3360
3301	GACTCGACCCGCTGTACCTTACGTCGCACTTCGAGGGTCACTCGAGACAGGCCAGACGCA	3360
3361	GCTGATGTGGAAAGCTCCCGGGGAGAGAGCTGACGCTCGCTGGAGGCGGACGCAACCCGCG	3420
3361	GCTGATGTGGAAAGCTCCCGGGGAGAGAGCTGACGCTCGCTGGAGGCGGACGCAACCCGCG	3420
3421	ACTGCGCTCAACACTTCAAGAACATCTCTGACTGATGAGCCACCCGCGCACAGCCAGGCGGA	3480
3421	ACTGCGCTCAACACTTCAAGAACATCTCTGACTGATGAGCCACCCGCGCACAGCCAGGCGGA	3480
3481	GAGCGAACAACAGAGAGCCCTGTCAAGCGCGGCTCTAAGTCCACAGGAGGGAGGGGCGGCG	3540
3481	GAGCGAACAACAGAGAGCCCTGTCAAGCGCGGCTCTAAGTCCACAGGAGGGAGGGGCGGCG	3540
3541	CACACCCAGGCGCGGACCGCTGGAGTGTGAGGCTGAGTGAAGTGTGTCGCGAGGCGCTG	3600
3541	CACACCCAGGCGCGGACCGCTGGAGTGTGAGGCTGAGTGAAGTGTGTCGCGAGGCGCTG	3600
3601	CATGTCCGGCTTGAAGGCTGAGTGTCCCGGCTGAGGCTGAGGAGTGTGCACAGCCAAAGGCT	3660
3601	CATGTCCGGCTTGAAGGCTGAGTGTCCCGGCTGAGGCTGAGGAGTGTGCACAGCCAAAGGCT	3660
3661	GAGTGTCCAGACACCTGCGCTTCACTTCCCAACAGGCTGAGGCTCGCTCCACCCCA	3720
3661	GAGTGTCCAGACACCTGCGCTTCACTTCCCAACAGGCTGAGGCTCGCTCCACCCCA	3720
3721	GGGCGAGCTTTCCTCACACAGGAGCCGGCTTCACTCCCAANTAGGAATATGTCATCC	3780
3721	GGGCGAGCTTTCCTCACACAGGAGCCGGCTTCACTCCCAANTAGGAATATGTCATCC	3780
3781	CCAGATTGCGCAATTGTTCAACCCCTGCGCTGCCCTCTTTTGCCTTCCACCCCAACATCC	3840
3781	CCAGATTGCGCAATTGTTCAACCCCTGCGCTGCCCTCTTTTGCCTTCCACCCCAACATCC	3840
3841	AGGTGGAACCTTGAAGAGAACCTTGGAGAGCTCTGGGAATTTTGGAGTACCAAGATGTG	3900
3841	AGGTGGAACCTTGAAGAGAACCTTGGAGAGCTCTGGGAATTTTGGAGTACCAAGATGTG	3900
3901	CCCTGTACACAGGCGACGACCTTGACCTGAGTGGGGTCTCCTGTGGTCAAAATTGGGGG	3960
3901	CCCTGTACACAGGCGACGACCTTGACCTGAGTGGGGTCTCCTGTGGTCAAAATTGGGGG	3960
3961	GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTTACGTTTGAATAAAAAA 4015	
3961	GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTTACGTTTGAATAAAAAA 4015	

RESULT 12
AD182171
ID AD182171 standard; cDNA; 4015 BP.
XX

AD182171;
22-APR-2004 (first entry)
Human cDNA encoding telomerase reverse transcriptase.
Human; gs; gene; embryonic stem cell; pluripotent stem cell;
abnormal cell growth; malignancy; differentiation.
Homo sapiens.
US2003224411-A1.
04-DEC-2003.
13-MAR-2003; 2003US-00388578.
13-MAR-2003; 2003US-00388578.
(STAN/) STANTON L W.
(BRAN/) BRANDENBERGER R.
(GOLD/) GOLD J D.
(IRVI/) IRVING J M.
(MAND/) MANDALAM R.
(MOKM/) MOK M.
(SHEL/) SHELTON D.
Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;
Mok M, Shelton D;
WPI. 2004-119701/12.
P-PSDB: AD182172.
Assessing culture of undifferentiated primate pluripotent stem cells by
detecting expression of markers e.g., Zic family member 3, other than
human telomerase reverse transcriptase/octamer binding transcription
factor.
Claim 1; SEQ ID NO 1; 106bp; English.
The invention relates to assessing a culture of undifferentiated primate
pluripotent stem cells (pPS, e.g. embryonic stem cells), involving
detecting expression of markers (MRI) e.g. Zic family member 3 (ZIC3), as
given in specification, other than human telomerase reverse transcriptase
(hTERT) or octamer binding transcription factor (Oct3/4, or a marker
(MR2) such as cripto or podocalyxin-like protein and hTERT and/or Oct3/4
or second marker chosen from (MR2). Also included are maintaining (M2)
pPS cells in a pluripotent state (involves causing them to express one of
the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypohelical
protein Flt20582, Forkhead box H1 (FOXH1), Zinc finger protein, Hsdl,
KRAB-zinc finger protein SZF1-1 or zinc finger protein of cerebellum
ZIC3, or any other marker (MR4) chosen from PBD protein Jade-1 (Jade-1),
kruppel-like zinc finger protein (ZNF300), etc., as given in the
specification), causing pPS cells to differentiate into a particular
tissue type by causing them to express one of the markers chosen from
(MR3) or (MR4) (or markers chosen from GATA binding protein 3 (GATA3),
core promoter element binding protein (COPEB), etc., as given in the
specification), maintaining pPS cells in a pluripotent state (involves
culturing pPS cells or their progeny in the presence of a normally
secreted protein that is encoded by a gene that down-regulated upon
differentiation of human embryonic stem (hES) cells, chosen from
Fibillin 3 gene, Lefty B gene, ZIC3 gene, EphA1 gene, etc., as given in
the specification), causing pPS cells to differentiate (involves
culturing pPS cells or their progeny in the presence of a normally
secreted protein that is encoded by a gene that up-regulated upon
differentiation of hES cells, chosen from P311 protein gene, Tax
interaction protein 1 gene, KIA0853 protein gene, Keratin 19 (KRT 19)
gene, etc., as given in the specification), causing an encoding sequence
to be preferentially expressed in undifferentiated pPS cells, causing an
encoding sequence to be preferentially expressed in differentiated cells,
sorting (M4) differentiated cells from less differentiated cells
(involves separating cells expressing a surface marker chosen from any
one of MRI from cells not expressing the marker), causing pPS cells to

CC proliferate without differentiation, identifying genes that are up or
CC down regulated during differentiation of pps cells, and a kit (II) for
CC assessing a culture of pps cells by M1. The method, (M1) is useful for
CC assessing culture of undifferentiated primate pluripotent stem cells and
CC for assessing the growth characteristics of a cell population. The cell
CC population has been obtained by culturing cells from human blastocyst or
CC from a human patient suspected of having a clinical condition related to
CC abnormal cell growth. The method further involves determining whether the
CC cell population is pluripotent from the marker expression and assessing
CC whether the patient has a malignancy from the marker expression. The
CC present sequence is a cDNA whose expression is down regulated in
CC pluripotent stem cells.

SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match	Score	DB	Length
100.0%	4015	12	4015

Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGCGTCTCTGCTGCGCAGTGGAGCCCTGGCCCGGCCACCCCGGATGCC 60

Db 1 GCAGCGCTGCGTCTCTGCTGCCACGTGGAGCCCTGGCCCGGCCACCCCGCATGCC 60

61 GCGCGTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTCT 120

Db 61 GCGCGTCCCGCTGCCGAGCCGCTCCCTGCTGCCGAGCCACTACCGGAGGTCT 120

121 GCCGCTGGCAAGTTCTGTCGCGCCTGGGCCCCAGGCTGGCTGGTGCAGCCGG 180

Dh 121 GCGCTGGCCACGTTTCGTCGCGCCACGAGCGCTGGCGCTGTCAGCGCG 180

181 GGAACCGGCGCTTTACGGGCGCGCTGGTGGCCACGTCCTTGTCGCGTGGCCACGCGACGC 240

[illegible][illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

[illegible][illegible][illegible]

UD 361 GCGGAGGGCCCCCGGGCCCGACCAACACCAAGGAGCGACGA 720

421 CCTGCCAACACGGTGAACGACGACCTGCGGGAGCGGGCGTGGGAGCAGCAGCG 480

DB 421 CCTGCCAACACGCTGACCCGACGCATCTGCGGGGAGCGGGCGTGGGGCTGGCTGCTGGC 480

481 CCGCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACCGCTGCGCGCTCTTGTGCTGGT 540

Db 481 CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCAGCGCTGCGGCTCTTTGTGCTGGT 540

541 GGCTCCAGCTGCGCTACCAAGTGTGCGGGCGCCGCTGTACCAGCTCGGCGTGCCAC 600

Db 541 GCGTCCAGCTGGCGCTACCAAGTGTGCCGGCCGCTGTACCAAGCTCGCGCTGCCAC 600

601 TCAGGCCCGCCCCCGCCACACGCTAGTGACCCCGAAGCGCTTGGATGCGAACGGC 660

Db 601 TCAGGCCCGGCCCGCCACACGCTAGTGACCCCGAAGCGTCTGGATGCGAACGGGC 660

661 CTGGAACCATAGCGTCAGGAGGCCGGGTCCCCCTGGGCCCTGCCAGCCCCGGGTGCAG 720

Db 661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGGCTGCCAGCCCCGGGTGCAG 720

721 GAGCGCGGGCAGTGCCACCGAAGTCTGCCGTTGCCCAAGAGGCCCAAGCGTGCGC 780

Db 721 GAGCGCGGGGCGAGTCTGCCGTTGCCCAAGAGGCCCAAGCGTGGCG 780

781 TGCCTGAGCCGAGCGCCGTTGGCAGGGTCTTGGCCCAACCGGCAAGAC 840

Db 781 TGCCCTGAGCCGGAAGGAGCGCCCGTTGGGACAGGGTCTTGAGGCCACCCCGGACAGAC 840
QY 841 GCGTGAACGAGAGACCGGTGTTCTGTGTGTGTCACTGACAGACCCCGCAAGAAC 900
Db 841 GCGTGAACGAGAGACCGGTGTTCTGTGTGTGTCACTGACAGACCCCGCAAGAAC 900
QY 901 CACCTCTTTGAGAGGTGCGCTCTCTGACAGCGCCCACTCCCACTCAGTGGAGCGCA 960
Db 901 CACCTCTTTGAGAGGTGCGCTCTCTGACAGCGCCCACTCCCACTCAGTGGAGCGCA 960
QY 961 GCAACAAGCGGGGCCCCCATCTCAATCGCGGCCACCACTGCTTGGAGACAGCTTGTCC 1020
Db 961 GCAACAAGCGGGGCCCCCATCTCAATCGCGGCCACCACTGCTTGGAGACAGCTTGTCC 1020
QY 1021 CCGGAGTACGCGGAGACCAAGACCTTCTCTCTGAGGAGACAGAGAGAGTGGG 1080
Db 1021 CCGGAGTACGCGGAGACCAAGACCTTCTCTCTGAGGAGACAGAGAGAGTGGG 1080
QY 1081 GCCCTCTTCTACTAGCTCTCTGAGGCCAGCCTGACCTGAGCGCTTGGAGCTGTGA 1140
Db 1081 GCCCTCTTCTACTAGCTCTCTGAGGCCAGCCTGACCTGAGCGCTTGGAGCTGTGA 1140
QY 1141 GACCACTTTTGTGGTTCAGAGCCCTGAGATCCAGAGGACTCCCGCAGTTCGCCCT 1200
Db 1141 GACCACTTTTGTGGTTCAGAGCCCTGAGATCCAGAGGACTCCCGCAGTTCGCCCT 1200
QY 1201 GCGCCAGCGCTACTGGAATGAGGCCCTGTTTCTGAGAGCTGTTGGAGAACAGCGCA 1260
Db 1201 GCGCCAGCGCTACTGGAATGAGGCCCTGTTTCTGAGAGCTGTTGGAGAACAGCGCA 1260
QY 1261 GTCGCCCTTACGAGGATGCTCTCAAGACGCACTGCCCTGAGCTGCGGTCAACCCAGC 1320
Db 1261 GTCGCCCTTACGAGGATGCTCTCAAGACGCACTGCCCTGAGCTGCGGTCAACCCAGC 1320
QY 1321 AGCCGCTGTGTGTGCGCGGAGAAAGCCCGCTGTGTGGCGGCCCGGAGAGAGAA 1380
Db 1321 AGCCGCTGTGTGTGCGCGGAGAAAGCCCGCTGTGTGGCGGCCCGGAGAGAGAA 1380
QY 1381 CACAGACCCCGTGTGTGTGAGCTGCTCGGCAAGACAGAGCCCTGAGAGAGTGA 1440
Db 1381 CACAGACCCCGTGTGTGTGAGCTGCTCGGCAAGACAGAGCCCTGAGAGAGTGA 1440
QY 1441 CGGCTTGTGCGGAGCCCTGCTGCGCGCGGTGTGTGCCCAAGGCTGTGAGGCA 1500
Db 1441 CGGCTTGTGCGGAGCCCTGCTGCGCGCGGTGTGTGCCCAAGGCTGTGAGGCA 1500
QY 1501 CAACGAAAGCGGCTTCTCTCAAGAAACCAAGAACTTCTCTCTGAGAGATGCA 1560
Db 1501 CAACGAAAGCGGCTTCTCTCAAGAAACCAAGAACTTCTCTCTGAGAGATGCA 1560
QY 1561 GCTCTGCTGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
Db 1561 GCTCTGCTGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
QY 1621 GAGCCGAGGGGTTGCTGTGTCCGCGCAGAGACCGTCTGAGTGAAGTGAAGTGAAG 1680
Db 1621 GAGCCGAGGGGTTGCTGTGTCCGCGCAGAGACCGTCTGAGTGAAGTGAAGTGAAG 1680
QY 1681 CAGGTTCTGACAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1740
Db 1681 CAGGTTCTGACAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1740
QY 1741 TGTACGAGAGACAGCTTCAAAAGAACAGAGCTTCTTCTACCGAGAGTGTCTGAG 1800
Db 1741 TGTACGAGAGACAGCTTCAAAAGAACAGAGCTTCTTCTACCGAGAGTGTCTGAG 1800
QY 1801 CAGGTTCAAAAGATTGAAATCAAGACAGCTTGAAGAGGTTGAGTGAAGTGAAGTGAAG 1860
Db 1801 CAGGTTCAAAAGATTGAAATCAAGACAGCTTGAAGAGGTTGAGTGAAGTGAAGTGAAG 1860
QY 1861 GGAAGCAGAGGTGAGGAGATGAGGAGCCAGGCGGCTGCTGAGTGAAGTGAAGTGAAG 1920
Db 1861 GGAAGCAGAGGTGAGGAGATGAGGAGCCAGGCGGCTGCTGAGTGAAGTGAAGTGAAG 1920

QY 1921 CTTTCATCCCAAGGCTGACAGGCTGCGGCGATTTGAAACATGACATAGTGTGGAGC 1980
Db 1921 CTTTCATCCCAAGGCTGACAGGCTGCGGCGATTTGAAACATGACATAGTGTGGAGC 1980
QY 1981 CAGAAAGTTCCGAGAGAAAGAGGCGCAGGCTCTCACTTGAAGGTGAAGGCACTGTT 2040
Db 1981 CAGAAAGTTCCGAGAGAAAGAGGCGCAGGCTCTCACTTGAAGGTGAAGGCACTGTT 2040
QY 2041 CAGCGTCTCACTGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100
Db 2041 CAGCGTCTCACTGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100
QY 2101 CTTGAGAGATTCACAGAGGCTGAGGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 CTTGAGAGATTCACAGAGGCTGAGGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
QY 2161 GCGGCTGAGCTGATCTTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2220
Db 2161 GCGGCTGAGCTGATCTTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2220
QY 2221 GGAAGAGCTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2280
Db 2221 GGAAGAGCTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2280
QY 2281 TCGGTATGCGGTGATCAGAGAGCGCCAGTGGGCACTGCGCAAGGCTTCAAGAGCA 2340
Db 2281 TCGGTATGCGGTGATCAGAGAGCGCCAGTGGGCACTGCGCAAGGCTTCAAGAGCA 2340
QY 2341 CGTCTCTACTTGAAGACACTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2400
Db 2341 CGTCTCTACTTGAAGACACTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2400
QY 2401 GACAGGCGGCTGAGAGGAGTGGCGGTGATGAGAGAGAGTGGCGGTGATGAGAGAG 2460
Db 2401 GACAGGCGGCTGAGAGGAGTGGCGGTGATGAGAGAGAGTGGCGGTGATGAGAGAG 2460
QY 2461 CAGTGGCTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2520
Db 2461 CAGTGGCTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2520
QY 2521 CAACTCTTACGTCAGTGCAGAGGAGTCCGCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2580
Db 2521 CAACTCTTACGTCAGTGCAGAGGAGTCCGCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2580
QY 2581 CAGCCTGTCTACGAGTGCAGAGGAGTCCGCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2640
Db 2581 CAGCCTGTCTACGAGTGCAGAGGAGTCCGCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2640
QY 2641 GCTCTGCTGATGATGATTTCTTGTGTGACACTTCAAGGCTTCAAGGCTTCAAG 2700
Db 2641 GCTCTGCTGATGATGATTTCTTGTGTGACACTTCAAGGCTTCAAGGCTTCAAG 2700
QY 2701 CTTCTCAGAGGCTTGTGAGAGTGTCCGTAAGTGTGCTGTGCTGTGCTGTGCTGTG 2760
Db 2701 CTTCTCAGAGGCTTGTGAGAGTGTCCGTAAGTGTGCTGTGCTGTGCTGTGCTGTG 2760
QY 2761 GACAGTGTGAATCTTCCGTGAAGAGAGGCTTGTGAGAGGCTTGTGAGAGTGTG 2820
Db 2761 GACAGTGTGAATCTTCCGTGAAGAGAGGCTTGTGAGAGGCTTGTGAGAGTGTG 2820
QY 2821 GCGGCGCAGAGGCTTATCCCGTGTGAGGCGGCTGCTGAGTATCCCGAGCCCTGAG 2880
Db 2821 GCGGCGCAGAGGCTTATCCCGTGTGAGGCGGCTGCTGAGTATCCCGAGCCCTGAG 2880
QY 2881 GCAAGAGCTACTCAGCTATGCGGAGCTTCAAGAGGCTTCAAGGCTTCAAGGCTTCAAG 2940
Db 2881 GCAAGAGCTACTCAGCTATGCGGAGCTTCAAGAGGCTTCAAGGCTTCAAGGCTTCAAG 2940
QY 2941 CCGCTTCAAGGCTTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3000
Db 2941 CCGCTTCAAGGCTTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3000


```

OY 3001 TCACAGCCGTTTCTGATTTGAGGTGAACAGCCTCCAGACGGTGTGCACCAATCTA 3060
DB 3001 TCACAGCCGTTTCTGATTTGAGGTGAACAGCCTCCAGACGGTGTGCACCAATCTA 3060
OY 3061 CAAGATCCCTCTGCTGACGAGCGGTACAGGTTTCAACGATGTGTGCTGACGCTCCATTTCA 3120
DB 3061 CAAGATCCCTCTGCTGACGAGCGGTACAGGTTTCAACGATGTGTGCTGACGCTCCATTTCA 3120
OY 3121 TCAGCAAGTTTGGAGAAACCCCAATTTTCTGCGCGCTCATCTCTGACACGGCTCTCT 3180
DB 3121 TCAGCAAGTTTGGAGAAACCCCAATTTTCTGCGCGCTCATCTCTGACACGGCTCTCT 3180
OY 3181 CTGCTACTCATCTCTGAAAGCCCAAGAACCGAGGATGTGCTGTGGGGGCCAAGGCGCGCG 3240
DB 3181 CTGCTACTCATCTCTGAAAGCCCAAGAACCGAGGATGTGCTGTGGGGGCCAAGGCGCGCG 3240
OY 3241 CGGCGCTCTGCGCTCCGAGCGCGTGCAGTGTGTGCAACCAAGCATTCCTGTCTCAAGCT 3300
DB 3241 CGGCGCTCTGCGCTCCGAGCGCGTGCAGTGTGTGCAACCAAGCATTCCTGTCTCAAGCT 3300
OY 3301 GACTGACACCGGTGTACCTTACCTGCTCACTCTCTGCGGCTCATCTGACGACGCTCAAGCGCA 3360
DB 3301 GACTGACACCGGTGTACCTTACCTGCTCACTCTCTGCGGCTCATCTGACGACGCTCAAGCGCA 3360
OY 3361 GGTGAGTGGGAAAGCTCCGAGGAGCGAGCGTGAATGCTGTGCAACCGCGCCAGCGGCGCG 3420
DB 3361 GGTGAGTGGGAAAGCTCCGAGGAGCGAGCGTGAATGCTGTGCAACCGCGCCAGCGGCGCG 3420
OY 3421 ACTGCGCTGAGATTCCTGAAAGCATCTCTGACCTGATGAGCGCAACCGCGCCAGCGGCGCG 3480
DB 3421 ACTGCGCTGAGATTCCTGAAAGCATCTCTGACCTGATGAGCGCAACCGCGCCAGCGGCGCG 3480
OY 3481 GAGCAGACACCGAGCAGCCTGTGTACCGCGCGCTCTACCTGCTCCAGGAGAGGAGGCGCGCG 3540
DB 3481 GAGCAGACACCGAGCAGCCTGTGTACCGCGCGCTCTACCTGCTCCAGGAGAGGAGGCGCGCG 3540
OY 3541 CACACCCAGGCGCGCAGCGTGGAGTGTGAGGCGCTGAGTGAATGTTTGGCGAGGCGCTG 3600
DB 3541 CACACCCAGGCGCGCAGCGTGGAGTGTGAGGCGCTGAGTGAATGTTTGGCGAGGCGCTG 3600
OY 3601 CATGTCGGCTGAAAGCTGATGTGTGCGGCTGAGGCGCTGAGCGATGTCCAGCGCAAGGCGCT 3660
DB 3601 CATGTCGGCTGAAAGCTGATGTGTGCGGCTGAGGCGCTGAGCGATGTCCAGCGCAAGGCGCT 3660
OY 3661 GAGTGTCCAGACACCTGCGCTTTCATCTTCCCAAGAGCTGCGCTCCAGCGCGCA 3720
DB 3661 GAGTGTCCAGACACCTGCGCTTTCATCTTCCCAAGAGCTGCGCTCCAGCGCGCA 3720
OY 3721 GGGCGCAGCTTTCCTACAGGAGCGCGGCTTCCATCCCAATGAGTATGTCATCC 3780
DB 3721 GGGCGCAGCTTTCCTACAGGAGCGCGGCTTCCATCCCAATGAGTATGTCATCC 3780
OY 3781 CCAGATTCGCATTTGTTCAACCCCTGCGCTGCGCTCTTTCGCTTCCACCCCGCATCC 3840
DB 3781 CCAGATTCGCATTTGTTCAACCCCTGCGCTGCGCTCTTTCGCTTCCACCCCGCATCC 3840
OY 3841 AGGTGAGACCTCTGAGAGGAGCCCTGAGAGCTTGGGAAATTTGAGTACCAAGGTGTG 3900
DB 3841 AGGTGAGACCTCTGAGAGGAGCCCTGAGAGCTTGGGAAATTTGAGTACCAAGGTGTG 3900
OY 3901 CCCTGTACAGGCGAGGAGCCCTGAGAGCTGAGTGGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
DB 3901 CCCTGTACAGGCGAGGAGCCCTGAGAGCTGAGTGGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
OY 3961 GAGGTGCTGTGGGAGTAAATATGTAATATGATTTTCAATTTTGAAGAAAA 4015
DB 3961 GAGGTGCTGTGGGAGTAAATATGTAATATGATTTTCAATTTTGAAGAAAA 4015

```

RESULT 13
AAV72117
ID AAV72117 standard; cDNA; 4042 BP.
XX

```

AC AAV72117;
XX
DT 24-MAY-1999 (first entry)
XX
DE Human catalytic telomerase sub-unit cDNA.
XX
KW Human; catalytic telomerase subunit; therapy; diagnosis; htc; assay;
KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KW ageing; antisense; neoplastic cell; telomerase-related condition;
KW tumour cell; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 63..3461
FT /tag= a
FT /product= "catalytic telomerase subunit"
XX
PD 30-DEC-1998.
XX
PF 09-JUN-1998; 98WO-BP003468.
XX
PR 20-JUN-1997; 97DE-01026329.
PR 26-MAR-1998; 98DE-01013274.
PR 14-APR-1998; 98DE-01016496.
XX
PA (FARB ) BAYER AG.
XX
PI Hagen G, Slegmund H, Weichel W, Wlck M, Zubov D;
XX
DR MPI, 1999-081276/07.
XX
DR P-PSDB; AAM90251.
XX
PT New catalytically active subunit of human telomerase - used in the
PT modulation of telomerase activity, particularly for treating cancer and
PT ageing.
XX
PS Claim 4; Fig 1; 76pp; German.
XX
CC This sequence encodes a novel human catalytic telomerase sub-unit (hTC).
CC The encoded protein can be used in screening assays to identify
CC modulators of telomerase and to treat or inhibit cellular disorders.
CC death, defects and/or other pathological processes involving telomerase,
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense
CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit
XX
SQ Sequence 4042 BP; 684 A; 1364 C; 1277 G; 717 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 4015; DB 2; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GAGCGCTGCGTCTGCTGCGACGTTGGAGACCTTGCGCGCCGCGCGCGATGCC 60
DB 8 GAGCGCTGCGTCTGCTGCGACGTTGGAGACCTTGCGCGCCGCGCGCGATGCC 67
OY 61 GCGCGCTCCCGCTGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGTCT 120
DB 68 GCGCGCTCCCGCTGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGTCT 127
OY 121 GCGCGTGCACGTTGCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGTCTGCGCGCG 180
DB 121 GCGCGTGCACGTTGCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGTCTGCGCGCG 180

```

Db	128	GC	CGCTGGCCACGTTTGTGTGGGCGCTTGGGGCCCAAGGGCTGGCGGCTGGTGCAGCGCG	187
QY	181	GG	ACCAGGCGGCTTTTCGCGCGCTGTGGCCAGTACCTGATGTGGCTCGCCCGAGACG	240
Db	188	GG	ACCAGGCGGCTTTTCGCGCGCTGTGGCCAGTACCTGATGTGGCTCGCCCGAGACG	247
QY	241	AG	GCACCGCCCCCGCCCGCCCTCTTTCGCGCAGGTGTCTGTGCTGAAGAGCTGGTGGC	300
Db	248	AG	GCACCGCCCCCGCCCGCCCTCTTTCGCGCAGGTGTCTGTGCTGAAGAGCTGGTGGC	307
QY	301	CC	GAGTGTCTGACAGAGCTGTGCGAGGCGCGAGAGAAAGTGTGGCTTTCGGCTTCG	360
Db	308	CC	GAGTGTCTGACAGAGCTGTGCGAGGCGCGAGAGAAAGTGTGGCTTTCGGCTTCG	367
QY	361	GT	CTGTCTGGAACGGGGGCTCCGCGGGGGCCCCCGAAGCTTTTACCAACAGCTGTGCAGCTA	420
Db	368	GT	CTGTCTGGAACGGGGGCTCCGCGGGGGCCCCCGAAGCTTTTACCAACAGCTGTGCAGCTA	427
QY	421	CT	TGCGCCAAACAGGTGACCGAGCACTGTGGGGGGAACGGGGGAGTGGGGGCTGTGCTGG	480
Db	428	CT	TGCGCCAAACAGGTGACCGAGCACTGTGGGGGGAACGGGGGAGTGGGGGCTGTGCTGG	487
QY	481	CC	GGCTGGGCGACGACGTGTCTGTTCACCTGTGCGACGCTGTGCCTTTTGTGTGT	540
Db	488	CC	GGCTGGGCGCGACGACGTGTGTCTTCACCTGTGCGACGCTGTGCCTTTTGTGTGT	547
QY	541	GG	CTCCACAGCTGCGCTTACAGTGTGGGGGGCGCGCTGTACAGCTGTGGCGCTGCCAC	600
Db	548	GG	CTCCACAGCTGCGCTTACAGTGTGGGGGGCGCGCTGTACAGCTGTGGCGCTGCCAC	607
QY	601	TC	AGGCCCCGGCCCCCGCCACACGCTAAGTGAACCCGAAAGCGTCTGTGGAATGCGAACGGAC	660
Db	608	TC	AGGCCCCGGCCCCCGCCACACGCTAAGTGAACCCGAAAGCGTCTGTGGAATGCGAACGGAC	667
QY	661	CT	GGAACCATATGCGTTCAGGGAGAGCGCGGGGTCCCCCTGGGCTTGCCAGCCCGCGGTGCCAG	720
Db	668	CT	GGAACCATATGCGTTCAGGGAGAGCGCGGGGTCCCCCTGGGCTTGCCAGCCCGCGGTGCCAG	727
QY	721	GAG	GCGGCGGCGGAGCACTGTGCACGCCGAAGTCTGCCCTTGTGCCAAGAGGCGCCAGGCTGTGGCG	780
Db	728	GAG	GCGGCGGCGGAGCACTGTGCACGCCGAAGTCTGCCCTTGTGCCAAGAGGCGCCAGGCTGTGGCG	787
QY	781	TG	CCCTTGAACCGCGAGCGGACGCGCCGCTTGGGCGAGGGGTCTGGGCTCCACCCCGGCGAGAC	840
Db	788	TG	CCCTTGAACCGCGAGCGGACGCGCCGCTTGGGCGAGGGGTCTGGGCTCCACCCCGGCGAGAC	847
QY	841	GC	GTGGAACCAAGTGAACGCTGTCTGTGTGTGTCACTGTGCAGACCCGCGAGAGAGC	900
Db	848	GC	GTGGAACCAAGTGAACGCTGTCTGTGTGTGTCACTGTGCAGACCCGCGAGAGAGC	907
QY	901	CA	CTCTTTTGAAGGGGTGCTCTGTGGAACGCGGCCACTTCCACCATCCGTGGGCGGACA	960
Db	908	CA	CTCTTTTGAAGGGGTGCTCTGTGGAACGCGGCCACTTCCACCATCCGTGGGCGGACA	967
QY	961	GA	CAACACGCGGGGCCCCCATCAACATGGGGGCAACAAGTCCCTTGGGACAACGCTTGTTC	1020
Db	968	GA	CAACACGCGGGGCCCCCATCAACATGGGGGCAACAAGTCCCTTGGGACAACGCTTGTTC	1027
QY	1021	CC	CGGCTGTAGCGCGAACAAGCACTTCTCTTCACTCTCAGGCGACAAGAGACGCTGCG	1080
Db	1028	CC	CGGCTGTAGCGCGAACAAGCACTTCTCTTCACTCTCAGGCGACAAGAGACGCTGCG	1087
QY	1081	GC	CTCCCTCTTCTACATCAAGCTCTCTGAGGGCCAGCCTGACCTGGCGCTCGGAAGCTGTGGA	1140
Db	1088	GC	CTCCCTCTTCTACATCAAGCTCTCTGAGGGCCAGCCTGACCTGGCGCTCGGAAGCTGTGGA	1147
QY	1141	GA	CCATCTTTTCTGGAGTTCCAGAGCCCTGATCCAGGGACTCCCGCAGAGTTTCCCGGCT	1200
Db	1148	GA	CCATCTTTTCTGGAGTTCCAGAGCCCTGATCCAGGGACTCCCGCAGAGTTTCCCGGCT	1207
QY	1201	GC	CCACACGCGCTACCTGGCAAAATGCGGCGCTCTTTTCTGGAGCTGCTTGGGAACACGCGCA	1266
Db	1208	GC	CCACACGCGCTACCTGGCAAAATGCGGCGCTCTTTTCTGGAGCTGCTTGGGAACACGCGCA	1267

QY	1261	GTGCCCCCTAACGGGGGTGCTCTCTCAGAGCGCATCTGCCCGTGTGAGCTGGCTCAACCCAGC	1320
Db	1268	GTGCCCCCTAACGGGGGTGCTCTCTCAGAGCGCATCTGCCCGTGTGAGCTGGCTCAACCCAGC	1327
QY	1321	AGCCGGTGTCTGTGCGCCGGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCGAGAGAGAGGA	1380
Db	1328	AGCCGGTGTCTGTGCGCCGGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCGAGAGAGAGGA	1387
QY	1381	CACAGACCCCGGTGGCTGTGTGACGTGCTCGCCAGACAGACAGCCCTGTGGCAGGTGA	1440
Db	1388	CACAGACCCCGGTGGCTGTGTGACGTGCTCGCCAGACAGACAGCCCTGTGGCAGGTGA	1447
QY	1441	CGGCTTCTGAGGGGGCTGCGCCCGGCTGGTACCCCAAGCCTCTTGGGCTCAAGCA	1500
Db	1448	CGGCTTCTGAGGGGGCTGCGCCCGGCTGGTACCCCAAGCCTCTTGGGCTCAAGCA	1507
QY	1501	CAACGAAACGCGCTTCTCAGAGAAACCCAGAAAGTTATCTCCCTGGGAGAAAGCATGACAA	1560
Db	1508	CAACGAAACGCGCTTCTCAGAGAAACCCAGAAAGTTATCTCCCTGGGAGAAAGCATGACAA	1567
QY	1561	GCTCTCGCTGCAGAGAGCTGACGTGGAAAGTGAAGCTGCGGAGCTGCGCTTGGCTGCGCAG	1620
Db	1568	GCTCTCGCTGCAGAGAGCTGACGTGGAAAGTGAAGCTGCGGAGCTGCGCTTGGCTGCGCAG	1627
QY	1621	GAGCCCAAGGGGTTGGCTGTGTTCCGGGCGCAGAGCAACGCTGTGAGAGAGATCCTGGC	1680
Db	1628	GAGCCCAAGGGGTTGGCTGTGTTCCGGGCGCAGAGCAACGCTGTGAGAGAGATCCTGGC	1687
QY	1681	CAAGTTCTCTGCACTGGCTGATGAAGTGTGTACGTCTGACAGCTGCTAGGTCCTTCTTTTA	1740
Db	1688	CAAGTTCTCTGCACTGGCTGATGAAGTGTGTACGTCTGACAGCTGCTAGGTCCTTCTTTTA	1747
QY	1741	TGTCACGAGACACAGTTTCAAAAAGAACAGGCTTTTCTACCCGAAAGTGTCTGGAG	1800
Db	1748	TGTCACGAGACACAGTTTCAAAAAGAACAGGCTTTTCTACCCGAAAGTGTCTGGAG	1807
QY	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACAGCATTTGAAAGAGGTGACGTGCGGAGCTGTCTC	1860
Db	1808	CAAGTTGCAAAAGCATTTGGAAATCAGACAGCATTTGAAAGAGGTGACGTGCGGAGCTGTCTC	1867
QY	1861	GGAAGCAGAGGTGACAGGAGCATGCGGAAAGCCAGAGCCCGCCCTGTCTACGTTCCAGACTCCG	1920
Db	1868	GGAAGCAGAGGTGACAGGAGCATGCGGAAAGCCAGAGCCCGCCCTGTCTACGTTCCAGACTCCG	1927
QY	1921	CTTGATCCCCAGGCTGTACGAGGCTGCGGCGCATTTGTGTAAATGATGATCACTGCTGTGGAGAC	1980
Db	1928	CTTGATCCCCAGGCTGTACGAGGCTGCGGCGCATTTGTGTAAATGATGATCACTGCTGTGGAGAC	1987
QY	1981	CAGAAACGTTCCGACAGAGAAAGAGGGCCGAGCGTCTTCACTCTGAGAGGTGAAGGACCTGTT	2040
Db	1988	CAGAAACGTTCCGACAGAGAAAGAGGGCCGAGCGTCTTCACTCTGAGAGGTGAAGGACCTGTT	2047
QY	2041	CAGGTCCTCAATCAGACAGGGGGGGGGGGGCCCGCGCTCTCTGGGGGCGCTCTGTGCTGGG	2100
Db	2048	CAGGTCCTCAATCAGACAGGGGGGGGGGGGCCCGCGCTCTCTGGGGGCGCTCTGTGCTGGG	2107
QY	2101	CTTGACGATATCCACAGAGGCTGTGCGCACCTTCTGATCTGCTGCTGTGCGGGCCAGAGACC	2160
Db	2108	CTTGACGATATCCACAGAGGCTGTGCGCACCTTCTGATCTGCTGCTGTGCGGGCCAGAGACC	2167
QY	2161	GGCGGCTGACCTGTATCTTTTGTCAAAGTGTGATGTGAAGGGGGGTATGACATCTTCCCCCA	2220
Db	2168	GGCGGCTGACCTGTATCTTTTGTCAAAGTGTGATGTGAAGGGGGGTATGACATCTTCCCCCA	2227
QY	2221	GGAACAGGCTACGGAGGTATCTGCCAGACATCATCAAAACCCAGAAACAGCTATCTGCGTGG	2280
Db	2228	GGAACAGGCTACGGAGGTATCTGCCAGACATCATCAAAACCCAGAAACAGCTATCTGCGTGG	2287
QY	2281	TGCGTATGCGGTGTTCAGAGGCGCCCATGTGGGCACTGTCCGAAAGGCTTTCAGAGGCCA	2340
Db	2288	TGCGTATGCGGTGTTCAGAGGCGCCCATGTGGGCACTGTCCGAAAGGCTTTCAGAGGCCA	2347

2341 CGTCTCACTTGAAGACCTCCAGCCGTAATGCGACAGTTTCTGTGCTCACTTCAGAGA 2400
 2348 CGTCTCACTTGAAGACCTCCAGCCGTAATGCGACAGTTTCTGTGCTCACTTCAGAGA 2407
 2401 GACCAAGCCCGCTGAGGAGATGCCGTGTCTATCGAGCAGAGCTCTCTCTGAATGAGGCCAG 2460
 2408 GACCAAGCCCGCTGAGGAGATGCCGTGTCTATCGAGCAGAGCTCTCTCTGAATGAGGCCAG 2467
 2461 CAGTGGCCCTTTCAGAGTCTTCTTCCGCTTCAATGTCACCAAGCCGCTGATCATGAGGG 2520
 2468 CAGTGGCCCTTTCAGAGTCTTCTTCCGCTTCAATGTCACCAAGCCGCTGATCATGAGGG 2527
 2521 CAAGTCTCAAGTCAAGTCCAGGAGATCCCGAGGCTTCATCTCTCCAGCTGCTCTG 2580
 2528 CAAGTCTCAAGTCAAGTCCAGGAGATCCCGAGGCTTCATCTCTCCAGCTGCTCTG 2587
 2581 CAGCTGTGCTACGCGGACATGAGAAACAAGCTGTTTGGGGGATTCGGCGGAGCGGCT 2640
 2588 CAGCTGTGCTACGCGGACATGAGAAACAAGCTGTTTGGGGGATTCGGCGGAGCGGCT 2647
 2641 GCTCCTGGTTTGGGATGATTTCTGTGTTGTTGACACCTCACCTCACCCAGCGGAAAAC 2700
 2648 GCTCCTGGTTTGGGATGATTTCTGTGTTGTTGACACCTCACCTCACCCAGCGGAAAAC 2707
 2701 CTTCTCAAGAACCTGATGTCAGAGTGTCCCTGATATGAGCTGCTGATGTAATTTGCGGAA 2760
 2708 CTTCTCAAGAACCTGATGTCAGAGTGTCCCTGATATGAGCTGCTGATGTAATTTGCGGAA 2767
 2761 GACAGTGTGTAATTTCTCTGTGAAAGACGAGGCGCTGAGTGCACGCGCTTTTGTTCAGAT 2820
 2768 GACAGTGTGTAATTTCTCTGTGAAAGACGAGGCGCTGAGTGCACGCGCTTTTGTTCAGAT 2827
 2821 GCGGCGCCCAAGGCTATTTCCCTGTCGCGGCTGCTGCTGATACCCGGAACCTCGAAGGT 2880
 2828 GCGGCGCCCAAGGCTATTTCCCTGTCGCGGCTGCTGCTGATACCCGGAACCTCGAAGGT 2887
 2881 GCGAGCGCATCTACCTGATGATGCGCGGACCTCATCAGAGCCAGTCTGACCTTCAACCG 2940
 2888 GCGAGCGCATCTACCTGATGATGCGCGGACCTCATCAGAGCCAGTCTGACCTTCAACCG 2947
 2941 GCGCTTCAAGGCTGAGGAAACATGCTGCGAACTCTTTGGGGTCTTGGCGCTGAAGTG 3000
 2948 GCGCTTCAAGGCTGAGGAAACATGCTGCGAACTCTTTGGGGTCTTGGCGCTGAAGTG 3007
 3001 TCACAGCCCTGTTTCTGATGATTTGAGGTGAACAGCTCCGAGAGGTGTGACCAACATCTA 3060
 3008 TCACAGCCCTGTTTCTGATGATTTGAGGTGAACAGCTCCGAGAGGTGTGACCAACATCTA 3067
 3061 CAAGATCCCTCTGTCGACGCGTACAGTTCACGATGTGTGTCAGCTCCCATTTTCA 3120
 3068 CAAGATCCCTCTGTCGACGCGTACAGTTCACGATGTGTGTCAGCTCCCATTTTCA 3127
 3121 TCAGCAAGTTTGAAGAAACCCCAATTTTCTGCGCGTCACTCTGACACGCGCTCCCT 3180
 3128 TCAGCAAGTTTGAAGAAACCCCAATTTTCTGCGCGTCACTCTGACACGCGCTCCCT 3187
 3181 CTGCTACTCTCATCTCGAAGAACCAAGAACGAGAGATGTGCTGCGGAGCCAAAGGCGCGC 3240
 3188 CTGCTACTCTCATCTCGAAGAACCAAGAACGAGAGATGTGCTGCGGAGCCAAAGGCGCGC 3247
 3241 GCGGCTCTGCGCTCCGAGAGCGGTGACGATGAGTGTGTCACCAAGCAATTCCTGTCAGAGT 3300
 3248 GCGGCTCTGCGCTCCGAGAGCGGTGACGATGAGTGTGTCACCAAGCAATTCCTGTCAGAGT 3307
 3301 GACTGACACCGTGTCACTTACGTGCACTCTGAGGCTCACTCAGGACAGCCAGCGCA 3360
 3308 GACTGACACCGTGTCACTTACGTGCACTCTGAGGCTCACTCAGGACAGCCAGCGCA 3367
 3361 GCTGAGTGGAGAGCTCCCGGAGACGACGCTGATGCTCTGAGGCGCGGACCAACCCGCGC 3420
 3368 GCTGAGTGGAGAGCTCCCGGAGACGACGCTGATGCTCTGAGGCGCGGACCAACCCGCGC 3427
 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGATGATGGCCAGCCGCGCAAGCCAGGCGCA 3480

3428 ACTGCCCTCAGACTTCAAGACCATCTGAGATGAGCCACCGCGCAAGCCAGGCGCA 3487
 3481 GAGCAGACACAGAGCGCCCTGTCACGCGGCGTCAAGTCCAGAGGAGAGGCGGCGC 3540
 3488 GAGCAGACACAGAGCGCCCTGTCACGCGGCGTCAAGTCCAGAGGAGAGGCGGCGC 3547
 3541 CACACCAAGCGCCGACGCTGAGAGTCTGAGAGCTGATGATGTTTGGCCGAGGCTG 3600
 3548 CACACCAAGCGCCGACGCTGAGAGTCTGAGAGCTGATGATGTTTGGCCGAGGCTG 3607
 3601 CATGTCCGAGTGAAGCTGATGTCGCGCTGAGGCTTGAAGCTGAGGCTTGAAGGCT 3660
 3608 CATGTCCGAGTGAAGCTGATGTCGCGCTGAGGCTTGAAGCTGAGGCTTGAAGGCT 3667
 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGCTGAGGCTGAGGCTTGAAGGCT 3720
 3668 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGCTGAGGCTGAGGCTTGAAGGCT 3727
 3721 GGGCAGCTTTTCTCACAGAGCGCGGCTTCACTTCCCAAGAGCTGAGGCTTGAAGGCT 3780
 3728 GGGCAGCTTTTCTCACAGAGCGCGGCTTCACTTCCCAAGAGCTGAGGCTTGAAGGCT 3787
 3781 CCAGATTCGCAATTTGTTCAACCCCTGCGCTGCTTGTGCTTCAACCCCAATTC 3840
 3788 CCAGATTCGCAATTTGTTCAACCCCTGCGCTGCTTGTGCTTCAACCCCAATTC 3847
 3841 AGGTGGAACCTTGAAGAGACCTTGGAGCTCTGGGAATTTGGAGTACCAAAAGTGTG 3900
 3848 AGGTGGAACCTTGAAGAGACCTTGGAGCTCTGGGAATTTGGAGTACCAAAAGTGTG 3907
 3901 CCTGTACACAGGCGAGGACCTGACCTGATGAGGAGGCTCTGAGGCTCAAAATTTGGGG 3960
 3908 CCTGTACACAGGCGAGGACCTGACCTGATGAGGAGGCTCTGAGGCTCAAAATTTGGGG 3967
 3961 GAGGTGCTGTGGAGTAAATACTGAATATATGATTTTCAAGTTTGAAGAAAAA 4015
 3968 GAGGTGCTGTGGAGTAAATACTGAATATATGATTTTCAAGTTTGAAGAAAAA 4022

RESULT 14
 ABL53711
 ID ABL53711 standard; cDNA; 4070 BP.
 XX
 AC ABL53711;
 XX
 DT 17-JUN-2002 (first entry)
 XX
 DE Human telomerase catalytic subunit hTERT cDNA.
 XX
 KW hTERT; telomerase; reverse transcriptase; immortalisation; human;
 KW vaccine; enzyme; gene; ss.
 OS Homo sapiens.
 XX
 PN WO200216555-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-GB003726.
 XX
 PR 17-AUG-2000; 2000GB-00020246.
 PR 17-AUG-2000; 2000US-0225734P.
 XX
 PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX
 PI Jones CJ, Kipling DG, Wilkinson G, Mesarry B, Skinner JW;
 XX
 DR WPI; 2002-315462/35.
 XX
 PT Novel hTERT-immortalized cell line (human telomerase reverse
 PT transcriptase) useful for human vaccine production and preparation of
 PT antigen, such as a virus or virus-derived agent.

XX Example 1; Fig 1; 64bp; English.

CC The present sequence is that of hTERT cDNA in plasmid pGRN121. hTERT is
CC the catalytic subunit of human telomerase. Claimed immortalised cell
CC lines for use in vaccine production are adapted to express hTERT.
CC Suitable cell lines comprise human diploid fibroblasts, e.g. MRC-5 or
CC WI38 cells, transfected with hTERT cDNA or infected by a retrovirus
CC carrying hTERT cDNA, and are capable of supporting antigen production. A
CC method for preparing such cell lines using recombinant techniques is
CC provided. The cell lines are also used as a diagnostic test for the
CC presence of a virus, such as human cytomegalovirus, and to determine the
CC efficacy of antiviral agents by testing the capability of a modified
CC virus containing a reporter gene to infect the cells. The cell lines have
CC the ability, which can be impaired in cell lines immortalised by other
CC methods, of being able to support viral replication. The cells remain
CC morphologically suitable for viral/vaccine cultivation

XX Sequence 4070 BP; 670 A; 1383 C; 1296 G; 721 T; 0 U; 0 Other;

Query Match 100.0%; Score 4015; DB 6; Length 4070;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGCTGCTCTGCTGCGACAGTGGAGACCTGAGCCCGGACCCCGGACATGCG 60
DB GCAGCGCTGCTCTGCTGCGACAGTGGAGACCTGAGCCCGGACCCCGGACATGCG 80
QY 61 GCGCGCTCCCGCTGCGACCGCTGCGCTCTGCTGCGACAGCTACCGCGAGTGTCT 120
DB GCGCGCTCCCGCTGCGACCGCTGCGCTCTGCTGCGACAGCTACCGCGAGTGTCT 140
QY 121 GCGCGTGGGACAGTGTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB GCGCGTGGGACAGTGTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 200
QY 141 GCGCGTGGGACAGTGTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB GCGCGTGGGACAGTGTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 260
QY 181 GAGCGCGCGCGCTTTCGCGCGCTGCTGCGACAGTGTGCTGCTGCTGCTGCTG 240
DB GAGCGCGCGCGCTTTCGCGCGCTGCTGCGACAGTGTGCTGCTGCTGCTGCTGCT 260
QY 201 GAGCGCGCGCGCTTTCGCGCGCTGCTGCGACAGTGTGCTGCTGCTGCTGCTGCT 240
DB GAGCGCGCGCGCTTTCGCGCGCTGCTGCGACAGTGTGCTGCTGCTGCTGCTGCT 260
QY 241 AGCG 300
DB AGCG 320
QY 261 AGCG 340
DB AGCG 360
QY 301 CGAGTGTGCTGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB CGAGTGTGCTGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 380
QY 321 CGAGTGTGCTGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 400
DB CGAGTGTGCTGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 361 GCTGCTGAGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB GCTGCTGAGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 440
QY 381 GCTGCTGAGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 440
DB GCTGCTGAGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 460
QY 421 CTTGCGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB CTTGCGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 500
QY 441 CTTGCGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 500
DB CTTGCGCGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 520
QY 481 CCGGCGTGGGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB CCGGCGTGGGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 560
QY 501 CCGGCGTGGGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 560
DB CCGGCGTGGGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 580
QY 541 GCGTCCAGCTGCGCTACAGAGTGTGCGGCGCGCGCGCGCTGACAGCTCGGCGT 600
DB GCGTCCAGCTGCGCTACAGAGTGTGCGGCGCGCGCGCGCTGACAGCTCGGCGT 620
QY 561 GCGTCCAGCTGCGCTACAGAGTGTGCGGCGCGCGCGCGCTGACAGCTCGGCGT 620
DB GCGTCCAGCTGCGCTACAGAGTGTGCGGCGCGCGCGCGCTGACAGCTCGGCGT 640
QY 601 TCAAGCG 660
DB TCAAGCG 680
QY 621 TCAAGCG 680
DB TCAAGCG 700
QY 661 CTTGAGACCATAGAGTGTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
DB CTTGAGACCATAGAGTGTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 740
QY 681 CTTGAGACCATAGAGTGTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 740
DB CTTGAGACCATAGAGTGTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 760
QY 721 GAGGCGCGGCGGCGAGTGTGCGAGCGGAGTGTGCGGCGGCGGCGGCGGCGGCGG 780
DB GAGGCGCGGCGGCGAGTGTGCGAGCGGAGTGTGCGGCGGCGGCGGCGGCGGCGG 800

DB 741 GAGGCGCGGCGGCGAGTGTGCGAGCGGAGTGTGCGGCGGCGGCGGCGGCGGCGG 800
QY 781 TCGCCCTAGACCGCGGCGGACCGCGGTTGGGCGAGGGGCTGTTGGGCGACCGCGGAGGAC 840
DB TCGCCCTAGACCGCGGCGGACCGCGGTTGGGCGAGGGGCTGTTGGGCGACCGCGGAGGAC 860
QY 841 GCGTGGACCGAGTGTGACCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB GCGTGGACCGAGTGTGACCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920
QY 901 CACTCTTTTGAAGGTTGCGCTCTGCGACGCGCGCACTCCACCACTCGTGGGCGCGCA 960
DB CACTCTTTTGAAGGTTGCGCTCTGCGACGCGCGCACTCCACCACTCGTGGGCGCGCA 980
QY 961 GAGACACCGGCGGCG 1020
DB GAGACACCGGCGGCG 1040
QY 1021 CCGGCTGTAAGCGCGAGACCAAGCACTTCTCTACTCTCTAGGCGCAAGAGACAGCTGCG 1080
DB CCGGCTGTAAGCGCGAGACCAAGCACTTCTCTACTCTCTAGGCGCGCAAGAGACAGCTGCG 1100
QY 1081 GCGCTCTCTTCTACTCTAGCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB GCGCTCTCTTCTACTCTAGCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1160
QY 1141 GACCATCTTTCTGAGGTTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB GACCATCTTTCTGAGGTTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1220
QY 1161 GACCATCTTTCTGAGGTTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1220
DB GACCATCTTTCTGAGGTTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1240
QY 1201 GCGCGACGCTACTGCGCAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB GCGCGACGCTACTGCGCAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1280
QY 1221 GCGCGACGCTACTGCGCAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1280
DB GCGCGACGCTACTGCGCAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1300
QY 1261 GTGCGCTTACGCGGCTCTCTCAAGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
DB GTGCGCTTACGCGGCTCTCTCAAGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1340
QY 1281 GTGCGCTTACGCGGCTCTCTCAAGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1340
DB GTGCGCTTACGCGGCTCTCTCAAGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1360
QY 1321 AGCGCGTGTCTGCGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
DB AGCGCGTGTCTGCGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1400
QY 1341 AGCGCGTGTCTGCGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1400
DB AGCGCGTGTCTGCGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1420
QY 1381 CACAGACCGCGCGCTGCGCTGCTGCGCGACAGCGCGCGCGCGCGCGCGCGCGCG 1440
DB CACAGACCGCGCGCTGCGCTGCTGCGCGACAGCGCGCGCGCGCGCGCGCGCGCG 1460
QY 1401 CACAGACCGCGCGCTGCGCTGCTGCGCGACAGCGCGCGCGCGCGCGCGCGCGCG 1460
DB CACAGACCGCGCGCTGCGCTGCTGCGCGACAGCGCGCGCGCGCGCGCGCGCGCG 1480
QY 1441 CCGCTTCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
DB CCGCTTCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1520
QY 1461 CCGCTTCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1520
DB CCGCTTCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1540
QY 1501 CAAAGGACCGCGCGCTTCTCAAGAACCAAGAGTGTCTCTCTCTCTCTCTCTCTCT 1560
DB CAAAGGACCGCGCGCTTCTCAAGAACCAAGAGTGTGTCTCTCTCTCTCTCTCTCT 1580
QY 1521 CAAAGGACCGCGCGCTTCTCAAGAACCAAGAGTGTGTCTCTCTCTCTCTCTCT 1580
DB CAAAGGACCGCGCGCTTCTCAAGAACCAAGAGTGTGTCTCTCTCTCTCTCTCTCT 1600
QY 1561 GCTCTGCTGCGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1620
DB GCTCTGCTGCGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1640
QY 1581 GCTCTGCTGCGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1640
DB GCTCTGCTGCGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1660
QY 1621 GAGCGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1680
DB GAGCGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1700
QY 1641 GAGCGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1700
DB GAGCGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1720
QY 1681 CAAAGTCTGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB CAAAGTCTGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1760
QY 1701 CAAAGTCTGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1760
DB CAAAGTCTGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1780
QY 1741 TGTCAAGAGACCAAGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB TGTCAAGAGACCAAGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1820
QY 1761 TGTCAAGAGACCAAGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1820
DB TGTCAAGAGACCAAGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1840
QY 1801 CAAAGTGTGAGAGATGAGACAGCACTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB CAAAGTGTGAGAGATGAGACAGCACTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1880

Db	1821	CAAGTTGCAAAAGCAATTGGAAATCAACAGACATTGGAAGAGGTGCAGCTGCCGGAGCTGTCTC	1880
Qy	1861	GGAAGCAGAGGTCAGGCGAGCATTCGGGAAAGCCAGGCCCGCCCTGTGTGACGTGCAGACTTCG	1920
Db	1881	GGAAGCAGAGGTCAGGCGAGCATTCGGGAAAGCCAGGCCCGCCCTGTGTGACGTGCAGACTTCG	1940
Qy	1921	CTTCATCCCAAGCTGACGGGGCTGCGGCCGATTGTGAACATGGAATTACGTCTGTGGAGC	1980
Db	1941	CTTCATCCCAAGGCTGACGGGGCTGCGGCCGATTGTGAACATGGAATTACGTCTGTGGAGC	2000
Qy	1981	CAGAACGTTCCGCAAGAAAAGAGGGCCGACGCTCACTCCGAGGGGTGAAGGACACTGTT	2040
Db	2001	CAGAACGTTCCGCAAGAAAAGAGGGCCGACGCTCTCACTCCGAGGGGTGAAGGACACTGTT	2060
Qy	2041	CAGCGTGTCTAACTACGACGGGGCGCGGCCCGCCCTCTGTGGCGCTCTGTGTGG	2100
Db	2061	CAGCGTGTCTAACTACGACGGGGCGCGGCCCGCCCTCTGTGGCGCTCTGTGTGG	2120
Qy	2101	CCTGGAAGCATATCCACAGGGCCTTGCGGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2160
Db	2121	CCTGGAAGCATATCCACAGGGCCTTGCGGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2180
Qy	2161	GCCGCTGAGCTGATCTTTGTCAAGGTGGAATGTGACGGGGCGGTATACGACACTATCCCCCA	2220
Db	2181	GCCGCTGAGCTGATCTTTGTCAAGGTGGAATGTGACGGGGCGGTATACGACACTATCCCCCA	2240
Qy	2221	GGACAGGCTCAACGAGAGTCATTCGCGAGCATCATAAACCCGACGAACAGTACTCGTGTG	2280
Db	2241	GGACAGGCTCAACGAGAGTCATTCGCGAGCATCATAAACCCGACGAACAGTACTCGTGTG	2300
Qy	2281	TGCGTATTCGCTGTGTCCAGAAAGCCGCCCATAGGGACGTCGCGCAAGCCTTCAGAGCCA	2340
Db	2301	TGCGTATTCGCTGTGTCCAGAAAGCCGCCCATAGGGACGTCGCGCAAGCCTTCAGAGCCA	2360
Qy	2341	CGTCTCTACCTTGAACAGACCTCCAGCCGCTTAATGAGTAAGTTGCTGCTACCTGACGGA	2400
Db	2361	CGTCTCTACCTTGAACAGACCTCCAGCCGCTTAATGAGTAAGTTGCTGCTACCTGACGGA	2420
Qy	2401	GACCAGCCCGCTGAGAGGATGTCGCTGTGATGAGCAGAGCTCTCTCCCTGAATGAGGCCAG	2460
Db	2421	GACCAGCCCGCTGAGAGGATGTCGCTGTGATGAGCAGAGCTCTCTCCCTGAATGAGGCCAG	2480
Qy	2461	CAGTGGCCTCTTCGACGCTCTTCTTACGCTTCAATGTGCACACGCGCGTCAACAGGG	2520
Db	2481	CAGTGGCCTCTTCGACGCTCTTCTTACGCTTCAATGTGCACACGCGCGTCAACAGGG	2540
Qy	2521	CAAGTCTTCACTGTCAGATGTCAGAGGGGATCCGCAAGGGCTCACTCTTCACAGCTGTCTG	2580
Db	2541	CAAGTCTTCACTGTCAGATGTCAGAGGGGATCCGCAAGGGCTCACTCTTCACAGCTGTCTG	2600
Qy	2581	CAGCCTGTGCTACGGCGCATGAGGAAACAAGCTGTTTCGGGGATTCGGCGGGACGGGCT	2640
Db	2601	CAGCCTGTGCTACGGCGCATGAGGAAACAAGCTGTTTCGGGGATTCGGCGGGACGGGCT	2660
Qy	2641	GCTCTCGGTTGTGTGATGATTTCTTGTGGTGAACACTCACTCAACCCACGCGAAAC	2700
Db	2661	GCTCTCGGTTGTGTGATGATTTCTTGTGGTGAACACTCACTCAACCCACGCGAAAC	2720
Qy	2701	CTTCTCTCAGAACCTCTGTGCCAGGTGTCCCTGAGATATGGCTGTGTGTGAACCTTGCGGA	2760
Db	2721	CTTCTCTCAGAACCTCTGTGTGCCAGGTGTCCCTGAGATATGGCTGTGTGTGAACCTTGCGGA	2780
Qy	2761	GACAGTGTGTAACCTTCCCTGTATGAAAGAGAGAGGCCCTGTGGTGTGACGCTTTTGTTCAGAT	2820
Db	2781	GACAGTGTGTAACCTTCCCTGTATGAAAGAGAGAGGCCCTGTGGTGTGACGCTTTTGTTCAGAT	2840
Qy	2821	GCCGCGCCACCGCTTATTCCTCTGTGTGCGCTGTCTGTGATACCGCGAACCTTGAGAGT	2880
Db	2841	GCCGCGCCACCGCTTATTCCTCTGTGTGCGCTGTCTGTGATACCGCGAACCTTGAGAGT	2900
Qy	2881	GCAGAGCGACTACTCTCAGCTATATGCCCGGACCTTCAATCAAGACCAAGCTTCACTTCAACCG	2940
Db	2901	GCAGAGCGACTACTCTCAGCTATATGCCCGGACCTTCAATCAAGACCAAGCTTCACTTCAACCG	2960

QY	2941	TCGCGTTCAAGGCTTGGAGAGAAATGCGTCCGAACTCTTTGGGGCTCTTGGCGCTGAAGTG	3000
DB	2961	CGGCTTCAAGGCTGAGAGAAATGCGCTCGAAACTCTTTGGGGCTCTTGGCGCTGAAGTG	3020
QY	3001	TCACAGCTGTGTTTGTGATTTTGACAGTGAACAGCTCCAGACGGTGTGACCAATCTTA	3060
DB	3021	TCACAGCTGTGTTTGTGATTTTGACAGTGAACAGCTCCAGACGGTGTGACCAATCTTA	3080
QY	3061	CAAGATCTCTGCTGTCAGGCGTACAGGTTTACGCAATGTGTGCTGCAGCTCCCATTTCA	3120
DB	3081	CAAGATCTCTCTGCTGTCAGGCGTACAGGTTTACGCAATGTGTGCTGCAGCTCCCATTTCA	3140
QY	3121	TCAGAGATTGGAAGAACCCCAATTTTCTGAGCGGTCAATCTCTGACAGGCTCCCT	3180
DB	3141	TCAGAGATTGGAAGAACCCCAATTTTCTGAGCGGTCAATCTCTGACAGGCTCCCT	3200
QY	3181	CTGCTACTCCATCTCTGAAGGCGAAGAACGACGGAGATGTGCTGAGGGGCGCAAGGCGCGCG	3240
DB	3201	CTGCTACTCCATCTCTGAAGGCGAAGAACGACGGAGATGTGCTGAGGGGCGCAAGGCGCGCG	3260
QY	3241	CGGCGCTTGTGCGCTCCAGAGCGGTGCGATGGCTGTGCAACCAACATTTCCGTCAAGCT	3300
DB	3261	CGGCGCTTGTGCGCTCCAGAGCGGTGCGATGGCTGTGCAACCAACATTTCCGTCAAGCT	3320
QY	3301	GACTCGACACCGGTGTCACTACGTGCGCACTCTTGAGGCTCACTCAGGACAGCCAGACGCA	3360
DB	3321	GACTCGACACCGGTGTCACTACGTGCGCACTCTTGAGGCTCACTCAGGACAGCCAGACGCA	3380
QY	3361	GCTGAGTCTGGAAGCTCCCGGGGAGCGAGCTGACGTCCCTGGAAGGCCGACGCCAACCCGGC	3420
DB	3381	GCTGAGTCTGGAAGCTCCCGGGGAGCGAGCTGACGTCCCTGGAAGGCCGACGCCAACCCGGC	3440
QY	3421	ACTGCGCTCAACACTTCAAGACATCTCTGGAATGGAATGGAATGGGCAACCGGCCACAGCCAGCGGA	3480
DB	3441	ACTGCGCTCAACACTTCAAGACATCTCTGGAATGGAATGGAATGGGCAACCGGCCACAGCCAGCGGA	3500
QY	3481	GAGCAGACACCGAGCAGCGCTGTCAACGCCGGCTCTACGTCCAGAGAGAGAGGGGCGGCGC	3540
DB	3501	GAGCAGACACCGAGCAGCGCTGTCAACGCCGGCTCTACGTCCAGAGAGAGAGGGGCGGCGC	3560
QY	3541	CACACCCAGGCGCCGACCGCTGGGAGTCTGAAGGCTTGAGTGAAGTCTTTGGCCGAGCGCTG	3600
DB	3561	CACACCCAGGCGCCGACCGCTGGGAGTCTGAAGGCTTGAGTGAAGTCTTTGGCCGAGCGCTG	3620
QY	3601	CATGTCGGGCTGAAGGCTGAGTGTCTCGGCTAGGCGCTGACGAGAGTGTCAACCCAAAGGCT	3660
DB	3621	CATGTCGGGCTGAAGGCTGAGTGTCTCGGCTAGGCGCTGACGAGAGTGTCAACCCAAAGGCT	3680
QY	3661	GAGTGTCCAGACACCTGCGCTTTCACATTTCCCAACAGGCTGGCGCTGCTCCACCCCA	3720
DB	3681	GAGTGTCCAGACACCTGCGCTTTCACATTTCCCAACAGGCTGGCGCTGCTCCACCCCA	3740
QY	3721	GGGGCAGCTTTTCCACACAGAGGCGGGGCTTCCACTCCCAATAGGAATAGTCAATCC	3780
DB	3741	GGGGCAGCTTTTCCACACAGAGGCGGGGCTTCCACTCCCAATAGGAATAGTCAATCC	3800
QY	3781	CCAGAATTGCGCAATTTTCAACCCCTTGCGGCTGCGCTCTTTGCGCTTCCACCCCAACATCC	3840
DB	3801	CCAGAATTGCGCAATTTTCAACCCCTTGCGGCTGCGCTCTTTGCGCTTCCACCCCAACATCC	3860
QY	3841	AGGTGGAACCCCTGAGAAAGAACCTCTGGGAGCTCTGGGAAATTTGGAAGTGAACCAAGGTGTG	3900
DB	3861	AGGTGGAACCCCTGAGAAAGAACCTCTGGGAGCTCTGGGAAATTTGGAAGTGAACCAAGGTGTG	3920
QY	3901	CCCTGTACACAGGCGAGACCTCGACCTGAGTGGGGGTCCCTGTGGGTCAAAATTGGGGG	3960
DB	3921	CCCTGTACACAGGCGAGACCTCGACCTGAGTGGGGGTCCCTGTGGGTCAAAATTGGGGG	3980
QY	3961	GAGGTGCTGTGGGAGTAAATACTAGAAATATATGAGTTTTTAAGTTTGAAGAAAAA 4015	
DB	3981	GAGGTGCTGTGGGAGTAAATACTAGAAATATATGAGTTTTTAAGTTTGAAGAAAAA 4035	


```
RESULT 15
AAZ08150
ID AAZ08150 standard; cDNA; 4015 BP.
XX
AC AAZ08150;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human telomerase reverse transcriptase cDNA.
XX
KW Human telomerase reverse transcriptase; hTERT; telomerase; hEST2;
KW catalytic protein component; cell proliferative capacity;
KW cell immortality; neoplastic phenotype; diagnostic application;
KW prognostic application; telomerase related condition; cancer;
KW therapeutic agent; telomerase expression; telomerase activity; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /*tag= a
FT /product= "Human telomerase reverse transcriptase"
FT /transl_except= (pos:1877..1879, aa:Gln)
XX
XX MO9950279-A1.
XX 07-OCT-1999.
XX
XX 31-MAR-1999; 99MO-US007160.
XX
XX 31-MAR-1998; 98US-00052919.
XX
XX (GERO-) GERON CORP.
XX (UYTB-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB,
XX Andrews WH;
XX WPI; 1999-610834/52.
XX P-PSDB; AAY28881.
XX
XX Antisense polynucleotides for human telomerase reverse transcriptase used
XX for diagnosing or treating cancer.
XX
XX Claim 1; Fig 1; 31pp; English.
XX
XX The present sequence encodes for human telomerase reverse transcriptase
XX (hTERT). This is the catalytic protein component of telomerase and is also
XX referred to as hEST2. This correlates with cell proliferative capacity,
XX cell immortality, and the development of a neoplastic phenotype. Human
XX TRT antisense oligonucleotides are useful for diagnostic or prognostic
XX applications to telomerase related conditions, including cancer. They are
XX also useful as therapeutic agents, for inhibition of telomerase
XX expression and activity
XX
XX Sequence 4015 BP; 663 A; 1364 C; 1274 G; 714 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 4013.4; DB 2; Length 4015;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 4014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCAGCGCTGCTCTCTCTGCGACGTTGGAGAGCCCTGAGCCCGCCGCGAGTGC 60
XX DB 1 GCAGCGCTGCTCTCTCTGCGACGTTGGAGAGCCCTGAGCCCGCCGCGAGTGC 60
XX QY 61 GCGCGCTCCCGCGTGGCGAGCGGTGGCTCCCTGCTGGCGACGACTACCGGAGGTGCT 120
XX DB 61 GCGCGCTCCCGCGTGGCGAGCGGTGGCTCCCTGCTGGCGACGACTACCGGAGGTGCT 120
XX QY 121 GCGCGTGGCGACGTTCTGTCGCGCGCTGGAGGCCCGCCAGGCGTGGTGCAGCGCG 180
XX DB 121 GCGCGTGGCGACGTTCTGTCGCGCGCTGGAGGCCCGCCAGGCGTGGTGCAGCGCG 180
```

```
QY 181 GGAACCGCGGCGCTTTCCGCGCGCTGGTGGCCCAAGTCCCTGTGTGCTGCCCTGGAGCC 240
DB 181 GGAACCGCGGCGCTTTCCGCGCGCTGGTGGCCCAAGTCCCTGTGTGCTGCCCTGGAGCC 240
QY 241 ACGGCGCGCCCGCGCGCGCCCTCTTCCGCGAGGTCTCTGCTGGAAGAGTGGTGGC 300
DB 241 ACGGCGCGCCCGCGCGCGCCCTCTTCCGCGAGGTCTCTGCTGGAAGAGTGGTGGC 300
QY 301 CCGAGTCTGCGAGAGGCTGTGAGAGCGCGCGCGAAGAACTGTGACCTTGGCTTGGC 360
DB 301 CCGAGTCTGCGAGAGGCTGTGAGAGCGCGCGCGAAGAACTGTGACCTTGGCTTGGC 360
QY 361 GCTGCTGGAAGCGGAGCCCGCGGAGGCCCGCCGAGGCTTCAACACAGGTGCGAGCTA 420
DB 361 GCTGCTGGAAGCGGAGCCCGCGGAGGCCCGCCGAGGCTTCAACACAGGTGCGAGCTA 420
QY 421 CCTGCCCAACAGGTGACCGACGCACTGCGGAGAGCGGAGCGGTGAGGCTGCTGCG 480
DB 421 CCTGCCCAACAGGTGACCGACGCACTGCGGAGAGCGGAGCGGTGAGGCTGCTGCG 480
QY 481 CCGCGTGGCGGACGAGAGTGTCTGTTCACTGCTGGGAGGCTGCGGCTTTGTGCTGCT 540
DB 481 CCGCGTGGCGGACGAGAGTGTCTGTTCACTGCTGGGAGGCTGCGGCTTTGTGCTGCT 540
QY 541 GGCTCCAGCTGCGCTCAAGAGTGTGCGGAGCGCGCGCTGTACAGCTCGGCGCTGCCAC 600
DB 541 GGCTCCAGCTGCGCTCAAGAGTGTGCGGAGCGCGCGCTGTGTACAGCTCGGCGCTGCCAC 600
QY 601 TCAGGCGCGGCGCCCGCGCAACAGCTAGTGAACCCCGAAGCGCTGTGGATGGGA 660
DB 601 TCAGGCGCGGCGCCCGCGCAACAGCTAGTGAACCCCGAAGCGCTGTGGATGGGA 660
QY 661 CTGGAACCAATACGTCAGAGAGAGCGGAGTCCCTGTGGAGCTGCGAGCCCGGAGTGCAG 720
DB 661 CTGGAACCAATACGTCAGAGAGAGCGGAGTCCCTGTGGAGCTGCGAGCCCGGAGTGCAG 720
QY 721 GAGGCGCGGAGGCACTGTCAGCGCAAGTCTGCGCTGTGCGCAAGAGCCCGAGCGTGGCG 780
DB 721 GAGGCGCGGAGGCACTGTCAGCGCAAGTCTGCGCTGTGCGCAAGAGCCCGAGCGTGGCG 780
QY 781 TCCCTCTGAGCGCGAGCGCGCGCTTGGGCAAGGATCTTGGGCGCACCGGCGAGAGC 840
DB 781 TCCCTCTGAGCGCGAGCGCGCGCTTGGGCAAGGATCTTGGGCGCACCGGCGAGAGC 840
QY 841 GCGTGAACCGAGTGAACGTTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GCGTGAACCGAGTGAACGTTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 CACTCTTTTGAAGGAGTGTCTCTGTCAGCGCGCACTCCCAACCATCCGTGGGCGCGCA 960
DB 901 CACTCTTTTGAAGGAGTGTCTCTGTCAGCGCGCACTCCCAACCATCCGTGGGCGCGCA 960
QY 961 GCAACACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
DB 961 GCAACACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1021 CCGGTGTAGCGCGAGCAACGACTTCTCTACTCTCAGGCGCAAGAGAGCGAGTGGC 1080
DB 1021 CCGGTGTAGCGCGAGCAACGACTTCTCTACTCTCAGGCGCAAGAGAGCGAGTGGC 1080
QY 1081 GCGCTCTCTCTACTCTCTGAGGCGCGAGCTGAGCGCTGAGAGCTGTGGA 1140
DB 1081 GCGCTCTCTCTACTCTCTGAGGCGCGAGCTGAGCGCTGAGAGCTGTGGA 1140
QY 1141 GACCATCTTTCTGAGGTTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
DB 1141 GACCATCTTTCTGAGGTTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1201 GCGCCAGGCGTACTGCGCAAAATGCGGCGCGCGTGTCTGGAAGTGTGTGGAACACAGCGCA 1260
DB 1201 GCGCCAGGCGTACTGCGCAAAATGCGGCGCGCGTGTGTCTGGAAGTGTGTGGAACACAGCGCA 1260
```


OY	1261	TTGGCCCTCA	GGGGGGTGGCTTC	CAAGAGCA	CTGGCCGCTGGAGCTGGCTCA	CCCCAGC	1320			
Db	1261	GTGCCCCCTCA	GGGGGGTGGCTTC	CAAGAGCA	GTCCCGCTGGAGCTGGCTCA	CCCCAGC	1320			
OY	1321	AGCCGGTGTCTGTG	TCCCGGGAGAA	AGCCCA	GGGCTCTGTGGCGGCCCCCGAGAGAGAG	1380				
Db	1321	AGCCGGTGTCTGTG	TCCCGGGAGAA	AGCCCA	GGGCTCTGTGGCGGCCCCCGAGAGAGAG	1380				
OY	1381	CACAGACCCCGCTG	CGCTGTGTGCA	GTCTCCGCCAGCA	CAGCAGCCCTTGGCAGTGTGA	1440				
Db	1381	CACAGACCCCGCTG	CGCTGTGTGCA	GTCTCCGCCAGCA	CAGCAGCCCTTGGCAGTGTGA	1440				
OY	1441	CGGCTCTGTGGGGG	CTGGCTGGCCCGGCTGGTGGCC	CAGGCGCTCTGGGGCTCA	AGGCA	1500				
Db	1441	CGGCTCTGTGGGGG	CTGGCTGGCCCGGCTGGTGGCC	CAGGCGCTCTGGGGCTCA	AGGCA	1500				
OY	1501	CAACGAA	CGCGCTTCCTC	CAGAAACAC	CAAAAGTTCTATCTCCCTGGGGAAAGCATG	CAAA	1560			
Db	1501	CAACGAA	CGCGCTTCCTC	CAGAAACAC	CAAAAGTTCTATCTCCCTGGGGAAAGCATG	CAAA	1560			
OY	1561	GCTCTCGCTG	CAGAGCTGAC	GTGAAAGT	AGCGTGGGAGCTGCGCTTGGCTG	CGAG	1620			
Db	1561	GCTCTCGCTG	CAGAGCTGAC	GTGAAAGT	AGCGTGGGAGCTGCGCTTGGCTG	CGAG	1620			
OY	1621	GAGCCCA	GGGGTGGCTGT	TCCGGCCGAGAGCA	CGCTTGGGTGAGAGATCT	TGGC	1680			
Db	1621	GAGCCCA	GGGGTGGCTGT	TCCGGCCGAGAGCA	CGCTTGGGTGAGAGATCT	TGGC	1680			
OY	1681	CAAGTCTT	CGACCTGGATG	AGTGTATAGTGC	TGACGTCTCAGGTCTTCTCTTTTA		1740			
Db	1681	CAAGTCTT	CGACCTGGATG	AGTGTATAGTGC	TGACGTCTCAGGTCTTCTCTTTTA		1740			
OY	1741	TGTCA	CGGAGACA	CGTITTC	CAAAAGACAGGCTCTTTTTC	TCAACGGAAAGATGTCT	GGAG	1800		
Db	1741	TGTCA	CGGAGACA	CGA	GTTTCAAAAGAACAGGCTCTTTTTC	TCAACGGAAAGATGTCT	GGAG	1800		
OY	1801	CAAGTTG	CAAAAGCATTTG	GAATCAGAC	ACTTGAAGGGTGCAGCTGCGGGAGCTGTCTC		1860			
Db	1801	CAAGTTG	CAAAAGCATTTG	GAATCAGAC	ACTTGAAGGGTGCAGCTGCGGGAGCTGTCTC		1860			
OY	1861	GGAAGCA	AGGGTCAGG	CGACATCGG	GGAAAGCCAGGGCCGCTCGCTGACGCTC	CAGACTCGG	1920			
Db	1861	GGAAGCA	AGGGTCAGG	CGACATCGG	GGAAAGCCAGGGCCGCTCGCTGACGCTC	CAGACTCGG	1920			
OY	1921	CTTCAT	TCCCAAGCCTG	AGGGCTGCGGCGCATTTGT	GAACATGGA	CTACGTCTGTGGAGGC	1980			
Db	1921	CTTCAT	TCCCAAGCCTG	AGGGCTGCGGCGCATTTGT	GAACATGGA	CTACGTCTGTGGAGGC	1980			
OY	1981	CAGAA	CGTTCCG	CAGAGAA	AAAGAGGGCCGAGGTCTCA	CTCTGAGGGGTGAAGGCA	CTGTT	2040		
Db	1981	CAGAA	CGTTCCG	CAGAGAA	AAAGAGGGCCGAGGTCTCA	CTCTGAGGGGTGAAGGCA	CTGTT	2040		
OY	2041	CAGCGT	GTCAACTAC	AGCGGGCGGCGGCGCTCC	TGGGGCGGCTCTGTG	TGGGG	2100			
Db	2041	CAGCGT	GTCAACTAC	AGCGGGCGGCGGCGCTCC	TGGGGCGGCTCTGTG	TGGGG	2100			
OY	2101	CCTG	GACATATTC	CAAGAGG	CGCTGCGGACCTTCG	TGCTGGGTGTGCGGGCC	CAGAGACC	2160		
Db	2101	CCTG	GACATATTC	CAAGAGG	CGCTGCGGACCTTCG	TGCTGGGTGTGCGGGCC	CAGAGACC	2160		
OY	2161	GCCG	CTGAGCTGTAT	CTTTGTTC	AGATGATGAGGCGCGCTGAC	AGACACCATCCCA	2220			
Db	2161	GCCG	CTGAGCTGTAT	CTTTGTTC	AGATGATGAGGCGCGCTGAC	AGACACCATCCCA	2220			
OY	2221	GGA	CAAGGCTC	ACGAGGTC	ATGCGCAGATCAT	CAAAACCCAGAA	CAAGTACTGTGGCG	2280		
Db	2221	GGA	CAAGGCTC	ACGAGGTC	ATGCGCAGATCAT	CAAAACCCAGAA	CAAGTACTGTGGCG	2280		
OY	2281	TGG	GTATGCGCTGTG	ATCCAAAGG	CGCCCATATGGG	CAAGTGGCAAGGCGCTTCA	AGAGGCA	2340		
Db	2281	TGG	GTATGCGCTGTG	ATCCAAAGG	CGCCCATATGGG	CAAGTGGCAAGGCGCTTCA	AGAGGCA	2340		
OY	2341	CGT	CTCTAC	CTTTGAC	AGACTTC	CACGCGTACATG	GACAGATTTCTGGCTCA	CTG	CAGAG	2400

Db	2341	CGTCTTACCTTGA	CACACCTCCAGCGCTACATG	CCAGCACTGTGGCTCACCTG	CAGGA	2400	
Qy	2401	GACCAAGCCCGTGA	GGGATGCGCTGTCATCGAC	AGACTCCTCCTGAA	TGAGCCAG	2460	
Db	2401	GACCAGCCCCGTGA	GGGATGCCGTGCTCATCGAC	AGAGCTCCTCCTGAA	TGAGGCGAG	2460	
Qy	2461	CNATGGCCCTTGA	CGCTTCTCCAGGCTTCA	TGTCACACAGCGCGTGGGCAT	CAAGGG	2520	
Db	2461	CATGGCCCTTGA	CGCTTCTCCAGGCTTCA	TGTCACACAGCGCGTGGGCAT	CAAGGG	2520	
Qy	2521	CAAGTCTCACTG	CCAGTGCAGGGGATCCCG	CAGGGCTCCATCTTCCA	CGCTGCTCTG	2580	
Db	2521	CAAGTCTCACTG	CCAGTGCAGGGGATCCCG	CAGGGCTCCATCTTCCA	CGCTGCTCTG	2580	
Qy	2581	CAGCCTTGCTAC	GGGCAATGAGAA	CAAGCTTTGCGGGATTTGG	GGGGGACGGGCT	2640	
Db	2581	CAGCCTTGCTAC	GGGCAATGAGAA	CAAGCTTTGCGGGATTTGG	GGGGGACGGGCT	2640	
Qy	2641	GCTCTCGCTTGGT	TGGATGATTTTCTTG	TGGTGAACCTCACCTCA	CCACGGGAAAC	2700	
Db	2641	GCTCTCGCTTGGT	TGGATGATTTTCTTG	TGGTGAACCTCACCTCA	CCACGGGAAAC	2700	
Qy	2701	CTTCTCTAGAG	CCCTGGTCCAGGATGCTCC	TGAGTATGGCTGCTGTGA	ACTTGGCGGAA	2760	
Db	2701	CTTCTCTAGAG	CCCTGGTCCAGGATGCTCC	TGAGTATGGCTGCTGTGA	ACTTGGCGGAA	2760	
Qy	2761	GACAGTGTGA	CTTCCCTGTGA	AGAGAGGCGCTGGTGGCA	CGGCTTTGTTCA	2820	
Db	2761	GACAGTGTGA	CTTCCCTGTGA	AGAGAGGCGCTGGTGGCA	CGGCTTTGTTCA	2820	
Qy	2821	GCCGGCCCA	CGGCTTATTCCTCTG	TGTGGGCTGTCTGTCTG	ATACCCGGACCTTGGAGT	2880	
Db	2821	GCCGGCCCA	CGGCTTATTCCTCTG	TGTGGGCTGTCTGTGTATAC	CCGGACCTTGGAGT	2880	
Qy	2881	GCAGAGGCA	CTACTCCAGCTATG	CCCGGACCTCATAGAG	CCAGCTTCAACCG	2940	
Db	2881	GCAGAGGCA	CTACTCCAGCTATG	CCCGGACCTCATAGAG	CCAGCTTCAACCG	2940	
Qy	2941	CGGCTTCAAG	GCTGGGAGAA	CATGCGTGGCAA	CTCTTTGGGGTCTTGGCGGCTGA	2940	
Db	2941	CGGCTTCAAG	GCTGGGAGAA	CATGCGTGGCAA	CTCTTTGGGGTCTTGGCGGCTGA	2940	
Qy	3001	TCACAGCTGTTT	TCGATTTGCA	GGTGAACGCTTCA	CAGCGTGTGCA	CAACA	3060
Db	3001	TCACAGCTGTTT	TCGATTTGCA	GGTGAACGCTTCA	CAGCGTGTGCA	CAACA	3060
Qy	3061	CAAGATCCTCG	GTGAGAGGCGTAC	AGGTTTCA	GCAGATGTGTGCA	AGCTCCCATTTCA	3120
Db	3061	CAAGATCCTCG	GTGAGAGGCGTAC	AGGTTTCA	GCAGATGTGTGCA	AGCTCCCATTTCA	3120
Qy	3121	TCAGCAATTTGA	AGAA	CCCCAATTTTCTCG	GGCTCATCTCTG	CA	3180
Db	3121	TCAGCAATTTGA	AGAA	CCCCAATTTTCTCG	GGCTCATCTCTG	CA	3180
Qy	3181	CTGCTACTCC	ATCCTGAAGCA	AGCAAGCGAGGATG	CGCTGGGGGCGAA	GGGCGCCG	3240
Db	3181	CTGCTACTCC	ATCCTGAAGCA	AGCAAGCGAGGATG	CGCTGGGGGCGAA	GGGCGCCG	3240
Qy	3241	CGGCTCTG	CCCTCCAGAGCGCGTGA	GTGCTGTGCA	CCAAACATTTCTGTCA	AGCT	3300
Db	3241	CGGCTCTG	CCCTCCAGAGCGCGTGA	GTGCTGTGCA	CCAAACATTTCTGTCA	AGCT	3300
Qy	3301	GACTGCA	ACCGTGTCA	CTTCA	GTGCACTCTTGGGTG	CACTCAGGACAGCCAGAGCGCA	3360
Db	3301	GACTGCA	ACCGTGTCA	CTTCA	GTGCACTCTTGGGTG	CACTCAGGACAGCCAGAGCGCA	3360
Qy	3361	GCTGAGTGA	AGCTCCCGGGAG	AGAGCGTGA	CTGCTTGGAGGCG	CAGCAACCCGGC	3420
Db	3361	GCTGAGTGA	AGCTCCCGGGAG	AGAGCGTGA	CTGCTTGGAGGCG	CAGCAACCCGGC	3420
Qy	3421	ACTGCGCTCA	AGCTTCA	AGACATCTTGA	ATGCTCA	CCGCCCA	3480
Db	3421	ACTGCGCTCA	AGCTTCA	AGACATCTTGA	ATGCTCA	CCGCCCA	3480

```

Db 3421 ACTGCCCTAGACTTGAAGACCATCTCTGACGTGATGAGCCACCGCCACAGCCAGGCCGA 3480
QY 3481 GAGCAGACACACAGCAGCCCTGTGACGCGCGGCTCTAGTCCAGAGGAGGAGGCGGCC 3540
Db 3481 GAGCAGACACACAGCAGCCCTGTGACGCGCGGCTCTAGTCCAGAGGAGGAGGCGGCC 3540
QY 3541 CACACCCAGGCCCGCAGCCGCTGAGAGCTTGAGGCTGAGTGTGTTGGCCGAGGCTTG 3600
Db 3541 CACACCCAGGCCCGCAGCCGCTGAGAGCTTGAGGCTGAGTGTGTTGGCCGAGGCTTG 3600
QY 3601 CATGTCCGCTGAAGCTGAGTGTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Db 3601 CATGTCCGCTGAAGCTGAGTGTGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
QY 3661 GAGTGTCAAGCAGCAGCTGCGCTTCTACATTCCTCCACAGGCTGAGGCTGAGGCTGAGGCT 3720
Db 3661 GAGTGTCAAGCAGCAGCTGCGCTTCTACATTCCTCCACAGGCTGAGGCTGAGGCTGAGGCT 3720
QY 3721 GGGCCAGCTTTTCTCTACAGAGAGCCCGGCTTCACTCCCAATAGAAATAGTCAATCC 3780
Db 3721 GGGCCAGCTTTTCTCTACAGAGAGCCCGGCTTCACTCCCAATAGAAATAGTCAATCC 3780
QY 3781 CCAGATTCGCAATGTTTCAACCCCTGCGCTGCTTTCCTTCCATGAGGCTGAGGCTGAGGCT 3840
Db 3781 CCAGATTCGCAATGTTTCAACCCCTGCGCTGCTTTCCTTCCATGAGGCTGAGGCTGAGGCT 3840
QY 3841 AGGTGAGACCTTGAGAGAGACCTGAGAGCTTGAGAAATTTGAGTGAACCAAGGTGTG 3900
Db 3841 AGGTGAGACCTTGAGAGAGACCTGAGAGCTTGAGAAATTTGAGTGAACCAAGGTGTG 3900
QY 3901 CCTGTACACAGGCGAGAGACCTTGACCTGAGATGAGGCTCCTGTGAGTCAAAATTTGAGG 3960
Db 3901 CCTGTACACAGGCGAGAGACCTTGACCTGAGATGAGGCTCCTGTGAGTCAAAATTTGAGG 3960
QY 3961 GAGGTGCTGTGGAGTAAATCTGAATATATGAGTGTTCAGTTTGAAGAAAAA 4015
Db 3961 GAGGTGCTGTGGAGTAAATCTGAATATATGAGTGTTCAGTTTGAAGAAAAA 4015

```

Search completed: October 30, 2004, 00:00:24
 Job time : 1776 secs

Db 61 GCGGCTCCCGCTGCGAAGCCGCTGCTCCCTGCTGCGACCACTACCGCGAGGTGCT 120
QY 121 GCCGCTGACCACTTGTGTGCGGCGCTGAGGAGCCCAAGGCTGCGGCTGGTGCAGGCGG 180
Db 121 GCCGCTGACCACTTGTGTGCGGCGCTGAGGAGCCCAAGGCTGCGGCTGGTGCAGGCGG 180
QY 181 GGAAGGCGGCGCTTTCGCGCGCTGTGTGCGCCAGTGCCTGTGTGCGCTGAGGAGCG 240
Db 181 GGAAGGCGGCGCTTTCGCGCGCTGTGTGCGCCAGTGCCTGTGTGCGCTGAGGAGCG 240
QY 241 AGCGCGGCG 300
Db 241 AGCGCGGCG 300
QY 301 CCGAGTGTGCTGAGAGGCTGTGCGAGGCGCGCGAGAAAGTGTGCGCGCTTGGCTTCCG 360
Db 301 CCGAGTGTGCTGAGAGGCTGTGCGAGGCGCGCGAGAAAGTGTGCGCGCTTGGCTTCCG 360
QY 361 GCTGTGAGACGAGGAGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 361 GCTGTGAGACGAGGAGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 CCGCGCCCAACGCTGTGACGCACTGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCG 480
Db 421 CCGCGCCCAACGCTGTGACGCACTGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCG 480
QY 481 CCGCGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 481 CCGCGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 GCGTCCAGCTGCGCTTACCAAGGTGTGCGGAGCGCGCGCTGTACCAAGCTGCGCTG 600
Db 541 GCGTCCAGCTGCGCTTACCAAGGTGTGCGGAGCGCGCGCTGTACCAAGCTGCGCTG 600
QY 601 TAGAGCG 660
Db 601 TAGAGCG 660
QY 661 CTGGAACCACTAGCGTCAAGGAGGAGCGGAGGAGCGGAGGAGGAGGAGGAGGAGG 720
Db 661 CTGGAACCACTAGCGTCAAGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 GAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 721 GAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 TGCG 840
Db 781 TGCG 840
QY 841 GCGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 GCGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 CACTCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db 901 CACTCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 GAGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 961 GAGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 CCGCGGTGTAGCGAGACCAAGCACTTCTCTACTCTCTAGGAGCAAGAGAGGAGTGG 1080
Db 1021 CCGCGGTGTAGCGAGACCAAGCACTTCTCTACTCTCTAGGAGCAAGAGAGGAGTGG 1080
QY 1081 GCGCTCTCTTCTACTAGCTCTGTAGGAGCGAGCTGTGAGGAGTGTGAGGAGTGTGAG 1140
Db 1081 GCGCTCTCTTCTACTAGCTCTGTAGGAGCGAGCTGTGAGGAGTGTGAGGAGTGTGAG 1140
QY 1141 GAGCAATCTTCTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1141 GAGCAATCTTCTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200

QY 1201 GCCCAGCGCTACTGACAAATGCGGCGCGCTGTTTCTGAGAGCTGTGGAACCAAGCGCA 1260
Db 1201 GCCCAGCGCTACTGACAAATGCGGCGCGCTGTTTCTGAGAGCTGTGGAACCAAGCGCA 1260
QY 1261 GTGCGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db 1261 GTGCGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
QY 1321 AGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Db 1321 AGCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
QY 1381 CACAGACCGCGCTGCGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Db 1381 CACAGACCGCGCTGCGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
QY 1441 CCGCTTCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
Db 1441 CCGCTTCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
QY 1501 CACAGAGCGCGCTTCTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db 1501 CACAGAGCGCGCTTCTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
QY 1561 GCTCTGCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
Db 1561 GCTCTGCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
QY 1621 GAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
Db 1621 GAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
QY 1681 CAAAGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
Db 1681 CAAAGTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
QY 1741 TGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
Db 1741 TGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
QY 1801 CAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
Db 1801 CAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
QY 1861 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Db 1861 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
QY 1921 CTTCAATCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Db 1921 CTTCAATCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1981 CAGAAAGTTCGCGAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Db 1981 CAGAAAGTTCGCGAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
QY 2041 CAGCGGTGTCACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
Db 2041 CAGCGGTGTCACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
QY 2101 CTTGAGAGATATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
Db 2101 CTTGAGAGATATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
QY 2161 GCGCGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
Db 2161 GCGCGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
QY 2221 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
Db 2221 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280

2281 TGGGATGCGGTGTCAGAGAGCGGCCCATGAGGCGCTCCGCAAGGCTTCAAGAGCCA 2340
2281 TGGGATGCGGTGTCAGAGAGCGGCCCATGAGGCGCTCCGCAAGGCTTCAAGAGCCA 2340
2341 CCGTCTCTAAGTGAAGAGAGCTCCAGGCTGATGAGAGAGGCTTCTGAGAGGA 2400
2341 CCGTCTCTAAGTGAAGAGAGCTCCAGGCTGATGAGAGAGGCTTCTGAGAGGA 2400
2401 GAGCAGCCCGGTGAGGAGTCCGCTGATGAGAGAGGCTTCTGAGAGAGGCTGAG 2460
2401 GAGCAGCCCGGTGAGGAGTCCGCTGATGAGAGAGGCTTCTGAGAGAGGCTGAG 2460
2461 CAGTGGCTCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 2520
2461 CAGTGGCTCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 2520
2521 CAGTGGCTCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 2580
2521 CAGTGGCTCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 2580
2581 GAGCAGCCCGGTGAGGAGTCCGCTGATGAGAGAGGCTTCTGAGAGAGGCTGAG 2640
2581 GAGCAGCCCGGTGAGGAGTCCGCTGATGAGAGAGGCTTCTGAGAGAGGCTGAG 2640
2641 GCTCTGCGGTGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGG 2700
2641 GCTCTGCGGTGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGG 2700
2701 CTTCTCTAAGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGG 2760
2701 CTTCTCTAAGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGG 2760
2761 GAGCAGCCCGGTGAGGAGTCCGCTGATGAGAGAGGCTTCTGAGAGAGGCTGAG 2820
2761 GAGCAGCCCGGTGAGGAGTCCGCTGATGAGAGAGGCTTCTGAGAGAGGCTGAG 2820
2821 GCGGAGCCCAAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCT 2880
2821 GCGGAGCCCAAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCT 2880
2881 GAGAGAGGAGTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 2940
2881 GAGAGAGGAGTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 2940
2941 GCGGCTTCAAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCT 3000
2941 GCGGCTTCAAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCT 3000
3001 TCACAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3060
3001 TCACAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3060
3061 CAGAGTCTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3120
3061 CAGAGTCTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3120
3121 TCAGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3180
3121 TCAGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3180
3181 CTGCTACTCTCATCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3240
3181 CTGCTACTCTCATCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3240
3241 CCGGCTCTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3300
3241 CCGGCTCTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3300
3301 GAGTGGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3360
3301 GAGTGGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3360
3361 GCTGAGTGGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3420

3361 GCTGAGTGGAGAGGCTTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3420
3421 ACTGCTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3480
3421 ACTGCTCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3480
3481 GAGCAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3540
3481 GAGCAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3540
3541 CACACCCAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3600
3541 CACACCCAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3600
3601 CATGTCGGCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3660
3601 CATGTCGGCTGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3660
3661 GAGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3720
3661 GAGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3720
3721 GGGCAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3780
3721 GGGCAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3780
3781 CAGAGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3840
3781 CAGAGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3840
3841 AGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3900
3841 AGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGG 3900
3901 CCGTGTACAGAGGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3960
3901 CCGTGTACAGAGGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 3960
3961 GAGGTGCTGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 4015
3961 GAGGTGCTGTGGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAGAGAGGCTTCTGAG 4015

RESULT 2

US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1

Query Match 100.0%; Score 4015; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTfT"
/note= "human telomerase reverse
transcriptase (hTfT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224
Query Match 100.0%; Score 4015; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

421 CTTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGGCTGCTGCTGCG 480
481 CCGGTGGGCGACGACGTGCTGCTTACCTGCTGGGACGCTGGCGCTCTTTGGCTGT 540
481 CCGGTGGGCGACGACGTGCTGCTTACCTGCTGGGACGCTGGCGCTCTTTGGCTGT 540
541 GGGTCCACGCTGCGCTACCGAGTGTGCGGGCGCGCTGTACCAAGCTCGAGCTGCGAC 600
541 GGGTCCACGCTGCGCTTACCGAGTGTGCGGGCGCGCTGTACCAAGCTCGAGCTGCGAC 600
601 TCAGGCGCGGCGCGCGCGACGCTAGTGAAGCTTGAAGGCTTGGGATGCGAACGCGG 660
601 TCAGGCGCGGCGCGCGCGACGCTAGTGAAGCTTGAAGGCTTGGGATGCGAACGCGG 660
661 CTGGAACCATAGCTGCAAGGAGGCGGGGGTCCCTGAGGCTTGGACGCGGCTGGAG 720
661 CTGGAACCATAGCTGCAAGGAGGCGGGGGTCCCTGAGGCTTGGACGCGGCTGGAG 720
721 GAGGCGCGGGGCAAGTGCACGCGGAGCTGCTGCTGAGTGCACCTGCGCAAGGCTCGGCGC 780
721 GAGGCGCGGGGCAAGTGCACGCGGAGCTGCTGCTGAGTGCACCTGCGCAAGGCTCGGCGC 780
781 TCCCTCTGAGCGCGGAGCGCGGCGCGCTTGGGCAAGGCTTGGGCAAGGCTTGGGCAAG 840
781 TCCCTCTGAGCGCGGAGCGCGGCGCGCTTGGGCAAGGCTTGGGCAAGGCTTGGGCAAG 840
841 GGTGGACCGAGTGCACGCGGCTTCTGCTGAGTGCACCTGCGCAAGGCTCGGCGC 900
841 GGTGGACCGAGTGCACGCGGCTTCTGCTGAGTGCACCTGCGCAAGGCTCGGCGC 900
901 CACTCTTTTGAAGGCTGCTCTCTGCGACGCGGCACTTCCCAAGCTTCTGCGGCGCGCA 960
901 CACTCTTTTGAAGGCTGCTCTCTGCGACGCGGCACTTCCCAAGCTTCTGCGGCGCGCA 960
961 GCACCAAGGCGGCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 1020
961 GCACCAAGGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGGCGG 1020
1021 CCGGCTGTAAGCGCGAGACCAAGCACTTCTTACTTCTTACTTCTTACTTCTTACTTCTT 1080
1021 CCGGCTGTAAGCGCGAGACCAAGCACTTCTTACTTCTTACTTCTTACTTCTTACTTCTT 1080
1081 GCGCTCTCTTCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140
1081 GCGCTCTCTTCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140
1141 GACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
1141 GACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
1201 GCGGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1260
1201 GCGGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1260
1261 GTCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1320
1261 GTCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1320
1321 AGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1380
1321 AGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1380
1381 CACAGACCGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1440
1381 CACAGACCGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1440
1441 CCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1500
1441 CCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1500
1501 CACGAAAGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1560
1501 CACGAAAGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1560

Db	1501	CAAGSAAAGCCGGCTTCTCTCAGAGAAACACCAAGAATTATCTCTCGGGGAAAGCATGCCAA	1500
Qy	1561	GCTCTCGCTGCAGAGAGCTGACGCTGAGATGAGCGTGCGGACATGCGCTTGAGCGTCAG	1620
Db	1561	GCTCTCGCTGCAGAGAGCTGACGCTGAGATGAGCGTGCGGACATGCGCTTGAGCGTCAG	1620
Qy	1621	GAGCCCAAGGGGTTGGCTGTGTTTCGGGCGGCAGAGACCGTCTGGGTGAGAGATCTGGC	1680
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTTCGGGCGGCAGAGACCGTCTGGGTGAGAGATCTGGC	1680
Qy	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGCTCAGCGTGCACAGTCTTTCTTTTA	1740
Db	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGCTCAGCGTGCACAGTCTTTCTTTTA	1740
Qy	1741	TGTCAACGAGAACCAAGTTTCAAAAAGACAGGCTCTTTTCTTCAACGGAAAGTGTCTGAG	1800
Db	1741	TGTCAACGAGAACCAAGTTTCAAAAAGACAGGCTCTTTTCTTCAACGGAAAGTGTCTGAG	1800
Qy	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACACACTTGAAGAAGGCTGACGCTGCAGGAGCTGT	1860
Db	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACACACTTGAAGAAGGCTGACGCTGCAGGAGCTGT	1860
Qy	1861	GGAAGCAGAGGTCAGGCGAGCATTCGGGGAAGCCAGGCGCCGCTCGCTGACGTCAGACTCG	1920
Db	1861	GGAAGCAGAGGTCAGGCGAGCATTCGGGGAAGCCAGGCGCCGCTCGCTGACGTCAGACTCG	1920
Qy	1921	CTTCATCCCAAGCGCTGACGGGCTGTGCGGCGCATTTGTGAACAATGACATCAGTCGTGGAGC	1980
Db	1921	CTTCATCCCAAGCGCTGACGGGCTGTGCGGCGCATTTGTGAACAATGACATCAGTCGTGGAGC	1980
Qy	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGGTGAAGGCACTGTT	2040
Qy	2041	CAGCGTGTCTCAACTACGAGCGGGGCGGGGCGCCGCGGCTCTCGGGCGGCTCGTGTGG	2100
Db	2041	CAGCGTGTCTCAACTACGAGCGGGGCGGGGCGCCGCGGCTCTCGGGCGGCTCGTGTGG	2100
Qy	2101	CCTGAGCAGATATCCACAGGGGCTGTGCGGACCTTCGTGCTGGGTGTGCGGGCCACAGACC	2160
Db	2101	CCTGAGCAGATATCCACAGGGGCTGTGCGGACCTTCGTGCTGGGTGTGCGGGCCACAGACC	2160
Qy	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTCGACACATCTCCCA	2220
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTCGACACATCTCCCA	2220
Qy	2221	GGAACGGCTCACGAGGATCATGCCAGGATCATCAAACCCAGAACAGATCACTGTGTGCG	2280
Db	2221	GGAACGGCTCACGAGGATCATGCCAGGATCATCAAACCCAGAACAGATCACTGTGTGCG	2280
Qy	2281	TCGGTATCCGTTGATCCAGAAAGGCGCCCATATGGGACATCTCGCAAGGCGCTTCAAGAGCA	2340
Db	2281	TCGGTATCCGTTGATCCAGAAAGGCGCCCATATGGGACATCTCGCAAGGCGCTTCAAGAGCA	2340
Qy	2341	CGTCTCTACCTTTCAGACAGCTTCAGCGGTCATATGAGACAGTTGCGTCACTTCAGAGA	2400
Db	2341	CGTCTCTACCTTTCAGACAGCTTCAGCGGTCATATGAGACAGTTGCGTCACTTCAGAGA	2400
Qy	2401	GACACGCCCCGCTGAGAGGATGCCGTTGTATGAGACAGAGCTCTCTCCCTGAATGAGGCCAG	2460
Db	2401	GACACGCCCCGCTGAGAGGATGCCGTTGTATGAGACAGAGCTCTCTCCCTGAATGAGGCCAG	2460
Qy	2461	CAGTGGCGCTTTCAGAGCTCTTCTCTACGCTTCAATGTGCCACACAGCGCGTGCAGATCAGGG	2520
Db	2461	CAGTGGCGCTTTCAGAGCTCTTCTCTACGCTTCAATGTGCCACACAGCGCGTGCAGATCAGGG	2520
Qy	2521	CAAGTCTTACGTCAGGTGCAGAGGGGATCCCGAGGGCTCAATCTCTCAACGCTGCTGTG	2580
Db	2521	CAAGTCTTACGTCAGGTGCAGAGGGGATCCCGAGGGCTCAATCTCTCAACGCTGCTGTG	2580
Qy	2581	CAGCGTGTGTCTACGGCGCATGTGAACAACAAGCTGTGTTTCGGGGAATTCGGCGGAGCGGCT	2640
Db	2581	CAGCGTGTGTCTACGGCGCATGTGAACAACAAGCTGTGTTTCGGGGAATTCGGCGGAGCGGCT	2640

OY	2641	GCTCTGCGATTGGTGGATGATTTCTTGTTGGTGAACCTACCTCAACCCACGGGAAAC	2700
Db	2641	GCTCTGCGATTGGTGGATGATTTCTTGTTGGTGAACCTACCTCAACCCACGGGAAAC	2700
OY	2701	CTTCCTCAGGACCCCTGGATCCGAGGGTGTCCCTAGATATGGCTGCGTGGTGAACCTTGGCGAA	2760
Db	2701	CTTCCTCAGGACCCCTGGATCCGAGGGTGTCCCTAGATATGGCTGCGTGGTGAACCTTGGCGAA	2760
OY	2761	GACAGTGTGAACCTTCCCTGTGAAGACAGAGCCCTGGGTGGCAACGGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGAACCTTCCCTGTGAAGACAGAGCCCTGGGTGGCAACGGCTTTTGTTCAGAT	2820
OY	2821	GC CGGACCACGGCCTATATTCCTCTGTGCGGCTCTGCTGGATATCCGGAACCTTGAAGT	2880
Db	2821	GC CGGACCACGGCCTATATTCCTCTGTGCGGCTCTGCTGGATATCCGGAACCTTGAAGT	2880
OY	2881	GCAGAGGACTACTTCACAGCTATGCCCGGACCTTCATCAGAACAGTCTCACTTCAACCG	2940
Db	2881	GCAGAGGACTACTTCACAGCTATGCCCGGACCTTCATCAGAACAGTCTCACTTCAACCG	2940
OY	2941	CGGCTTCAAGGCTGGAGGAACATGCGCTCGCAACTCTTGGGGCTCTTGC GGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGAGGAACATGCGCTCGCAACTCTTGGGGCTCTTGGGGCTGAAGTG	3000
OY	3001	TCACAGCCTGTTTCTGGAATTTGACAGTGAACAGCCTTCAGACGGTGTGCACCAATCTA	3060
Db	3001	TCACAGCCTGTTTCTGGAATTTGACAGTGAACAGCCTTCAGACGGTGTGCACCAATCTA	3060
OY	3061	CAAAATCTCTCTGCTGACAGGCTACAGATTCAAGCAATGTGTGTGACAGCTCCCATTTCA	3120
Db	3061	CAAAATCTCTCTGCTGACAGGCTACAGATTCAAGCAATGTGTGTGACAGCTCCCATTTCA	3120
OY	3121	TCAGCAAGTTTGGAAAGAACCCCAATTTTCTCTCGAGTCACTCTGTGACAGCGCTCCCT	3180
Db	3121	TCAGCAAGTTTGGAAAGAACCCCAATTTTCTCTCGAGTCACTCTGTGACAGCGCTCCCT	3180
OY	3181	CTGCTACTCCATCTTGAAAGCCAAAGAACGACGGATGTCCGTGGGGGCCAAGGGCGCTGC	3240
Db	3181	CTGCTACTCCATCTTGAAAGCCAAAGAACGACGGATGTCCGTGGGGGCCAAGGGCGCTGC	3240
OY	3241	CGGCGCTCTGCGCTCCGAGGCGGAGCTGGCTGGGCAACCAAGCAATTCGCTCAAGCT	3300
Db	3241	CGGCGCTCTGCGCTCCGAGGCGGAGCTGGCTGGGCAACCAAGCAATTCGCTCAAGCT	3300
OY	3301	GACTCGAACCCGCTGTCACTTACGTGCCACTTCTGGGGTCACTCAGGACAGGCCACAGACGA	3360
Db	3301	GACTCGAACCCGCTGTCACTTACGTGCCACTTCTGGGGTCACTCAGGACAGGCCACAGACGA	3360
OY	3361	GCTGAGTGTGAAGCTCCCGGGGAGAGAGCTGTACTGTGCGCTGGAGGCTCGTAGCCAAACCCGGC	3420
Db	3361	GCTGAGTGTGAAGCTCCCGGGGAGAGAGCTGTACTGTGCGCTGGAGGCTCGTAGCCAAACCCGGC	3420
OY	3421	ACTGCCCTCAGACTTCAAAAGCAATCTCTGTGAGCTGTATGGCCACCGCCCAACACAGGCCGA	3480
Db	3421	ACTGCCCTCAGACTTCAAAAGCAATCTCTGTGAGCTGTATGGCCACCGCCCAACACAGGCCGA	3480
OY	3481	GAGCAGACACCCAGAGCCTCTGTCAAGCCCGGCTCTTACGTCCAGAGGAGGAGGGGCGGCTC	3540
Db	3481	GAGCAGACACCCAGAGCCTCTGTCAAGCCCGGCTCTTACGTCCAGAGGAGGAGGGGCGGCTC	3540
OY	3541	CACACCCAGGCGCGCACCGCTGGAGGTCTGAGGCTGTAGTAGTGTGTTGGCCGAGGCTTG	3600
Db	3541	CACACCCAGGCGCGCACCGCTGGAGGTCTGAGGCTGTAGTAGTGTGTTGGCCGAGGCTTG	3600
OY	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGCTGAGGCTGTAGGGAATGTCTCAAGCGGACT	3660
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGCTGAGGCTGTAGGGAATGTCTCAAGCGGACT	3660
OY	3661	GAGGTCTCAGACACCTGCGCTTTCATCTTCCCAAGCTGCGGGCTCCGCTCAACCCCA	3720
Db	3661	GAGGTCTCAGACACCTGCGCTTTCATCTTCCCAAGCTGCGGGCTCCGCTCAACCCCA	3720

QY	3721	GGGCCAGCTTTTCCACACAGAGACCCGGCTTCACATCCCAATGAAATAGTCATCC	3780
QY	3721	GGGCCAGCTTTTCCACACAGAGACCCGGCTTCACATCCCAATGAAATAGTCATCC <td>3780</td>	3780
Db	3721	GGGCCAGCTTTTCCACACAGAGACCCGGCTTCACATCCCAATGAAATAGTCATCC	3780
QY	3781	CCGAGTTGCCATTTGTTCACCCCTCTGCGCCTCTCTTTGCTTCCATCCCAACATCC	3840
Db	3781	CCGAGTTGCCATTTGTTCACCCCTCTGCGCCTCTCTTTGCTTCCATCCCAACATCC	3840
QY	3841	AGGTGGAGACCTTGAGAGAGGACCCCTGGAGGCTCTGGGAATTTTGAGTGAACAAAGGTGG	3900
Db	3841	AGGTGGAGACCTTGAGAGAGGACCCCTGGAGGCTCTGGGAATTTTGAGTGAACAAAGGTGG	3900
QY	3901	CCCTGTACACAGCCGACGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAATTTGGGGG	3960
Db	3901	CCCTGTACACAGCCGACGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAATTTGGGGG	3960
QY	3961	GAGGTCTGTGGGAGTAAATACTCAATATATGAGTTTTCAGTTTGGAAAAAA	4015
Db	3961	GAGGTCTGTGGGAGTAAATACTCAATATATGAGTTTTCAGTTTGGAAAAAA	4015

RESULT 4

US-09-953-052-1
Application MS/09953052

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

TITLE OF INVENTION: Antisense Compositions for Detecting and

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA

APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/974,588
FILING DATE: 13-NOV-1997

```

?      APPLICATION NUMBER: WO PCT/US97/17618
?      FILING DATE: 01-OCT-1997
?      APPLICATION NUMBER: WO PCT/US97/17885
?      FILING DATE: 01-OCT-1997
?      ATTORNEY/AGENT INFORMATION:
?          NAME: Parent, Annette S.
?          REGISTRATION NUMBER: 42,058
?          REFERENCE/DOCKET NUMBER: 015389-003600US
?      TELECOMMUNICATION INFORMATION:
?          TELEPHONE: (415) 576-0200
?          TELEFAX: (415) 576-0300
?      INFORMATION FOR SEQ ID NO: 1:
?          SEQUENCE CHARACTERISTICS:
?              LENGTH: 4015 base pairs
?              TYPE: nucleic acid
?              STRANDEDNESS: single
?              TOPOLOGY: linear
?              MOLECULE TYPE: cDNA
?          FEATURE:
?              NAME/KEY: CDS
?              LOCATION: 56..3454
?              OTHER INFORMATION: /product= "human telomerase reverse
?                  transcriptase (hTERT)"
?      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
?      US-09-953-052-1

```

SEQUENCE DESCRIPTION:	SEQ ID NO: 1:
US-09-953-052-1	

Query Match	100.0%;	Score 4015;	DB 9;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4015;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

[illegible]

QY 661 CTGGAACCATAGGCTCAGGGAGGCGGGGTCCCTGGGGCTGGCAAGCCCGGGGTGGAG 720
| | | | |
Db 661 CTGGAACCATAGGCTCAGGGAGGCGGGGTCCCTGGGGCTGGCAAGCCCGGGGTGGAG 720
| | | | |
QY 721 GAGGCGCGGGGCAAGTGCAGCGGAGAGTCTGCGTTGCCAAGAGGCGCAGGCGTGGCCG 780
| | | | |
Db 721 GAGGCGCGGGGCAAGTGCAGCGGAGAGTCTGCGTTGCCAAGAGGCGCAGGCGTGGCCG 780
| | | | |
QY 781 TCCCTCTGAGCGGAGCGGAGCGCGCTTGGGCAAGGGGTCTTGGGCCACCCGCGAGAGC 840
| | | | |
Db 781 TCCCTCTGAGCGGAGCGGAGCGCGCTTGGGCAAGGGGTCTTGGGCCACCCGCGAGAGC 840
| | | | |
QY 841 GGGTGGACCGAGTGAACCGGTGTTCTGTGTGGTGTACCTTGCAGAGCCCGCGAAGAAAC 900
| | | | |
Db 841 GGGTGGACCGAGTGAACCGGTGTTCTGTGTGGTGTACCTTGCAGAGCCCGCGAAGAAAC 900
| | | | |
QY 901 CACCTCTTGGAGAGGTGCGCTCTTGGCAAGCGCCACTCCACCCATCCGTGGGCGGCA 960
| | | | |
Db 901 CACCTCTTGGAGAGGTGCGCTCTTGGCAAGCGCCACTCCACCCATCCGTGGGCGGCA 960
| | | | |
QY 961 GCAACAACGCGGAGCGCCCAATCCATCGCGGCAACGCTCCCTGGGACAAGCTTTGTCC 1020
| | | | |
Db 961 GCAACAACGCGGAGCGCCCAATCCATCGCGGCAACGCTCCCTGGGACAAGCTTTGTCC 1020
| | | | |
QY 1021 CCGGGGTAGCGCGAGACCAAGCATCTTCTTACTCTTCAAGGAGCAAGAGAGAGCTGGG 1080
| | | | |
Db 1021 CCGGGGTAGCGCGAGACCAAGCATCTTCTTACTCTTCAAGGAGCAAGAGAGAGCTGGG 1080
| | | | |
QY 1081 GCGCTCTTCTTACTTCTAGCTCTTGAAGGCGCAGCTGAGCTGGAGCTCGAGAGCTCTGGA 1140
| | | | |
Db 1081 GCGCTCTTCTTACTTCTAGCTCTTGAAGGCGCAGCTGAGCTGGAGCTCGAGAGCTCTGGA 1140
| | | | |
QY 1141 GACCAATCTTCTTGGGTTCCAGGCGCTGATGCCAGGAACTCCCCGAGGTTGCCGCTT 1200
| | | | |
Db 1141 GACCAATCTTCTTGGGTTCCAGGCGCTGATGCCAGGAACTCCCCGAGGTTGCCGCTT 1200
| | | | |
QY 1201 GCGCCAGCGCTTCTGAGCAATCGGCGCCCTGTTTCTTGAAGCTGTGGAGAACAGCGGCA 1260
| | | | |
Db 1201 GCGCCAGCGCTTCTGAGCAATCGGCGCCCTGTTTCTTGAAGCTGTGGAGAACAGCGGCA 1260
| | | | |
QY 1261 GTGCGCCCTTACGGGAGTCTCTTCAAGAGAGAGCTGCGCTGCGAGCTGCGGTCAACCCAGC 1320
| | | | |
Db 1261 GTGCGCCCTTACGGGAGTCTCTTCAAGAGAGAGCTGCGCTGCGAGCTGCGGTCAACCCAGC 1320
| | | | |
QY 1321 AGCGGCTGTCTGTGCGCGGAGAGGCCCAAGGCTGTGGCGGCGCCGAGAGAGAGA 1380
| | | | |
Db 1321 AGCGGCTGTCTGTGCGCGGAGAGGCCCAAGGCTGTGGCGGCGCCGAGAGAGAGA 1380
| | | | |
QY 1381 CACAGACCCCCGCTGCTGTGTGAGTGTCTCCGCGAGACAGAGAGCCCTTGGAGGTGTA 1440
| | | | |
Db 1381 CACAGACCCCCGCTGCTGTGTGAGTGTCTCCGCGAGACAGAGAGCCCTTGGAGGTGTA 1440
| | | | |
QY 1441 CGGCTTCTGAGCGGAGCTGCTGCGCGGAGTGGGCCCCAGGCTCTTGGGGCTCCAGGGA 1500
| | | | |
Db 1441 CGGCTTCTGAGCGGAGCTGCTGCGCGGAGTGGGCCCCAGGCTCTTGGGGCTCCAGGGA 1500
| | | | |
QY 1501 CAAAGAACGCGCTTCTTCAAGAACCAAGAAATTCACTCTCCCTGGGAGAGATGCCAA 1560
| | | | |
Db 1501 CAAAGAACGCGCTTCTTCAAGAACCAAGAAATTCACTCTCCCTGGGAGAGATGCCAA 1560
| | | | |
QY 1561 GCTTCTGCTGCAAGAGCTGAGCTGGAAGATGAGAGCTGCGGAGATGCGCTTGGTGGCAG 1620
| | | | |
Db 1561 GCTTCTGCTGCAAGAGCTGAGCTGGAAGATGAGAGCTGCGGAGATGCGCTTGGTGGCAG 1620
| | | | |
QY 1621 GAGCCAGAGGAGTGGCTGTGTTCCGGCCGAGAGACCTGTGCGTGAAGAGATCTTGGC 1680
| | | | |
Db 1621 GAGCCAGAGGAGTGGCTGTGTTCCGGCCGAGAGACCTGTGCGTGAAGAGATCTTGGC 1680
| | | | |
QY 1681 CAAATTCTGCACTGAGCTGATGATGTGTAAGTGTGAGCTGTGAGCTGTCAAGTCTTTTAA 1740
| | | | |
Db 1681 CAAATTCTGCACTGAGCTGATGATGTGTAAGTGTGAGCTGTGAGCTGTCAAGTCTTTTAA 1740
| | | | |
QY 1740 CAAATTCTGCACTGAGCTGATGATGTGTAAGTGTGAGCTGTGAGCTGTCAAGTCTTTTAA 1740
| | | | |
Db 1740 CAAATTCTGCACTGAGCTGATGATGTGTAAGTGTGAGCTGTGAGCTGTCAAGTCTTTTAA 1740
| | | | |

QY 1741 TGTACAGAGACACAGTTTCAAAAGAACAGGCTCTTTTCTACCCGAAAGATGTCTGAG 1800
| | | | |
Db 1741 TGTACAGAGACACAGTTTCAAAAGAACAGGCTCTTTTCTACCCGAAAGATGTCTGAG 1800
| | | | |
QY 1801 CAAATTGCAAAAGATTTGAAATCAGACAGCACTTGAAGAGGTGCACTGCGGAGCTGTG 1860
| | | | |
Db 1801 CAAATTGCAAAAGATTTGAAATCAGACAGCACTTGAAGAGGTGCACTGCGGAGCTGTG 1860
| | | | |
QY 1861 GGAAGCAGAGGTGAGGAGATCCGGAAGAGGAGGCGGCGGCGGCTGTGAGCTGCAAGCTCCG 1920
| | | | |
Db 1861 GGAAGCAGAGGTGAGGAGATCCGGAAGAGGAGGCGGCGGCGGCTGTGAGCTGCAAGCTCCG 1920
| | | | |
QY 1921 CTTTATCCCAAGGCTGAGAGGCTGCGGCGGAGTTGTGAACATGAGTACTAGTGTGGAGC 1980
| | | | |
Db 1921 CTTTATCCCAAGGCTGAGAGGCTGCGGCGGAGTTGTGAACATGAGTACTAGTGTGGAGC 1980
| | | | |
QY 1981 CAGAAAGTTCCGAGAGAAAGAGGAGCGAGGCTCTCACTTGAAGGTGAAGGCACTGTT 2040
| | | | |
Db 1981 CAGAAAGTTCCGAGAGAAAGAGGAGCGAGGCTCTCACTTGAAGGTGAAGGCACTGTT 2040
| | | | |
QY 2041 CAGCTGTCTCAATCAGAGAGGAGCGGCGGCGGCGGCGGCTCTTGGGCGCTCTGTGTGGG 2100
| | | | |
Db 2041 CAGCTGTCTCAATCAGAGAGGAGCGGCGGCGGCGGCGGCTCTTGGGCGCTCTGTGTGGG 2100
| | | | |
QY 2101 CCGGAGCAATATCCAGAGGAGCGCTGAGCACTTGTGTGCTGTGTGCGGAGCCAGGAGCC 2160
| | | | |
Db 2101 CCGGAGCAATATCCAGAGGAGCGCTGAGCACTTGTGTGCTGTGTGCGGAGCCAGGAGCC 2160
| | | | |
QY 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGAGGCTGACAGCACTATCCCA 2220
| | | | |
Db 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGAGGCTGACAGCACTATCCCA 2220
| | | | |
QY 2221 GGAAGAGCTCAGAGAGGTATGTGAGAGATCATCAAAACCCAGAAACAGTACTGTGGGG 2280
| | | | |
Db 2221 GGAAGAGCTCAGAGAGGTATGTGAGAGATCATCAAAACCCAGAAACAGTACTGTGGGG 2280
| | | | |
QY 2281 TCGGATAGCGGTGTCTCAAGAGGCGGCGGCTGAGGAGAGGCTTCAAGAGGCA 2340
| | | | |
Db 2281 TCGGATAGCGGTGTCTCAAGAGGCGGCGGCTGAGGAGAGGCTTCAAGAGGCA 2340
| | | | |
QY 2341 CGTCTCTACCTTGAAGAGCTTCAAGCGCTGATGAGAGAGTGTGTGCTGACCTGAGGA 2400
| | | | |
Db 2341 CGTCTCTACCTTGAAGAGCTTCAAGCGCTGATGAGAGAGTGTGTGCTGACCTGAGGA 2400
| | | | |
QY 2401 GACAGCGCGCTGAGAGAGTGTGTGTGATGAGAGAGTGTGTGATGAGAGAGTGTGTGAT 2460
| | | | |
Db 2401 GACAGCGCGCTGAGAGAGTGTGTGTGATGAGAGAGTGTGTGATGAGAGAGTGTGTGAT 2460
| | | | |
QY 2461 CAGTGGCGCTTGAAGAGTGTGTGTGATGAGAGAGTGTGTGATGAGAGAGTGTGTGAT 2520
| | | | |
Db 2461 CAGTGGCGCTTGAAGAGTGTGTGTGATGAGAGAGTGTGTGATGAGAGAGTGTGTGAT 2520
| | | | |
QY 2521 CAAATCTACAGTCAAGTGCAGAGGAGATCCGAGAGGCTTCACTCTTCCAGCTGTCTG 2580
| | | | |
Db 2521 CAAATCTACAGTCAAGTGCAGAGGAGATCCGAGAGGCTTCACTCTTCCAGCTGTCTG 2580
| | | | |
QY 2581 CAGCTGTGTCTACGCGGAGATGAGAGAACAGCTGTTTGGGAGATTTGGCGGAGCGGCT 2640
| | | | |
Db 2581 CAGCTGTGTCTACGCGGAGATGAGAGAACAGCTGTTTGGGAGATTTGGCGGAGCGGCT 2640
| | | | |
QY 2641 GCTCTGCGGTGTTGAGATGATTTCTGTGTGATGACCTCACTCAACCCAGCGGAAAC 2700
| | | | |
Db 2641 GCTCTGCGGTGTTGAGATGATTTCTGTGTGATGACCTCACTCAACCCAGCGGAAAC 2700
| | | | |
QY 2701 CTTCTCAGAGACCTTGTGTGAGAGTGTCTCTGAGTATGAGCTGTGTGAGTGTGTGAG 2760
| | | | |
Db 2701 CTTCTCAGAGACCTTGTGTGAGAGTGTCTCTGAGTATGAGCTGTGTGAGTGTGTGAG 2760
| | | | |
QY 2761 GACAGTGTGAACTTCTCTGTGAGAGAGAGGCTTGGTGTGAGAGGCTTGTGTGAGT 2820
| | | | |
Db 2761 GACAGTGTGAACTTCTCTGTGAGAGAGAGGCTTGGTGTGAGAGGCTTGTGTGAGT 2820
| | | | |
QY 2821 GCGGCGCAGCGGCTATTCCTGCTGTGAGAGGCTGTGATGAGTATCCGGAACCTGAGGT 2880
| | | | |
Db 2821 GCGGCGCAGCGGCTATTCCTGCTGTGAGAGGCTGTGATGAGTATCCGGAACCTGAGGT 2880
| | | | |

DB 2821 GCGGCGCCACGCGCTATTCCTCCGAGTGGCGCTGCTGAGTACCAGACCTTGAGCT 2880
QY 2881 GCAGAGGACTACTCCAGCTATGCGGAGCTTCATCAGAGCCAGTCTCACCCTCAACCG 2940
DB 2881 GCAGAGGACTACTCCAGCTATGCGGAGCTTCATCAGAGCCAGTCTCACCCTCAACCG 2940
QY 2941 CCGCTTCAGAGCTGGAGAGACATGCGTGGCAACTCTTTGGGGTCTTTCGGCTGAAAGT 3000
DB 2941 CCGCTTCAGAGCTGGAGAGACATGCGTGGCAACTCTTTGGGGTCTTTCGGCTGAAAGT 3000
QY 3001 TCACAGGCTTTCTGATTTGAGAGTGAACAGCTCCAGAGGCTGAGACCAATCTA 3060
DB 3001 TCACAGGCTTTCTGATTTGAGAGTGAACAGCTCCAGAGGCTGAGACCAATCTA 3060
QY 3061 CAAGATCTCTGCTGAGGCGTACAGATTCAAGATGTGCTGAGCTCCATTCA 3120
DB 3061 CAAGATCTCTGCTGAGGCGTACAGATTCAAGATGTGCTGAGCTCCATTCA 3120
QY 3121 TCACAGATTTGAGAGACCCACATTTTCTGCGGCTATCTGACACCGGCTCCCT 3180
DB 3121 TCACAGATTTGAGAGACCCACATTTTCTGCGGCTATCTGACACCGGCTCCCT 3180
QY 3181 CTGCTATCTCCATCTCTGAAGCAAGACGAGGATGCTGCGGCGCAAGGCGCGC 3240
DB 3181 CTGCTATCTCCATCTCTGAAGCAAGACGAGGATGCTGCGGCGCAAGGCGCGC 3240
QY 3241 CCGGCTCTCTGCTCCAGAGGCGCTGAGTGGCTGTGCTGACCAAGCATTTCTGCTCAAGCT 3300
DB 3241 CCGGCTCTCTGCTCCAGAGGCGCTGAGTGGCTGTGCTGACCAAGCATTTCTGCTCAAGCT 3300
QY 3301 GACTGCAACCGTGTCACTGACGTCAGTCTGAGGCTGACTGAGACAGCCAGCGCA 3360
DB 3301 GACTGCAACCGTGTCACTGACGTCAGTCTGAGGCTGACTGAGACAGCCAGCGCA 3360
QY 3361 GCTGAGTGGAGAGTCCCGGAGAGAGCGCTGACTGCTGAGGCGCGCAAGCCGCGC 3420
DB 3361 GCTGAGTGGAGAGTCCCGGAGAGAGCGCTGACTGCTGAGGCGCGCAAGCCGCGC 3420
QY 3421 ACTGCTCTCAAGCTTCAAGACATCTGAGTGAAGTGGCAACCGCCAGAGGCGCA 3480
DB 3421 ACTGCTCTCAAGCTTCAAGACATCTGAGTGAAGTGGCAACCGCCAGAGGCGCA 3480
QY 3481 GAGCAGACACGAGCGCTGTCAAGCGCGGCTCTACGTCCAGAGAGGAGGCGCGC 3540
DB 3481 GAGCAGACACGAGCGCTGTCAAGCGCGGCTCTACGTCCAGAGAGGAGGCGCGC 3540
QY 3541 CACACCGAGGCGCGAGCGCTGAGGCTGAGGCTGAGTGAAGTGGCGCGAGGCGCTG 3600
DB 3541 CACACCGAGGCGCGAGCGCTGAGGCTGAGGCTGAGTGAAGTGGCGCGAGGCGCTG 3600
QY 3601 CATGTCGCGCTGAAGGCTGAGTGGCGGCTGAGGCTGAGGAGGCTGAGGAGGCT 3660
DB 3601 CATGTCGCGCTGAAGGCTGAGTGGCGGCTGAGGCTGAGGAGGCTGAGGAGGCT 3660
QY 3661 GAGTGTCCAGACACCTGCTGCTTCACTTCCCAAGAGTGGCGCTGAGGCTGAGGCT 3720
DB 3661 GAGTGTCCAGACACCTGCTGCTTCACTTCCCAAGAGTGGCGCTGAGGCTGAGGCT 3720
QY 3721 GGGGCGAGCTTTCTGACAGAGAGCGGCTTCCATCCCAATAGAAATGTCATCC 3780
DB 3721 GGGGCGAGCTTTCTGACAGAGAGCGGCTTCCATCCCAATAGAAATGTCATCC 3780
QY 3781 CGAGATTTGCGCATGTTTCAAGCTGCGCTGCTGCTTTCATCCACCCACCATCC 3840
DB 3781 CGAGATTTGCGCATGTTTCAAGCTGCGCTGCTGCTTTCATCCACCCACCATCC 3840
QY 3841 AGGTGAGAGCCTGAGAGAGACCTTGGAGGCTTGGAGATTTGGAGTCAACAAAGTGTG 3900
DB 3841 AGGTGAGAGCCTGAGAGAGACCTTGGAGGCTTGGAGATTTGGAGTCAACAAAGTGTG 3900
QY 3901 CCTGTACACAGGCGAGAGACCTTGGAGCTGAGTGGGGGCTTGGAGGCTCAATTTGGGGG 3960
DB 3901 CCTGTACACAGGCGAGAGACCTTGGAGCTGAGTGGGGGCTTGGAGGCTCAATTTGGGGG 3960

DB 3901 CCTGTACACAGGCGAGAGACCTTGGAGCTGAGTGGGGGCTTGGAGGCTCAATTTGGGGG 3960
QY 3961 GAGGTGCTGGGGAGTAAATTAATGATATATAGATTTTCAAGTTTGAAGAAAA 4015
DB 3961 GAGGTGCTGGGGAGTAAATTAATGATATATAGATTTTCAAGTTTGAAGAAAA 4015
RESULT 5
US-10-053-758-224
Sequence 224, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Ingriner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
Query Match 100.0%; Score 4015; DB 14; Length 4015;


```

; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

```

```

Query Match      100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GCAGCGCTGCTCTCTGCGCAGCGTGGAGAGCCCTGAGCCCGGACCCCGGAGTGGC 60
DB 1 GCAGCGCTGCTCTCTGCGCAGCGTGGAGAGCCCTGAGCCCGGACCCCGGAGTGGC 60
QY 61 GCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGAGCCACTACCGAGGTGCT 120
DB 61 GCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGAGCCACTACCGAGGTGCT 120
QY 121 GCGCGCTGCGCAGCTTGTGTGCGGCGCTGGGGCCCGAGGCTGGCTGTGAGCGCG 180
DB 121 GCGCGCTGCGCAGCTTGTGTGCGGCGCTGGGGCCCGAGGCTGGCTGTGAGCGCG 180
QY 181 GGAACCGGAGGCTTTCGCGCGCTGGTGGCCAGTGTCTGTGTGGTGGCTTGGGAGCG 240
DB 181 GGAACCGGAGGCTTTCGCGCGCTGGTGGCCAGTGTCTGTGTGGTGGCTTGGGAGCG 240
QY 241 ACGGCGCGCCCGCCCGCCCTCTCTTCCGCGCAGTGTCTGTGCTGAAGAGCTGTGAGC 300
DB 241 ACGGCGCGCCCGCCCGCCCTCTCTTCCGCGCAGTGTCTGTGCTGAAGAGCTGTGAGC 300
QY 301 CCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGGAGAACTGTGCTTGGCTTGGC 360
DB 301 CCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGGAGAACTGTGCTTGGCTTGGC 360
QY 361 GGTGCTGAGAGGCGCGCGCGCGCGCGCGCGCGCTTCAACAGAGGTGGGAGCTA 420
DB 361 GGTGCTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCTTCAACAGAGGTGGGAGCTA 420
QY 421 CCTGCGCAACACGAGTGAACGACGCTGCGGAGAGCGGAGCGTGGGAGCTGTGCTGCG 480
DB 421 CCTGCGCAACACGAGTGAACGACGCTGCGGAGAGCGGAGCGTGGGAGCTGTGCTGCG 480
QY 481 CCGCGTGGGAGAGCGTGTGCTGCTGCTGCTGCGACGCTGCGGCTCTTTGTGTGGT 540
DB 481 CCGCGTGGGAGAGCGTGTGCTGCTGCTGCTGCGACGCTGCGGCTCTTTGTGTGGT 540
QY 541 GGTGCTCAGCTGCTGCTACAGAGTGTGCGGCGCGCGCTGTACAGCTGCGGCTGCCAC 600
DB 541 GGTGCTCAGCTGCTGCTACAGAGTGTGCGGCGCGCGCTGTACAGCTGCGGCTGCCAC 600
QY 601 TCAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGTGCAGAGCGG 660
DB 601 TCAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGAGTGCAGAGCGG 660
QY 661 CTGGAACCAATAGCTGAGGAGGCGCGGAGTCCCTGCGGAGCTTGCAGCGCGGAGT 720
DB 661 CTGGAACCAATAGCTGAGGAGGCGCGGAGTCCCTGCGGAGCTTGCAGCGCGGAGT 720
QY 721 GAGGCGCGGAGGAGTGTGCGAGCGAGTGTGCGGCTTGCAGAGCGCGAGGCTGTGGCC 780
DB 721 GAGGCGCGGAGGAGTGTGCGAGCGAGTGTGCGGCTTGCAGAGCGCGAGGCTGTGGCC 780
QY 781 TGCGCGCTGAGCGGAGCGAGCGCGCGCTGTGGGAGGAGTCTGTGGCCCGAGAGCG 840
DB 781 TGCGCGCTGAGCGGAGCGAGCGCGCGCTGTGGGAGGAGTCTGTGGCCCGAGAGCG 840
QY 841 GCGTGAACCGAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GCGTGAACCGAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900

```

```

QY 901 CACCTCTTGAAGGAGCGCTCTGTGCAAGCGCCACTCCACCCATCCGTGGGCGGCA 960
DB 901 CACCTCTTGAAGGAGCGCTCTGTGCAAGCGCCACTCCACCCATCCGTGGGCGGCA 960
QY 961 GCAACAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGTGTC 1020
DB 961 GCAACAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGTGTC 1020
QY 1021 CCGGAGTACGCGGAGAGCAACACACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1080
DB 1021 CCGGAGTACGCGGAGAGCAACACACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1081 GCCCTCTCTCTACTGAGCTCTGTGAGGCGCGAGCTGTGAGGCTGTGAGGCTGTGGA 1140
DB 1081 GCCCTCTCTCTACTGAGCTCTGTGAGGCGCGAGCTGTGAGGCTGTGAGGCTGTGGA 1140
QY 1141 GACCATCTTCTGTGGTTCAGGCGCTTGAATGCCAGGAGTCTCCCGAGGTTGCCGCTT 1200
DB 1141 GACCATCTTCTGTGGTTCAGGCGCTTGAATGCCAGGAGTCTCCCGAGGTTGCCGCTT 1200
QY 1201 GCGCCAGCGCTACTGAGCAATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
DB 1201 GCGCCAGCGCTACTGAGCAATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261 GTGCGCGCTTACGAGGAGCGCTCTCAAGAGCGAGCGCGCGAGCTGTGAGTCAAGCCAGC 1320
DB 1261 GTGCGCGCTTACGAGGAGCGCTCTCAAGAGCGAGCGCGCGAGCTGTGAGTCAAGCCAGC 1320
QY 1321 AGCGGAGTGTGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGAG 1380
DB 1321 AGCGGAGTGTGTGTGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGAG 1380
QY 1381 CACAGACCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
DB 1381 CACAGACCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 1441 CGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
DB 1441 CGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
QY 1501 CAACGAGCGCGCTTCTCTAGAGAACCAAGAGTTCATCTCTCTGGGAGAGCATCCAA 1560
DB 1501 CAACGAGCGCGCTTCTCTAGAGAACCAAGAGTTCATCTCTCTGGGAGAGCATCCAA 1560
QY 1561 GCTTCTGCTGCAAGAGCTGACGTGAATGAGCGTGGAGCTGTGCTGTGCTGTGCGAG 1620
DB 1561 GCTTCTGCTGCAAGAGCTGACGTGAATGAGCGTGGAGCTGTGCTGTGCTGTGCGAG 1620
QY 1621 GAGCCAGGAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
DB 1621 GAGCCAGGAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 1681 CAAGTCTCTGCACTGCTGATGATGTGATGCTGTGAGTGTCTAGGCTCTTCTTTA 1740
DB 1681 CAAGTCTCTGCACTGCTGATGATGTGATGCTGTGAGTGTCTAGGCTCTTCTTTA 1740
QY 1741 TGTCAAGAGACACGCTTCAAAAGAACAGGCTCTTTTCTTCAAGAGAGTGTCTGAG 1800
DB 1741 TGTCAAGAGACACGCTTCAAAAGAACAGGCTCTTTTCTTCAAGAGAGTGTCTGAG 1800
QY 1801 CAAGTTGCAAAACATTTGAAATGACAGCACTTGAAGAGGAGTGTGCGGAGCTGTC 1860
DB 1801 CAAGTTGCAAAACATTTGAAATGACAGCACTTGAAGAGGAGTGTGCGGAGCTGTC 1860
QY 1861 GGAAGAGAGTCTAGGAGCATCTGGGAGAGCGAGCGCGCGCTGTGAGCTGTCCAGCTCCG 1920
DB 1861 GGAAGAGAGTCTAGGAGCATCTGGGAGAGCGAGCGCGCGCTGTGAGCTGTCCAGCTCCG 1920
QY 1921 CTTTATCCCAAGCTGACGAGGCTGTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
DB 1921 CTTTATCCCAAGCTGACGAGGCTGTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980

```

QY 1981 CAGAGCTTCCGAGAGAAAGAGGCGCAGAGCTTCACTTGAAGGTGAAGCACTTT 2040
 Db 1981 CAGAGCTTCCGAGAGAAAGAGGCGCAGAGCTTCACTTGAAGGTGAAGCACTTT 2040
 QY 2041 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2100
 Db 2041 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2100
 QY 2101 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2160
 Db 2101 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2160
 QY 2161 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2220
 Db 2161 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2220
 QY 2221 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2280
 Db 2221 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2280
 QY 2281 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2340
 Db 2281 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2340
 QY 2341 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2400
 Db 2341 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2400
 QY 2401 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2460
 Db 2401 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2460
 QY 2461 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2520
 Db 2461 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2520
 QY 2521 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2580
 Db 2521 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2580
 QY 2581 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2640
 Db 2581 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2640
 QY 2641 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2700
 Db 2641 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2700
 QY 2701 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2760
 Db 2701 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2760
 QY 2761 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2820
 Db 2761 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2820
 QY 2821 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2880
 Db 2821 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2880
 QY 2881 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2940
 Db 2881 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 2940
 QY 2941 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3000
 Db 2941 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3000
 QY 3001 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3060
 Db 3001 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3060
 QY 3061 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3120

Db 3061 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3120
 QY 3121 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3180
 Db 3121 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3180
 QY 3181 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3240
 Db 3181 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3240
 QY 3241 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3300
 Db 3241 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3300
 QY 3301 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3360
 Db 3301 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3360
 QY 3361 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3420
 Db 3361 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3420
 QY 3421 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3480
 Db 3421 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3480
 QY 3481 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3540
 Db 3481 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3540
 QY 3541 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3600
 Db 3541 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3600
 QY 3601 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3660
 Db 3601 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3660
 QY 3661 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3720
 Db 3661 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3720
 QY 3721 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3780
 Db 3721 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3780
 QY 3781 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3840
 Db 3781 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3840
 QY 3841 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3900
 Db 3841 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3900
 QY 3901 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3960
 Db 3901 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 3960
 QY 3961 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 4015
 Db 3961 CAGAGCTTCACTTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGT 4015

RESULT 7

US-10-054-295-224

 / Sequence 224, Application US/10054295
 / Publication No. US2003004953A1

GENERAL INFORMATION:

 APPLICANT: Cech, Thomas R.
 Ligner, Joachim
 Nakamura, Toru
 Chapman, Karen B.

Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-295-224
Query Match 100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

241 ACGGCGCCCCCGCGCCCTCTCTCCGACGAGTGTCTCTGAGAGAGCTGTGCG 300
241 ACGGCGCCCCCGCGCCCTCTCTCCGACGAGTGTCTCTGAGAGAGCTGTGCG 300
301 CCGAGTGTGACAGAGCTGTGTGAGCGCGCGCGAGAAAGTGTGCTTGGCTTGGC 360
301 CCGAGTGTGACAGAGCTGTGTGAGCGCGCGCGAGAAAGTGTGCTTGGCTTGGC 360
361 GCTGTGAGACGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
361 GCTGTGAGACGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
421 CCGGCGCAACAGAGTGTGACGAGCTGTGAGGGGGGGGGGGGGGGGGGGGGGGGG 480
421 CCGGCGCAACAGAGTGTGACGAGCTGTGAGGGGGGGGGGGGGGGGGGGGGGGGG 480
481 CCGGCGTGTGAGACGAGCTGTGTGACCTGTGTGACGCTGTGTGTGTGTGTGTGT 540
481 CCGGCGTGTGAGACGAGCTGTGTGACCTGTGTGACGCTGTGTGTGTGTGTGTGT 540
541 GGTCTCCAGCTGTGCTTACAGAGTGTGTGCGGGGGGGGGGGGGGGGGGGGGGGGG 600
541 GGTCTCCAGCTGTGCTTACAGAGTGTGTGCGGGGGGGGGGGGGGGGGGGGGGGGG 600
601 TCAGGGCGGG 660
601 TCAGGGCGGG 660
661 CTGGAACCATAGCTGTGAGGAGGCGGGGGTCCCTGTGGGCTTCCAGCCCGGGTGTGAG 720
661 CTGGAACCATAGCTGTGAGGAGGCGGGGGTCCCTGTGGGCTTCCAGCCCGGGTGTGAG 720
721 GAGGGCGGGGGGAGTGTGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
721 GAGGGCGGGGGGAGTGTGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
781 TGGCCCTGAGCGGAGCGGAGCGCGGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
781 TGGCCCTGAGCGGAGCGGAGCGCGGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
841 GCGTGTGACGAGTGTGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
841 GCGTGTGACGAGTGTGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
901 CACTCTTTGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
901 CACTCTTTGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
961 GACACACGG 1020
961 GACACACGG 1020
1021 CCGGAGTGTGAGCGGAGACCAAGCACTTCTCTTACTCTGAGGAGCAAGAGAGCTGTGCG 1080
1021 CCGGAGTGTGAGCGGAGACCAAGCACTTCTCTTACTCTGAGGAGCAAGAGAGCTGTGCG 1080
1081 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
1081 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
1081 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
1081 GCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
1141 GACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
1141 GACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
1141 GACCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
1201 GCGCCAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
1201 GCGCCAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
1261 GTGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
1261 GTGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320

QY 1321 AGCCGAGTCTGATCCCGAGAGAACCCAGAGGCTCTGTGGCGGCCCGGAGAGAGAGA 1380
DB 1321 AGCCGAGTCTGATCCCGAGAGAACCCAGAGGCTCTGTGGCGGCCCGGAGAGAGAGA 1380
QY 1381 CAGAGACCCCGGCTGCTGTGTGAGCTGCTCCGACAGACAGAGCCCTCTGGAGGTGTA 1440
DB 1381 CAGAGACCCCGGCTGCTGTGTGAGCTGCTCCGACAGACAGAGCCCTCTGGAGGTGTA 1440
QY 1441 CGGCTTCTGAGGAGGCTGCTGAGGCGGCTGAGTGGCCCGAGGCTCTGGAGGTGTA 1500
DB 1441 CGGCTTCTGAGGAGGCTGCTGAGGCGGCTGAGTGGCCCGAGGCTCTGGAGGTGTA 1500
QY 1501 CAAAGAACCGGCTTCTCTAGAGAACCAAGAAATCTCTCTGGAGAGATGCCAA 1560
DB 1501 CAAAGAACCGGCTTCTCTAGAGAACCAAGAAATCTCTCTGGAGAGATGCCAA 1560
QY 1561 GCTCTGCTGAGAGAGCTGAGCTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 GCTCTGCTGAGAGAGCTGAGCTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 GAGCCGAGGAGTGGCTGCTGCTGAGGCGAGAGACAGCTCTGCTGAGAGAGATCTGGC 1680
DB 1621 GAGCCGAGGAGTGGCTGCTGCTGAGGCGAGAGACAGCTCTGCTGAGAGAGATCTGGC 1680
QY 1681 CAAAGTCTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 CAAAGTCTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 TGTTCAGGAGAACCAAGCTTTTAAAGAACAGAGCTTTTCTAACGAGAGAGTCTGGAG 1800
DB 1741 TGTTCAGGAGAACCAAGCTTTTAAAGAACAGAGCTTTTCTAACGAGAGAGTCTGGAG 1800
QY 1801 CAAAGTCTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 1801 CAAAGTCTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 GGAAGCAGAGAGTCAAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 GGAAGCAGAGAGTCAAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 CTTTCATCCCAAGCTGAG 1980
DB 1921 CTTTCATCCCAAGCTGAG 1980
QY 1981 CAGAGCTTCCGAG 2040
DB 1981 CAGAGCTTCCGAG 2040
QY 2041 CAGGAGTCTCACTAAG 2100
DB 2041 CAGGAGTCTCACTAAG 2100
QY 2101 CTTGAGAGATTCACAG 2160
DB 2101 CTTGAGAGATTCACAG 2160
QY 2161 GCGGCTGAGAGCTGATCTTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
DB 2161 GCGGCTGAGAGCTGATCTTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
QY 2221 GAGAGAGCTCAAGAGAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
DB 2221 GAGAGAGCTCAAGAGAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
QY 2281 TCGGTAAGCGGTGATCCAG 2340
DB 2281 TCGGTAAGCGGTGATCCAG 2340
QY 2341 CGTCTACCTTGAAG 2400
DB 2341 CGTCTACCTTGAAG 2400
QY 2401 GAGCAG 2460

DB 2401 GAGCAG 2460
QY 2461 CAGTGGAGCTTTCAG 2520
DB 2461 CAGTGGAGCTTTCAG 2520
QY 2521 CAAAGTCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2580
DB 2521 CAAAGTCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2580
QY 2581 CAGCTGTCTACAG 2640
DB 2581 CAGCTGTCTACAG 2640
QY 2641 GCTCTGAGTGTGAG 2700
DB 2641 GCTCTGAGTGTGAG 2700
QY 2701 CTTCTCTAG 2760
DB 2701 CTTCTCTAG 2760
QY 2761 GAG 2820
DB 2761 GAG 2820
QY 2821 GCGGAG 2880
DB 2821 GCGGAG 2880
QY 2881 GAG 2940
DB 2881 GAG 2940
QY 2941 CCGCTTCAAG 3000
DB 2941 CCGCTTCAAG 3000
QY 3001 TCAAG 3060
DB 3001 TCAAG 3060
QY 3061 CAAAGTCTCTGAG 3120
DB 3061 CAAAGTCTCTGAG 3120
QY 3121 TCAAG 3180
DB 3121 TCAAG 3180
QY 3181 CTTGAG 3240
DB 3181 CTTGAG 3240
QY 3241 CCGGCTTCTGAG 3300
DB 3241 CCGGCTTCTGAG 3300
QY 3301 GAGTCAAG 3360
DB 3301 GAGTCAAG 3360
QY 3361 GCTGAGTCTGAG 3420
DB 3361 GCTGAGTCTGAG 3420
QY 3421 ACTGAGCTTCAAG 3480
DB 3421 ACTGAGCTTCAAG 3480
QY 3481 GAGCAG 3540

Db 2821 GCCGCGCCGACGCTATTCCTCCGTCGCGCTGCTGCTGATACCCGGAACCTCGAGGT 2880
Qy 2881 GCAGAGCGACTACTCAGCTATGCGCGACCTCCATCAGAGCGAGCTCAGCTTCAACCG 2940
Db 2881 GCAGAGCGACTACTCAGCTATGCGCGACCTCCATCAGAGCGAGCTCAGCTTCAACCG 2940
Qy 2941 CGGCTTCAAGGCTGAGAGGACATGCTGCAAACTCTTTGGGAGTCTTTCGCGCTGAGTG 3000
Db 2941 CGGCTTCAAGGCTGAGAGGACATGCTGCAAACTCTTTGGGAGTCTTTCGCGCTGAGTG 3000
Qy 3001 TCACAGCTGTTTCTGAGATTTGAGGTGAACAGCTCCAGAGCGTGTGACCAACATCTA 3060
Db 3001 TCACAGCTGTTTCTGAGATTTGAGGTGAACAGCTCCAGAGCGTGTGACCAACATCTA 3060
Qy 3061 CAAGATCCCTGCTGAGAGCGCTTACAGCTTACAGATGCTGAGCTGAGCTCCCATTTCA 3120
Db 3061 CAAGATCCCTGCTGAGAGCGCTTACAGCTTACAGATGCTGAGCTGAGCTCCCATTTCA 3120
Qy 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGCTCATCTGTGACAGCGCTCCCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGCTCATCTGTGACAGCGCTCCCT 3180
Qy 3181 CTGCTACTCATCTGTAAGAACCAAGAACCGAGGATGTGCTGAGGCGGCAAGGCGCGC 3240
Db 3181 CTGCTACTCATCTGTAAGAACCAAGAACCGAGGATGTGCTGAGGCGGCAAGGCGCGC 3240
Qy 3241 CGGCTTCTGCTGCTGAGAGCGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Db 3241 CGGCTTCTGCTGCTGAGAGCGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Qy 3301 GACTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Db 3301 GACTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Qy 3361 GCTGAGTGGAGGCTTCCGCGGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Db 3361 GCTGAGTGGAGGCTTCCGCGGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Qy 3421 ACTGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 3480
Db 3421 ACTGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 3480
Qy 3481 GAGCAGACACGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3481 GAGCAGACACGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Qy 3541 CACACCCAGGCGCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
Db 3541 CACACCCAGGCGCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
Qy 3601 CATGCTCCGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Db 3601 CATGCTCCGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Qy 3661 GAGTGTCCAGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Db 3661 GAGTGTCCAGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Qy 3721 GGGCGAGCTTCTTCTCAAGAGAGCGCGCTTCTCACTCCCAATAGAAATAGTCCATCC 3780
Db 3721 GGGCGAGCTTCTTCTCAAGAGAGCGCGCTTCTCACTCCCAATAGAAATAGTCCATCC 3780
Qy 3781 CCAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
Db 3781 CCAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
Qy 3841 AGGTGAGACCTGAG 3900
Db 3841 AGGTGAGACCTGAG 3900
Qy 3901 CCTGTGACAG 3960
Db 3901 CCTGTGACAG 3960

Qy 3961 GAGTGTCTGTGGAG 4015
Db 3961 GAGTGTCTGTGGAG 4015

RESULT 9
US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Deming, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; PRIOR FILING DATE: 2002-03-21
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

Query Match 100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 GCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Qy 61 GGGCGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 GGGCGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 121 GCGCTGAGCAAGTTCGTCGAGCGAGCTGAGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 GCGCTGAGCAAGTTCGTCGAGCGAGCTGAGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 GGAACCGGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 GGAACCGGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 241 AGGCG 300
Db 241 AGGCG 300
Qy 301 CCGAGTGTGAG 360
Db 301 CCGAGTGTGAG 360
Qy 361 GCTGCTGAG 420
Db 361 GCTGCTGAG 420
Qy 421 CCTGCCAACAAG 480
Db 421 CCTGCCAACAAG 480
Qy 481 CCGCGTGGAG 540
Db 481 CCGCGTGGAG 540

481 CGCGTGGGGGAGAGAGTGTGTGTCACCTGCTGGACGCGTGGCGCTCTTTGTGTGTGT 540
QY 541 GGGTCCCAAGTGGGCTTACCAAGTGTGGGGCGCGCTGTATCACTATGGGCGCTTGGCAC 600
Db 541 GGGTCCCAAGTGGGCTTACCAAGTGTGGGGCGCGCTGTATCACTATGGGCGCTTGGCAC 600
QY 601 TCAGAGCGGGCGCGCGCACAGCTAGTGGACCCCGAAGGCGTCTGGAGATGCGAAGGAGC 660
Db 601 TCAGAGCGGGCGCGCGCACAGCTAGTGGACCCCGAAGGCGTCTGGAGATGCGAAGGAGC 660
QY 661 CTGGAAACATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCTGTCCAGCCCGGGTGCAG 720
Db 661 CTGGAAACATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCTGTCCAGCCCGGGTGCAG 720
QY 721 GAAGCGCGGGGGGAGTGGCCAGCGGAAGTCTGCGGTTGCCAAGAGGCCAGGCGTGGCGC 780
Db 721 GAAGCGCGGGGGGAGTGGCCAGCGGAAGTCTGCGGTTGCCAAGAGGCCAGGCGTGGCGC 780
QY 781 TGGCCCTGAGCGGAGCGGACGCGCGCTTGGGAGGGGTCTTGGGCGCACCCGCGGAGAGC 840
Db 781 TGGCCCTGAGCGGAGCGGACGCGCGCTTGGGAGGGGTCTTGGGCGCACCCGCGGAGAGC 840
QY 841 GCGTGAACGAGTGAACCGGT 900
Db 841 GCGTGAACGAGTGAACCGGT 900
QY 901 CACTCTTTTGAAGGT 960
Db 901 CACTCTTTTGAAGGT 960
QY 961 GCACCAAGCGGGCGCGCGCATCATGCGCGGACCAAGTCCCTGGGAGACGCGCTTGTTC 1020
Db 961 GCACCAAGCGGGCGCGCGCATCATGCGCGGACCAAGTCCCTGGGAGACGCGCTTGTTC 1020
QY 1021 CCGCGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGGAGCAAGAGAGAGCTGCG 1080
Db 1021 CCGCGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGGAGCAAGAGAGAGCTGCG 1080
QY 1081 GCGCTCTCTCTACT 1140
Db 1081 GCGCTCTCTCTACT 1140
QY 1141 GACCATCTTCT 1200
Db 1141 GACCATCTTCT 1200
QY 1201 GCGCGAGCGCTACTGGAATGCGCGCGCTGTCTGTGAGCTGTGTGGAAACACGCGGCA 1260
Db 1201 GCGCGAGCGCTACTGGAATGCGCGCGCTGTCTGTGAGCTGTGTGGAAACACGCGGCA 1260
QY 1261 GTGCGCCCTAGCGGGGTGCTCTCAAGAGCACTGCGCGCTGAGAGCTGCGGTCAACCCAGC 1320
Db 1261 GTGCGCCCTAGCGGGGTGCTCTCAAGAGCACTGCGCGCTGAGAGCTGCGGTCAACCCAGC 1320
QY 1321 AGCGGTGTCTGTGCTCGCGGAGAAAGCCCAAGGCTCTGTGCGGCGCGCGCGAGAGAGGA 1380
Db 1321 AGCGGTGTGTGCTCGCGGAGAAAGCCCAAGGCTCTGTGCGGCGCGCGCGAGAGAGGA 1380
QY 1381 CACAGAGCCCGGTGCTGT 1440
Db 1381 CACAGAGCCCGGTGCTGT 1440
QY 1441 CGGCGTGTGTGCGGCTGTGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
Db 1441 CGGCGTGTGTGCGGCTGTGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
QY 1501 CAAAGAGCGCGCTTCTCTCAAGAAACACCAAGAGTTCTCTCTGTGGAGAGCATGCGCAA 1560
Db 1501 CAAAGAGCGCGCTTCTCTCAAGAAACACCAAGAGTTCTCTCTGTGGAGAGCATGCGCAA 1560
QY 1561 GCTCTCGCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1620
Db 1561 GCTCTCGCTGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1620

1621 GAGCCCAAGGGGT 1680
QY 1621 GAGCCCAAGGGGT 1680
Db 1621 GAGCCCAAGGGGT 1680
QY 1681 CAAAGTCTGTGCTGT 1740
Db 1681 CAAAGTCTGTGCTGT 1740
QY 1741 TGTCAAGGAGACCAAGT 1800
Db 1741 TGTCAAGGAGACCAAGT 1800
QY 1801 CAAAGTGTCAAGATTTGGAATCAGACACTTGAAGAGGTGTGAGCTTGGGAGCTGTTC 1860
Db 1801 CAAAGTGTCAAGATTTGGAATCAGACACTTGAAGAGGTGTGAGCTTGGGAGCTGTTC 1860
QY 1861 GGAAGCAGAGTGTGAGGAGCATGCGGAAAGCCAGGCGCGCGCTGTGAGCTGTCAAGCTCG 1920
Db 1861 GGAAGCAGAGTGTGAGGAGCATGCGGAAAGCCAGGCGCGCGCTGTGAGCTGTCAAGCTCG 1920
QY 1921 CTTCAATCCCAAGCGTGTGAGGCGTGTGAGGCGATGTGAAATGAACTGAGCTGTGAGGAGC 1980
Db 1921 CTTCAATCCCAAGCGTGTGAGGCGTGTGAGGCGATGTGAAATGAACTGAGCTGTGAGGAGC 1980
QY 1981 CAGAAAGTTCGCGAGAGAAAGAGGAGCGAGGCTGTCACTTGAAGGCTGAAAGCACTGTT 2040
Db 1981 CAGAAAGTTCGCGAGAGAAAGAGGAGCGAGGCTGTCACTTGAAGGCTGAAAGCACTGTT 2040
QY 2041 CAGCGTGTCAATCAAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
Db 2041 CAGCGTGTCAATCAAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
QY 2101 CCGTGAAGATATCAAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2160
Db 2101 CCGTGAAGATATCAAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2160
QY 2161 GCGCGCTGTGAGCTTGT 2220
Db 2161 GCGCGCTGTGAGCTTGT 2220
QY 2221 GGAAGAGCTCAGGAGAGT 2280
Db 2221 GGAAGAGCTCAGGAGAGT 2280
QY 2281 TCGGTATGCGGT 2340
Db 2281 TCGGTATGCGGT 2340
QY 2341 CGTCTTACTTGTGACAGACCTTCAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 CGTCTTACTTGTGACAGACCTTCAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
QY 2401 GACCAAGCGCGTGAAGGAGT 2460
Db 2401 GACCAAGCGCGTGAAGGAGT 2460
QY 2461 CAGTGTGCTTGTGAGAGT 2520
Db 2461 CAGTGTGCTTGTGAGAGT 2520
QY 2521 CAAATCTTGTGAGAGT 2580
Db 2521 CAAATCTTGTGAGAGT 2580
QY 2581 CAGCTGTGTGTGAGAGT 2640
Db 2581 CAGCTGTGTGTGAGAGT 2640
QY 2641 GCTCTGCGT 2700
Db 2641 GCTCTGCGT 2700

2701 CTTCTCAGAGACCCCTGTCGAGGTGTCCCTGATGATGCTGCTGTAACCTTGGCGAA 2760
2701 CTTCTCAGAGACCCCTGTCGAGGTGTCCCTGATGATGCTGCTGTAACCTTGGCGAA 2760
2761 GACAGTGTGAACTTCTCTGTGAAAGACAGAGCCCTGAGTGGACCGCTTTTGTTCAGAT 2820
2761 GACAGTGTGAACTTCTCTGTGAAAGACAGAGCCCTGAGTGGACCGCTTTTGTTCAGAT 2820
2821 GCGCGGCGCAAGGCTGATTTCCCTGTCGAGGCTGCTGCTGATGATGATGATGATGATGAT 2880
2821 GCGCGGCGCAAGGCTGATTTCCCTGTCGAGGCTGCTGCTGATGATGATGATGATGATGAT 2880
2821 GCGCGGCGCAAGGCTGATTTCCCTGTCGAGGCTGCTGCTGATGATGATGATGATGATGAT 2880
2881 GAGAGAGCAGTACTCAGAGTATGCTCCGAGCTTCATCAGAGCAGTCTCAGCTTCAACCG 2940
2881 GAGAGAGCAGTACTCAGAGTATGCTCCGAGCTTCATCAGAGCAGTCTCAGCTTCAACCG 2940
2881 GAGAGAGCAGTACTCAGAGTATGCTCCGAGCTTCATCAGAGCAGTCTCAGCTTCAACCG 2940
2941 GCGCTTCAAGGCTGAGAGAACATGCTGCGAAACTCTTTGGGCTTTCGCGCTGAAGTG 3000
2941 GCGCTTCAAGGCTGAGAGAACATGCTGCGAAACTCTTTGGGCTTTCGCGCTGAAGTG 3000
3001 TCAAGGCTGTTTCTGAGATTTGAGAGTGAACAGGCTCCAGAGGCTGAGCAGCAACTCTA 3060
3001 TCAAGGCTGTTTCTGAGATTTGAGAGTGAACAGGCTCCAGAGGCTGAGCAGCAACTCTA 3060
3061 CAAGATCTCTCTGCTGACAGGCTGACAGGTTTCAAGGATGCTGCTGCTGCTGCTGCTGCT 3120
3061 CAAGATCTCTCTGCTGACAGGCTGACAGGTTTCAAGGATGCTGCTGCTGCTGCTGCTGCT 3120
3121 TCAGCAAGTTTGGAGAGAACCCCAATTTTCTGCGGCTGATCTGAGACGCGCTTCCCT 3180
3121 TCAGCAAGTTTGGAGAGAACCCCAATTTTCTGCGGCTGATCTGAGACGCGCTTCCCT 3180
3181 CTGCTACTCTCTCTGAGAGAACCCCAAGAACAGGAGTGTGCTGAGAGGAGGAGGAGGAGG 3240
3181 CTGCTACTCTCTCTGAGAGAACCCCAAGAACAGGAGTGTGCTGAGAGGAGGAGGAGGAGG 3240
3181 CTGCTACTCTCTCTGAGAGAACCCCAAGAACAGGAGTGTGCTGAGAGGAGGAGGAGGAGG 3240
3241 CGAGCCTCTGCTGCTGAGAGAACCCCAAGAACAGGAGTGTGCTGAGAGGAGGAGGAGGAGG 3300
3241 CGAGCCTCTGCTGCTGAGAGAACCCCAAGAACAGGAGTGTGCTGAGAGGAGGAGGAGGAGG 3300
3301 GACTGACACCGGTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
3301 GACTGACACCGGTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
3361 GCTGAGTGTGAGAGCTCCCGGAGCGACGCTGAGTGTGCTGAGAGGAGGAGGAGGAGGAGG 3420
3361 GCTGAGTGTGAGAGCTCCCGGAGCGACGCTGAGTGTGCTGAGAGGAGGAGGAGGAGGAGG 3420
3421 ACTGAGCCTGAGACTTCAAGACATCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3480
3421 ACTGAGCCTGAGACTTCAAGACATCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3480
3481 GAGCAGACACAGCAGACCCCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3481 GAGCAGACACAGCAGACCCCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3481 GAGCAGACACAGCAGACCCCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3481 GAGCAGACACAGCAGACCCCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3541 CACACCCAGGCGCGCAGCCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3600
3541 CACACCCAGGCGCGCAGCCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3600
3541 CACACCCAGGCGCGCAGCCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3600
3601 CATGTCGAGTGAAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3660
3601 CATGTCGAGTGAAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3660
3661 GAGTGTGAGCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3661 GAGTGTGAGCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3661 GAGTGTGAGCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3721 GGGCGAGCTTTTCTGACAGAGAGGCGGCTTTCATCTCCCAATAGAAATATCTCATTC 3780
3721 GGGCGAGCTTTTCTGACAGAGAGGCGGCTTTCATCTCCCAATAGAAATATCTCATTC 3780
3721 GGGCGAGCTTTTCTGACAGAGAGGCGGCTTTCATCTCCCAATAGAAATATCTCATTC 3780
3721 GGGCGAGCTTTTCTGACAGAGAGGCGGCTTTCATCTCCCAATAGAAATATCTCATTC 3780
3781 CAGATTCGCTGATTTGACAGAGGCGGCTTTCATCTCCCAATAGAAATATCTCATTC 3840

|||||
Db 3781 CCAGATTCGCTGATTTGACAGAGGCGGCTTTCATCTCCCAATAGAAATATCTCATTC 3840
Qy 3841 AGTGTGAGACCTTGAAGAGAGACCTGAGAGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 3900
Db 3841 AGTGTGAGACCTTGAAGAGAGACCTGAGAGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 3900
Qy 3901 CCCTGTACACAGAGAGAGACCTGAGAGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3960
Db 3901 CCCTGTACACAGAGAGAGACCTGAGAGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3960
Qy 3961 GAGTGTGAG 4015
Db 3961 GAGTGTGAG 4015
RESULT 10
US-10-044-692-1
Sequence 1, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-10-044-692-1

Query Match 100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCGTGGGCTCTGCTGCGACAGTGGAGAGCCCTGAGCCCGGACACCCCGCGATGCC 60
DB 1 GCAGCGTGGGCTCTGCTGCGACAGTGGAGAGCCCTGAGCCCGGACACCCCGCGATGCC 60
QY 61 GCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGAGCCACTACCGCGAGGTGCT 120
DB 61 GCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGAGCCACTACCGCGAGGTGCT 120
QY 121 GCGCGTGGCAGAGTGTGCTGCGGCGCTTGGGGCCCAAGGCTGGCGGTGTGCAAGCGCG 180
DB 121 GCGCGTGGCAGAGTGTGCTGCGGCGCTTGGGGCCCAAGGCTGGCGGTGTGCAAGCGCG 180
QY 181 GAACCCGCGCGGCTTCCGCGCGCTGGAGCCAGTGGCTGGTGGTGGCTCCGGGAGCG 240
DB 181 GAACCCGCGCGGCTTCCGCGCGCTGGAGCCAGTGGCTGGTGGTGGCTCCGGGAGCG 240
QY 241 ACGCGCGCCCGCGCGCCCTCTCTTCCGCGCAGGTGTCTGCTGCTGAAGAGCTGTGAGC 300
DB 241 ACGCGCGCCCGCGCGCCCTCTCTTCCGCGCAGGTGTCTGCTGCTGAAGAGCTGTGAGC 300
QY 301 CCGAGTGTCTGCAAGAGCTGTGCGAGCGCGCGCGGAAAGAGTGTGCTGCTGCGCTTCCG 360
DB 301 CCGAGTGTCTGCAAGAGCTGTGCGAGCGCGCGCGGAAAGAGTGTGCTGCTGCGCTTCCG 360
QY 361 GCTGCTGAGACGAGGCGCGCGGAGCGCCCGCGAGGCTTCAACCAAGCGTGGCGAGCTA 420
DB 361 GCTGCTGAGACGAGGCGCGCGGAGCGCCCGCGAGGCTTCAACCAAGCGTGGCGAGCTA 420
QY 421 CCGTCCCAACAGCGTGAACCGACTGCGGAGGAGCGGAGCGTGGAGGCTGTGCTGCG 480
DB 421 CCGTCCCAACAGCGTGAACCGACTGCGGAGGAGCGGAGCGTGGAGGCTGTGCTGCG 480
QY 481 CCGCGTGGGAGAGAGTGTGCTGCTGCTGCTGCGAGCGTGGCGCTCTTGTGTGGT 540
DB 481 CCGCGTGGGAGAGAGTGTGCTGCTGCTGCTGCGAGCGTGGCGCTCTTGTGTGGT 540
QY 541 GGTCTCCAGTGGCTTACAGAGTGTGCGGCGCGCGCTGTACCAAGTCTGAGCTGCGCAC 600
DB 541 GGTCTCCAGTGGCTTACAGAGTGTGCGGCGCGCGCTGTACCAAGTCTGAGCTGCGCAC 600
QY 601 TCAGGCGCGGCG 660
DB 601 TCAGGCGCGGCG 660
QY 661 CTGGAACCAATAGGCTAGGAGGAGCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 661 CTGGAACCAATAGGCTAGGAGGAGCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 GAGGCGCGGAGGAGTGGCGAGCGAGTGTGCGGTGCGCAAGAGGCGCGAGGCTGGCGC 780
DB 721 GAGGCGCGGAGGAGTGGCGAGCGAGTGTGCGGTGCGCAAGAGGCGCGAGGCTGGCGC 780
QY 781 TGGCCCTTGAAGCGGAGCGAGCGCGCTTGGGAGCGGAGTCTGGAGCCCAACCGGAGC 840
DB 781 TGGCCCTTGAAGCGGAGCGAGCGCGCTTGGGAGCGGAGTCTGGAGCCCAACCGGAGC 840
QY 841 GGTGAGACGAGTGAACCGGTGTTTCTGTGTGAGTCACTGCGCAACCGCGGAGAGC 900
DB 841 GGTGAGACGAGTGAACCGGTGTTTCTGTGTGAGTCACTGCGCAACCGCGGAGAGC 900

DB 841 GGTGAGACGAGTGAACCGGTGTTTCTGTGTGAGTCACTGCGCAACCGCGGAGAGC 900
QY 901 CACTCTTTGAGAGGAGGCGCTCTTGGACAGGCGCACTCCACCCATCCGTGGGCGGCA 960
DB 901 CACTCTTTGAGAGGAGGCGCTCTTGGACAGGCGCACTCCACCCATCCGTGGGCGGCA 960
QY 961 GCACACAGGAGGCG 1020
DB 961 GCACACAGGAGGCG 1020
QY 1021 CCGGTGTAGCGCGAGACCAACACTTCTCTACTCTTCTGAGCGACAGAGAGTGGC 1080
DB 1021 CCGGTGTAGCGCGAGACCAACACTTCTCTACTCTTCTGAGCGAGAGAGTGGC 1080
QY 1081 GCGCTCTCTTCTACTAGTCTGTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1081 GCGCTCTCTTCTACTAGTCTGTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1141 GACATCTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB 1141 GACATCTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1201 GCGCCAGCGCTACTGAGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB 1201 GCGCCAGCGCTACTGAGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1261 GTGCCCTTACGAGGAGTCTCTGAGAGCGACGCGCGCGCGCGCGCGCGCGCGCGCG 1320
DB 1261 GTGCCCTTACGAGGAGTCTCTGAGAGCGACGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1321 AGCGGCTGTCTGCTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
DB 1321 AGCGGCTGTCTGCTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1381 CACAGACCCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 CACAGACCCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 CGGCTTCTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 CGGCTTCTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 CAACGAGCGCGCTTCTCTGAGAGACCAAGAGTTCATCTTCTGAGGAGACATGCCA 1560
DB 1501 CAACGAGCGCGCTTCTCTGAGAGACCAAGAGTTCATCTTCTGAGGAGACATGCCA 1560
QY 1561 GCTCTGCTGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
DB 1561 GCTCTGCTGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
QY 1621 GAGCCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 GAGCCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 CAAGTCTCTGCACTGAGTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1740
DB 1681 CAAGTCTCTGCACTGAGTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1740
QY 1741 TGTCAAGAGAGACAGTTCATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 TGTCAAGAGAGACAGTTCATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 CAAGTTCGAAAGCACTTGAATCAGACACTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1801 CAAGTTCGAAAGCACTTGAATCAGACACTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 GGAAGCAAGAGTCAAG 1920
DB 1861 GGAAGCAAGAGTCAAG 1920
QY 1921 CTTTATCCCAAG 1980
DB 1921 CTTTATCCCAAG 1980

1981 CAGAACGTTCCGAGAGAAAAGAGGCGAGCGTCTACCTCGAGGGGTGAAGCACTGTT 2040
1981 CAGAACGTTCCGAGAGAAAAGAGGCGAGCGTCTACCTCGAGGGGTGAAGCACTGTT 2040
2041 CAGCGTCTCACTAGAGAGGCGGCGGCGCGCGCGCTCTTGGGCGCTCTGCTGCGG 2100
2041 CAGCGTCTCACTAGAGAGGCGGCGGCGCGCGCGCTCTTGGGCGCTCTGCTGCGG 2100
2101 CCGTGAACGATATTCAGAGAGGCGCTGCGGCGCTCTGCTGCTGCGGCGCGGCGG 2160
2101 CCGTGAACGATATTCAGAGAGGCGCTGCGGCGCTCTGCTGCTGCGGCGCGGCGG 2160
2161 GCGGCGCTGAGCTGATCTTGTCAAGGTGATGAGAGGCGGCGCTGAGAGCACTCCCA 2220
2161 GCGGCGCTGAGCTGATCTTGTCAAGGTGATGAGAGGCGGCGCTGAGAGCACTCCCA 2220
2221 GGAAGAGCTCAGAGAGGCTATCGCAGCATCATCAAAACCCAGAGACAGTATGCGTGG 2280
2221 GGAAGAGCTCAGAGAGGCTATCGCAGCATCATCAAAACCCAGAGACAGTATGCGTGG 2280
2281 TCGGTATGCGGTGCTCAAGAGGCGCGCGCGCTGCGGCGCGCTCTTCAAGAGCA 2340
2281 TCGGTATGCGGTGCTCAAGAGGCGCGCGCGCTGCGGCGCGCTCTTCAAGAGCA 2340
2341 CCGTCTACCTTGAAGAGCTCAGAGCGCTGATGAGAGAGTGTGCTGCTGAGAGG 2400
2341 CCGTCTACCTTGAAGAGCTCAGAGCGCTGATGAGAGAGTGTGCTGCTGAGAGG 2400
2401 GACAGAGCGCTGAGAGGATGCGCTGATGAGAGAGAGTCTCTCTGATAGAGGCGAG 2460
2401 GACAGAGCGCTGAGAGGATGCGCTGATGAGAGAGAGTCTCTCTGATAGAGGCGAG 2460
2401 GACAGAGCGCTGAGAGGATGCGCTGATGAGAGAGAGTCTCTCTGATAGAGGCGAG 2460
2461 CAGTGGCTCTTGAAGGCTCTTCTAGCTTCAATGAGCAGAGCGGCTGAGAGGCGAG 2520
2461 CAGTGGCTCTTGAAGGCTCTTCTAGCTTCAATGAGCAGAGCGGCTGAGAGGCGAG 2520
2521 CAGTGGCTCTTGAAGGCTCTTCTAGCTTCAATGAGCAGAGCGGCTGAGAGGCGAG 2580
2521 CAGTGGCTCTTGAAGGCTCTTCTAGCTTCAATGAGCAGAGCGGCTGAGAGGCGAG 2580
2581 CAGCTGTGCTAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2640
2581 CAGCTGTGCTAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2640
2641 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
2641 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
2701 CTTTCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
2701 CTTTCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
2761 GACAGTGTGAACCTTCTGTAAGAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
2761 GACAGTGTGAACCTTCTGTAAGAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
2821 GCGGCGCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2821 GCGGCGCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2881 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2881 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2941 CCGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
2941 CCGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
3001 TCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
3001 TCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060

3061 CAGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
3061 CAGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
3121 TCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
3121 TCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
3181 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
3181 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
3241 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
3241 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
3301 GACTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
3301 GACTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
3301 GACTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
3361 GCTGAGTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
3361 GCTGAGTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
3421 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
3421 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
3481 GAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
3481 GAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
3541 CAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
3541 CAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
3601 CAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3601 CAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
3661 GAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3661 GAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3721 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
3721 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
3781 CCGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
3781 CCGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
3841 AGGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3900
3841 AGGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3900
3901 CCGTGTACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
3901 CCGTGTACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
3961 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4015
3961 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4015

RESULT 11
US-10-044-539-1
; Sequence 1, Application US/10044539
; Publication No. US20030100033A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru

Db 1201 GCCCAGCGCTACTGCGAAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACCAACGCGCA 1260
Qy 1261 GTGCCCTTACGCGGAGTCTCTCTCAAGAAGCACTGCGCGTGGAGCTGGGTACCCACG 1320
Db 1261 GTGCCCTTACGCGGAGTCTCTCTCAAGAAGCACTGCGCGTGGAGCTGGGTACCCACG 1320
Qy 1321 AGCCGGTGTCTGTGCCCCGAGAGAGCCCAAGGCTGTGGCGGCCCCGAGAGAGAGA 1380
Db 1321 AGCCGGTGTCTGTGCCCCGAGAGAGCCCAAGGCTGTGGCGGCCCCGAGAGAGAGA 1380
Qy 1381 CACAGACCCCCCTGCGCTGTGTGAGCTGCTCGCGCACAGACAGAGGCCCTTGGAGGTGA 1440
Db 1381 CACAGACCCCCCTGCGCTGTGTGAGCTGCTCGCGCACAGACAGAGGCCCTTGGAGGTGA 1440
Qy 1441 CGGCTTGTGCGGAGCGCTGCGCGCGGCTGCGCGCGCTGCGCGCGCTGCGCGCGA 1500
Db 1441 CGGCTTGTGCGGAGCGCTGCGCGCGGCTGCGCGCGCTGCGCGCGCTGCGCGCGA 1500
Qy 1501 CAACGACCGCGCTTCTCTGAGAACACCAAGAGTTCACTCCCTGGAGAGCATGCGAA 1560
Db 1501 CAACGACCGCGCTTCTCTGAGAACACCAAGAGTTCACTCCCTGGAGAGCATGCGAA 1560
Qy 1561 GCTCTGCTGACAGAGCTGACGTGAAAGATGAGCGTGGAGACTGCGCTTGGCTGGAG 1620
Db 1561 GCTCTGCTGACAGAGCTGACGTGAAAGATGAGCGTGGAGACTGCGCTTGGCTGGAG 1620
Qy 1621 GAGCCCAAGGGGTGGCTGTGTTCGGGCGCGAGACCGTCTGCGAGAGATCTTGGC 1680
Db 1621 GAGCCCAAGGGGTGGCTGTGTTCGGGCGCGAGACCGTCTGCGAGAGATCTTGGC 1680
Qy 1681 CAAGTTCCTGCACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1681 CAAGTTCCTGCACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Qy 1741 TGTACGAGAGACCACTTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGTGAG 1800
Db 1741 TGTACGAGAGACCACTTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGTGAG 1800
Qy 1801 CAGTTTGCAGAGACCACTTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGTGAG 1860
Db 1801 CAGTTTGCAGAGACCACTTTTCAAAAGAACAGGCTCTTTTCTACCGAGAGATGTGAG 1860
Qy 1861 GGAAGAGAGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGG 1920
Db 1861 GGAAGAGAGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGG 1920
Qy 1921 CTTTCACTCCCAAGGCTGAGCGGCTGGCGCGATTTGAAACATGACATGATGATGATG 1980
Db 1921 CTTTCACTCCCAAGGCTGAGCGGCTGGCGCGATTTGAAACATGACATGATGATGATG 1980
Qy 1981 CAGAAAGTTCGCGAGAGAAAGAGGCGCGAGCTTCACTGAGAGTGAAGGCACTGTT 2040
Db 1981 CAGAAAGTTCGCGAGAGAAAGAGGCGCGAGCTTCACTGAGAGTGAAGGCACTGTT 2040
Qy 2041 CAGCGTGTCAACTAGAGAGGCGCGGCGCGCGCGCTCTGAGGAGCTGATGATGAG 2100
Db 2041 CAGCGTGTCAACTAGAGAGGCGCGGCGCGCGCGCTCTGAGGAGCTGATGATGAG 2100
Qy 2101 CTTGAGAGATATCAAGAGGCTGGGCGACTTTCGTGCTGTGTGCGGCGCGAGAGAG 2160
Db 2101 CTTGAGAGATATCAAGAGGCTGGGCGACTTTCGTGCTGTGTGCGGCGCGAGAGAG 2160
Qy 2161 GCGCGCTGAGCTGTATTTGTCAAGGTGAATGAGCGGCGCGTACGACACATCCCCA 2220
Db 2161 GCGCGCTGAGCTGTATTTGTCAAGGTGAATGAGCGGCGCGTACGACACATCCCCA 2220
Qy 2221 GGAAGAGGCTCAGAGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 2280
Db 2221 GGAAGAGGCTCAGAGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAG 2280
Qy 2281 TCGGTATGCGGTGTCCAGAGAGCGCGCATGAGGAGCTGTCGAGAGGCTTCAAGAGCA 2340
Db 2281 TCGGTATGCGGTGTCCAGAGAGCGCGCATGAGGAGCTGTCGAGAGGCTTCAAGAGCA 2340

Qy 2341 CGTCTCTACTTGAAGACCTTCAAGCGGATCATGCGACAGTTGATGCTCACTGAGAGA 2400
Db 2341 CGTCTCTACTTGAAGACCTTCAAGCGGATCATGCGACAGTTGATGCTCACTGAGAGA 2400
Qy 2401 GACAGCGCGCTGAGAGATGCGGTGTATGAGAGAGAGCTCTCTCTGATGAGGCGAG 2460
Db 2401 GACAGCGCGCTGAGAGATGCGGTGTATGAGAGAGAGCTCTCTCTGATGAGGCGAG 2460
Qy 2461 CAGTGGCTCTTGAAGCTTCTGAGCTTCAATGAGGAGAGAGAGAGAGAGAGAGAGAG 2520
Db 2461 CAGTGGCTCTTGAAGCTTCTGAGCTTCAATGAGGAGAGAGAGAGAGAGAGAGAGAG 2520
Qy 2521 CAACTCTGAGTCAAGTGCAGAGGAGATCCCGAGAGGCTCATCTCTCAAGCTGCTG 2580
Db 2521 CAACTCTGAGTCAAGTGCAGAGGAGATCCCGAGAGGCTCATCTCTCAAGCTGCTG 2580
Qy 2581 CAGCTGTGCTACGAGGAGATGAGAGAACAGCTGTTTGGGAGATTCGAGGAGAGAGCT 2640
Db 2581 CAGCTGTGCTACGAGGAGATGAGAGAACAGCTGTTTGGGAGATTCGAGGAGAGAGCT 2640
Qy 2641 GCTCTGCGTGTGTGATGATTTCTTGTGTGACCTCACTTCAACCCAGCGAGAAAC 2700
Db 2641 GCTCTGCGTGTGTGATGATTTCTTGTGTGACCTCACTTCAACCCAGCGAGAAAC 2700
Qy 2701 CTTTCTGAGAGACCTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2760
Db 2701 CTTTCTGAGAGACCTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2760
Qy 2761 GACAGTGTGAATCTTCCGTGAGAGACAGAGCGCTGAGTGCAGCGCTTGTTCAGAT 2820
Db 2761 GACAGTGTGAATCTTCCGTGAGAGACAGAGCGCTGAGTGCAGCGCTTGTTCAGAT 2820
Qy 2821 GCGGCGCAGCGGCTATTTCCCTGAGCGGCTGCTGCTGATGATGCCGAGCCTTGAAGT 2880
Db 2821 GCGGCGCAGCGGCTATTTCCCTGAGCGGCTGCTGCTGATGATGCCGAGCCTTGAAGT 2880
Qy 2881 GGAAGAGGATCTACAGTATGAGCGGAGCTCAATCAGAGGAGAGTCACTTCAACCG 2940
Db 2881 GGAAGAGGATCTACAGTATGAGCGGAGCTCAATCAGAGGAGAGTCACTTCAACCG 2940
Qy 2941 CCGCTTCAAGGCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 3000
Db 2941 CCGCTTCAAGGCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 3000
Qy 3001 TCAAGCTGTTTCTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTG 3060
Db 3001 TCAAGCTGTTTCTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTG 3060
Qy 3061 CAAAGTCTCTGCTGAGAGGCTGATCAAGGATTTTCAAGGATTTGAGATTTGAGATTT 3120
Db 3061 CAAAGTCTCTGCTGAGAGGCTGATCAAGGATTTTCAAGGATTTGAGATTTGAGATTT 3120
Qy 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGAGCGCTCATCTGACAGCGCTCCCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGAGCGCTCATCTGACAGCGCTCCCT 3180
Qy 3181 CTGCTACTCATCTGAGAAAGCCCAAGAGAGAGAGATGAGTGTGAGGAGCGCGC 3240
Db 3181 CTGCTACTCATCTGAGAAAGCCCAAGAGAGAGAGATGAGTGTGAGGAGCGCGC 3240
Qy 3241 CCGGCTCTGCGCTTCCAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3300
Db 3241 CCGGCTCTGCGCTTCCAGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3300
Qy 3301 GACTGAGACCGTGTACCTTACGTGCACTCTTGGAGGTACCTCAAGAGAGAGAGAGCA 3360
Db 3301 GACTGAGACCGTGTACCTTACGTGCACTCTTGGAGGTACCTCAAGAGAGAGAGAGCA 3360
Qy 3361 GCTGAGTGGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Db 3361 GCTGAGTGGAGAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420

QY 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
DB 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
QY 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
DB 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
QY 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
DB 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
DB 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
QY 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
DB 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
QY 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
DB 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
QY 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
DB 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
QY 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
DB 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
QY 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
DB 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
QY 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015
DB 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015

RESULT 12
US-10-325-810-1
Sequence 1, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181

QY 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
DB 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
QY 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
DB 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
QY 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
DB 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
DB 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
QY 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
DB 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
QY 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
DB 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
QY 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
DB 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
QY 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
DB 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
QY 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
DB 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
QY 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015
DB 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015

QY 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
DB 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
QY 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
DB 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
QY 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
DB 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
DB 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
QY 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
DB 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
QY 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
DB 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
QY 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
DB 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
QY 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
DB 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
QY 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
DB 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
QY 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015
DB 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015

QY 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
DB 3421 ACTGCTTCAAGCTTCAAGCATCTTGAATGATGACCCAGCCAGCCAGCCAGCCAG 3480
QY 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
DB 3481 GAGCAGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3540
QY 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
DB 3541 CACACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 3600
QY 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
DB 3601 CATGTCGGCTGAAGGCTGAGTGTCCGCTGAGAGCCTGAGCAGTGTCCAGCAGGAGCT 3660
QY 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
DB 3661 GAGTGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3720
QY 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
DB 3721 GGGCCAGCTTTTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3780
QY 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
DB 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCCCTGCTTCCCTTCCCTTCCCTTCCCTTCC 3840
QY 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
DB 3841 AGGTGAGACACCTTGAAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 3900
QY 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
DB 3901 CCCTGTACACAGGAGAGACCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTT 3960
QY 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015
DB 3961 GAGGTGCTGTGAGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4015

QY	2561	CAGCTGTGCTACAGGCGCAATGAGAAACAAGCTGTTGGGGGATTCGGCGGAGACGGGCT	2640
Db	2561	CAGCTGTGCTACAGGCGCAATGAGAAACAAGCTGTTGGGGGATTCGGCGGAGACGGGCT	2640
QY	2641	GCTCTGTGTTGGTGTGATGATTTCTTGTGTGTGACACTCACTTCAACCGACGCGAAAC	2700
Db	2641	GCTCTGTGTTGGTGTGATGATTTCTTGTGTGTGACACTCACTTCAACCGACGCGAAAC	2700
QY	2701	CTTCTCTAGAGACCTCGGTGCGAGGTGCTCTGAGTATGCTGTGCTGTGTGATCTTTCGGAA	2760
Db	2701	CTTCTCTAGAGACCTCGGTGCGAGGTGCTCTGAGTATGCTGTGCTGTGTGATCTTTCGGAA	2760
QY	2761	GACAGTGTGAACTTCCCTGTAGAGACGAGGCGCTGGTGGCACAGCTTTTGTTCAGAT	2820
Db	2761	GACAGTGTGAACTTCCCTGTAGAGACGAGGCGCTGGTGGCACAGCTTTTGTTCAGAT	2820
QY	2821	GCGGCGCCACGGGCTATTCCCTGTGTGGCGGCTGTGCTGTGATACCCGGACCTTGAAGT	2880
Db	2821	GCGGCGCCACGGGCTATTCCCTGTGTGGCGGCTGTGCTGTGATACCCGGACCTTGAAGT	2880
QY	2881	GCAGAGGCACTACTCAGATATCCCGAGACTTCATCAGAGCAGTCACTCACTTCAACG	2940
Db	2881	GCAGAGGCACTACTCAGATATCCCGAGACTTCATCAGAGCAGTCACTCACTTCAACG	2940
QY	2941	CGGCTTCAAGGCTGGGAGAACATGCGTGCAAACTTTTGGGAGTCTTGGCGGTGAAGT	3000
Db	2941	CGGCTTCAAGGCTGGGAGAACATGCGTGCAAACTTTTGGGAGTCTTGGCGGTGAAGT	3000
QY	3001	TCAAGCTGTGTTCTGGAATTGAGAGTGAACAAGCTCCAGAGAGGTGTACACAACTTA	3060
Db	3001	TCAAGCTGTGTTCTGGAATTGAGAGTGAACAAGCTCCAGAGAGGTGTACACAACTTA	3060
QY	3061	CAAGATCTCTCTGTGCGAGCGTACAGAGTTTCAAGCATGTGTGTGTGACAGTCCCATTTCA	3120
Db	3061	CAAGATCTCTCTGTGCGAGCGTACAGAGTTTCAAGCATGTGTGTGTGACAGTCCCATTTCA	3120
QY	3121	TCAGCAGTTTGGAAAGAACCCCAATTTTCTGGGCGTCACTCTTGAACAAGGCTCTCT	3180
Db	3121	TCAGCAGTTTGGAAAGAACCCCAATTTTCTGGGCGTCACTCTTGAACAAGGCTCTCT	3180
QY	3181	CTGTACTTCATCTCTGAAGCAAGCAAGACAGAGATGTGCTGGGGGCGAAGGGGCGCGC	3240
Db	3181	CTGTACTTCATCTCTGAAGCAAGCAAGACAGAGATGTGCTGGGGGCGAAGGGGCGCGC	3240
QY	3241	CGGCGCTCTGCTCCCTCGAGGCGCTGTGAGTGTGTGCGACCAAGCATTCCTGTCAAGT	3300
Db	3241	CGGCGCTCTGCTCCCTCGAGGCGCTGTGAGTGTGTGCGACCAAGCATTCCTGTCAAGT	3300
QY	3301	GACTCGACACGCTGTACACTTACGTGTGCACTTCCCTGGGGGTCACTCAGAGCAGGCGACGCA	3360
Db	3301	GACTCGACACGCTGTACACTTACGTGTGCACTTCCCTGGGGGTCACTCAGAGCAGGCGACGCA	3360
QY	3361	GCTGAGTTCGGAAGCTCCCGGGAGCGAGCTTGACTGCTCTGTGAAGGCGGAGCCAACCCGCGC	3420
Db	3361	GCTGAGTTCGGAAGCTCCCGGGAGCGAGCTTGACTGCTCTGTGAAGGCGGAGCCAACCCGCGC	3420
QY	3421	ACTGCGCTTGAGCTTCAAGACCATCTGTGACGTAGTATGAGTGTGTTGGTGGCGAGGCTGCA	3480
Db	3421	ACTGCGCTTGAGCTTCAAGACCATCTGTGACGTAGTATGAGTGTGTTGGTGGCGAGGCTGCA	3480
QY	3481	GAGCAGACACAGCAGCCTGTGTACGCGCGGAGCTTACGTCTCCAGAGGAGGAGGAGGCGGCGC	3540
Db	3481	GAGCAGACACAGCAGCCTGTGTACGCGCGGAGCTTACGTCTCCAGAGGAGGAGGAGGCGGCGC	3540
QY	3541	CACAACCAGGCGCGCACCGCTGTGAGTCTGAGGCTGTGATGATGTTTGGCGAGGCTG	3600
Db	3541	CACAACCAGGCGCGCACCGCTGTGAGTCTGAGGCTGTGATGATGTTTGGCGAGGCTG	3600
QY	3601	CATGTCCGCGTGAAGCTAGTGTCCGCTGAGAGGCTTACGAGAGTGTCCACCAAGGAGCT	3660
Db	3601	CATGTCCGCGTGAAGCTAGTGTCCGCTGAGAGGCTTACGAGAGTGTCCACCAAGGAGCT	3660
QY	3661	GAGTGTTCAGACACTCTCGCTTCACTTCCCAAGGCTGAGGCTCGGCTCCACCCCA	3720

Db	Sequence	Score	DB ID	Length	4015
Db	3661 GAGTGTCCAGCACCCTGCGCTTCTTCACTTCCACAGGGCTGCGCTCCACCCCA	3720			
Qy	3721 GGGCCAGCTTTTCTTCCACAGGAGCCGGCTCCACTCCACATAGGAATAGTCATCC	3780			
Db	3721 GGGCCAGCTTTTCTTCCACAGGAGCCGGCTTCCACTCCACATAGGAATAGTCATCC	3780			
Qy	3781 CCAGATTGCGCAATGTTTCACTCCCTGCGCCCTCTTTGCTTCCACCCCAACATCC	3840			
Db	3781 CCAGATTGCGCAATGTTTCACTCCCTGCGCCCTCTTTGCTTCCACCCCAACATCC	3840			
Qy	3841 AGGTGAGACCCCTGAGAAAGGACCTTGGAGCTCTGGAAATTTGGAGTGACCAAGGTG	3900			
Db	3841 AGGTGAGACCCCTGAGAAAGGACCTTGGAGCTCTGGAAATTTGGAGTGACCAAGGTG	3900			
Qy	3901 CCCTGTACACAGGCGAGACCCCTGCACTTGATGGGGTCCCTGTGGGTCAAAATTTGGGG	3960			
Db	3901 CCCTGTACACAGGCGAGACCCCTGCACTTGATGGGGTCCCTGTGGGTCAAAATTTGGGG	3960			
Qy	3961 GAGGTGCTGTGGGAGTAATAATCTGAATATATGATTTTCAGTTTGAATAAAAA	4015			
Db	3961 GAGGTGCTGTGGGAGTAATAATCTGAATATATGATTTTCAGTTTGAATAAAAA	4015			

OY	241	ACGGCCGCCCCCGCCGCCCCCTCTCTTCCGCAAGTGTCTCTGAAAGAGCTGGTGGC	300
Db	241	ACGGCCGCCCCCGCCGCCCCCTCTCTTCCGCAAGTGTCTCTGAAAGAGCTGGTGGC	300
OY	301	CCGAGTGTGAGAGAGCTGTGCGAGCGCGGCGGAAAGAACGTGTGAGCTTCCGACTTCG	360
Db	301	CCGAGTGTGAGAGAGCTGTGCGAGCGCGGCGGAAAGAACGTGTGTGGACTTCCGACTTCG	360
OY	361	GCTGTGAGACGGGGCCCGCGGGGGGCCCCCCCGAGGCTTCAACAACAGCTTGCAGCTTA	420
Db	361	GCTGTGAGACGGGGCCCGCGGGGGGCCCCCCCGAGGCTTCAACAACAGCTTGCAGCTTA	420
OY	421	CCTGCCCCCAACACGGTGAACCGAACGATGCGGGGGAGAGCGGGGCGTGGGGCTGTGCTGG	480
Db	421	CCTGCCCCCAACACGGTGAACCGAACGATGCGGGGGAGAGCGGGGCGTGGGGCTGTGCTGG	480
OY	481	CCGCGTGGGGACACGACGTGTGCTGTTCACCTCTGAGACGCTGCGCGCTCTTGTGTGGT	540
Db	481	CCGCGTGGGGACACACGTGTGCTGTTCACCTCTGTGGACGCTGCGCGCTCTTGTGTGGT	540
OY	541	GACTTCCACGCTGTGCGCTAACACAGTGTGTGGGCGCGCGCTGTACCAAGCTCGGCGCTGCAC	600
Db	541	GACTTCCACGCTGTGCGCTAACAGTGTGTGGGCGCGCGCTGTACCAAGCTCGGCGCTGCAC	600
OY	601	TCAGGCCCCGGCCCCCGGCCACACGCTAGTGTGAACCCCGAAGGGGTCTGGGAAATGCGAACGGG	660
Db	601	TCAGGCCCCGGCCCCCGGCCACACGCTAGTGTGAACCCCGAAGGGGTCTGGGAAATGCGAACGGG	660
OY	661	CTGGAACCATAGCGTGCAGGAGAGCGCGGGGTCCTCCCTGGGCTTGCACGCCCCGAGTGGAG	720
Db	661	CTGGAACCATAGCGTGCAGGAGAGCGCGGGGTCCTCCCTGGGCTTGCACGCCCCGAGTGGAG	720
OY	721	GAGGCGCGGGGSCAGTGTCCACGCGGAAAGTCTGCTGGTTCGCAAGAGGCCCAAGCTGTGCGC	780
Db	721	GAGGCGCGGGGSCAGTGTCCACGCGGAAAGTCTGCTGGTTCGCAAGAGGCCCAAGCTGTGCGC	780
OY	781	TGCCCCCTAAGCCGAGCGGAGCGCCCGTGTGGGCAAGGGGTCTGGGCGCAACCCGGSCAGAGAC	840
Db	781	TGCCCCCTAAGCCGAGCGGAGCGCCCGTGTGGGCAAGGGGTCTGTGGGCGCAACCCGGSCAGAGAC	840
OY	841	GCGTGGACCGAGTGAACGCTGTGTTCTGTGTGTGTGCACTTGCACAGACCCCGCGAAGAGC	900
Db	841	GCGTGGACCGAGTGAACGCTGTGTTCTGTGTGTGTGCACTTGCACAGACCCCGCGAAGAGC	900
OY	901	CACCTCTTTGAGAGGATGCGCTCTCTGTGGCAACGCGCACTTCCCAACCATTCGTGTGGGCGCGCA	960
Db	901	CACCTCTTTGAGAGGATGCGCTCTCTGTGGCAACGCGCACTTCCCAACCATTCGTGTGGGCGCGCA	960
OY	961	GCACCAAGCGGGGCCCCCGCATCCACATCGCGGCGACCAAGTCCCTGGGGCAAGGCTTGTGC	1020
Db	961	GCACCAAGCGGGGCCCCCGCATTCACATCGCGGCGACCAAGTCCCTGGGGCAAGGCTTGTGC	1020
OY	1021	CCCGGTGTACGCGGAGACCAAGCACTTCTCTTACCTCTCAGGCGCAAGAGAGCACTTGC	1080
Db	1021	CCCGGTGTACGCGGAGACCAAGCACTTCTCTTACCTCTCAGGCGCAAGAGAGCACTTGC	1080
OY	1081	GCGCTCTTTCTTACCTACGCTCTCTTGAAGGCCACGCTGACTTGGCGTGTGGAGGCTGTGGGA	1140
Db	1081	GCGCTCTTTCTTACCTACGCTCTCTTGAAGGCCACGCTGACTTGGCGTGTGGAGGCTGTGGGA	1140
OY	1141	GACCACTCTTTCTGGGTTCCAGGCGCTGTGAACGCACTGCGGAGGAGCTCCCGCGAGTTGCCCGGCT	1200
Db	1141	GACCACTCTTTCTGGGTTCCAGGCGCTGTGAACGCACTGCGGAGGAGCTCCCGCGAGTTGCCCGGCT	1200
OY	1201	GCCCCAGCGCTACTGTGGCAATGCGGCCCCCTGTTTCTGAGAGCTGCTTGGGAAACAAGCGCA	1260
Db	1201	GCCCCAGCGCTACTGTGGCAATGCGGCCCCCTGTTTCTGAGAGCTGCTTGGGAAACAAGCGCA	1260
OY	1261	GAGCCCCCTAACGGGGGTCTCTTCAACGCACTGCGCGCGTGTGGAGCTGGGCTACACCCAGC	1320
Db	1261	GAGCCCCCTAACGGGGGTCTCTTCAACGCACTGCGCGCGTGTGGAGCTGGGCTACACCCAGC	1320

QY	1321	AGCCGGTGTCTGTATCCCGGGAGAAAGCCCCCAAGGCTCTGTGTGGCGGCCCCCGAGAGAGAGGA	1380
Db	1321	AGCCGGTGTCTGTATCCCGGGAGAAAGCCCCCAAGGCTCTGTGTGGCGGCCCCCGAGAGAGAGGA	1380
QY	1381	CACAGACCCCCGTGTGGCCTGGTGACGTGTCCGACAGACAGCAGACCCTTGTGGCAGGTGT	1440
Db	1381	CACAGACCCCCGTGTGGCCTGGTGACGTGTCTCCGACAGACAGCAGACCCTTGTGGCAGGTGT	1440
QY	1441	CGGCTTCGTGTGGGCTTGTCCGCTGGCTGTGTGTCGCCCAAGGCTCTGTGGGCTCCAGGCA	1500
Db	1441	CGGCTTCGTGTGGGCTTGTCCGCTGGCTGTGTGTCGCCCAAGGCTCTGTGGGCTCCAGGCA	1500
QY	1501	CAAGGAACGCGCTTCTCTCAGAGAACCAACAGAACTTATCTCTCTGGGGAAGCATTCGCA	1560
Db	1501	CAAGGAACGCGCTTCTCTCAGAGAACCAACAAATTTATCTCTCTGGGGAAGCATTCGCA	1560
QY	1561	GCTCTCCGTGACAGAGAGCTGACGTGTGAAGATAGAGGTGTGGGACCTGTGGCTGTGGCAG	1620
Db	1561	GCTCTCCGTGACAGAGAGCTGACGTGTGAAGATAGAGGTGTGGGACCTGTGGCTGTGGCAG	1620
QY	1621	GAGCCCAAGGGGTGTGACTGTGTTCGGCGCAGAGCACCGTCTGTGGTGAAGAGATCTGTGC	1680
Db	1621	GAGCCCAAGGGGTGTGACTGTGTTCGGCGCAGAGCACCGTCTGTGGTGAAGAGATCTGTGC	1680
QY	1681	CAAGTTCTTCGACATGTGGCTGATGATGTGTACTGTGTGAGCTGTCAAGTCTTCTTTTA	1740
Db	1681	CAAGTTCTTCGACATGTGGCTGATGATGTGTACTGTGTGAGCTGTCAAGTCTTCTTTTA	1740
QY	1741	TGTACCGSAGACAGTTTCAAAAGAACAGGCTCTTTTCTTACCGSAAAGATGTCTGGAG	1800
Db	1741	TGTACCGSAGACAGGTTTCAAAAGAACAGGCTCTTTTCTTACCGSAAAGATGTCTGGAG	1800
QY	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTCTC	1860
Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTCTC	1860
QY	1861	GGAAGCAGAGGTCAAGCAGCATTCGGGAAGCCAGGCCCCGCTGTGAGTGTCAACATCTCG	1920
Db	1861	GGAAGCAGAGGTCAAGCAGCATTCGGGAAGCCAGGCCCCGCTGTGAGTGTCAACATCTCG	1920
QY	1921	CTTCAATCCCAAGGCTGACGGGCTGTGGGCGGATTTGTGAACATGTGACTGTGTGGAGC	1980
Db	1921	CTTCAATCCCAAGGCTGACGGGCTGTGGGCGGATTTGTGAACATGTGACTGTGTGGAGC	1980
QY	1981	CAGAACTTCCGACAGAGAAAGAGGGCCGACGCTCTCACTGTGAGGGTGAAGGACCTGTT	2040
Db	1981	CAGAACTTCCGACAGAGAAAGAGGGCCGACGCTCTCACTGTGAGGGTGAAGGACCTGTT	2040
QY	2041	CAGCGTGTCAACTTACAGAGCGGGCGGGCGCTCCGAGCTCTGTGGCGCTCTGTGTGTGG	2100
Db	2041	CAGCGTGTCAACTTACAGAGCGGGCGGGCGCTCCGAGCTCTGTGGCGCTCTGTGTGTGG	2100
QY	2101	CCTGGAACATATTCACAGGGCGCTGGCGGACCTTGTGTGTGTGTGTGTGGCGGCGGACCA	2160
Db	2101	CCTGGAACATATTCACAGGGCGCTGGCGGACCTTGTGTGTGTGTGTGTGGCGGCGGACCA	2160
QY	2161	GGCGGCTAGCTGTACTTGTGTCAAGGTGTGATGTGACGGGCGCGTATCGACACATCTCCCA	2220
Db	2161	GGCGGCTAGCTGTACTTGTGTCAAGGTGTGATGTGACGGGCGCGTATCGACACATCTCCCA	2220
QY	2221	GGACAGGCTCAACGAGGTCAATCGCCAGCATATCAAACTCCAGAACACATGACTGTGTGG	2280
Db	2221	GGACAGGCTCAACGAGGTCAATCGCCAGCATATCAAACTCCAGAACACATGACTGTGTGG	2280
QY	2281	TCCGTATCCCGTGTGTCAAGAGCGCGCCCATATGGGAGGTCCGCAAGGCTTCAAGAGGCA	2340
Db	2281	TCCGTATCCCGTGTGTCAAGAGCGCGCCCATATGGGAGGTCCGCAAGGCTTCAAGAGGCA	2340
QY	2341	CGTCTCTACTTGAACAGACTCTCAAGCGGTACATGTGACAGTTTGTGTGTGTCACTGTGACGA	2400
Db	2341	CGTCTCTACTTGAACAGACTCTCAAGCGGTACATGTGACAGTTTGTGTGTGTCACTGTGACGA	2400
QY	2401	GACCGGCCCGTGAAGAGTCCGCTCTCATCGACAGACTTCTTCTGAAATGAGGCCAG	2460

```

Db      2401  GACAGCCCGCTGAGGATGCGCTGTCATCAGAGAGAGCTCTCCCTGAATGAGGCGAG 2460
Qy      2461  CAGTGGCCCTTTCAGACGCTTCTCAACGTTTATGTGCGACACGCGCTGTGCATCAGGG 2520
Db      2461  CAGTGGCCCTTTCAGACGCTTCTCAACGTTTATGTGCGACACGCGCTGTGCATCAGGG 2520
Qy      2521  CAGTGGCCCTTTCAGACGCTTCTCAACGTTTATGTGCGACACGCGCTGTGCATCAGGG 2580
Db      2521  CAGTGGCCCTTTCAGACGCTTCTCAACGTTTATGTGCGACACGCGCTGTGCATCAGGG 2580
Qy      2581  CAGCTGTGTGCTACGCGCGACATGAGAAACAAGCTGTGCGGGATTCGCGGGAGCGGCT 2640
Db      2581  CAGCTGTGTGCTACGCGCGACATGAGAAACAAGCTGTGCGGGATTCGCGGGAGCGGCT 2640
Qy      2641  GCTCTGTGTGCTGTGATGATTTCTGTGTGATACCTCACTCACTCACTCACTCACTCA 2700
Db      2641  GCTCTGTGTGCTGTGATGATTTCTGTGTGATACCTCACTCACTCACTCACTCACTCA 2700
Qy      2701  CTTCCTCAGAGACCTGTGTGCGAGGTCTCTGAGTATGCGTGTGAGTGAATTCGAGAA 2760
Db      2701  CTTCCTCAGAGACCTGTGTGCGAGGTCTCTGAGTATGCGTGTGAGTGAATTCGAGAA 2760
Qy      2761  GACAGTGTAACTTCCCTGTGAAGAACAGAGCCCTGTGGTGGACGCGCTTTTGTTCAGAT 2820
Db      2761  GACAGTGTAACTTCCCTGTGAAGAACAGAGCCCTGTGGTGGACGCGCTTTTGTTCAGAT 2820
Qy      2821  GCGGCGCCACGCGCTATTTCCCTGTGTGCGAGCTGTGATACCGGACCGCTGAGGT 2880
Db      2821  GCGGCGCCACGCGCTATTTCCCTGTGTGCGAGCTGTGATACCGGACCGCTGAGGT 2880
Qy      2881  GCAGAGGACATCTCCAGCTATGCGCGACCTTCATCAGAGCGAGTCTCACTTCAACCG 2940
Db      2881  GCAGAGGACATCTCCAGCTATGCGCGACCTTCATCAGAGCGAGTCTCACTTCAACCG 2940
Qy      2941  CGGCTTCAAGAGCTGGAGAGAACATGCGTGCAGAACTTTGGGTCTTGGGTGAGT 3000
Db      2941  CGGCTTCAAGAGCTGGAGAGAACATGCGTGCAGAACTTTGGGTCTTGGGTGAGT 3000
Qy      3001  TCAAGCTGTCTGTGATTTGAGTGAAGTGAACAGCTTCAGAGCGTGTGACCAACATCTA 3060
Db      3001  TCAAGCTGTCTGTGATTTGAGTGAAGTGAACAGCTTCAGAGCGTGTGACCAACATCTA 3060
Qy      3061  CAAGATCTCTCTGTGAGGCGTGAAGGTTTCAAGCATGTGTCTCACTCCATTCA 3120
Db      3061  CAAGATCTCTCTGTGAGGCGTGAAGGTTTCAAGCATGTGTCTCACTCCATTCA 3120
Qy      3121  TCAGCAAGTTTGAAGAACCCCACTTTTCCGCGGTCTCTGACAGCGGCTCCCT 3180
Db      3121  TCAGCAAGTTTGAAGAACCCCACTTTTCCGCGGTCTCTGACAGCGGCTCCCT 3180
Qy      3181  CTGCTACTCATCTCTGAAGCAAGAACGAGGAGTGTGCTGGGGCCCAAGGGCGCGC 3240
Db      3181  CTGCTACTCATCTCTGAAGCAAGAACGAGGAGTGTGCTGGGGCCCAAGGGCGCGC 3240
Qy      3241  CGGCGCTGTGCGCTCCGAGGCGCTGAGTGTGCTGTGCGACCAAGCTTCTCTCAAGT 3300
Db      3241  CGGCGCTGTGCGCTCCGAGGCGCTGAGTGTGCTGTGCGACCAAGCTTCTCTCAAGT 3300
Qy      3301  GACTGTGACACCGTGTCACTGACCTGAGGCTGTGAGTGTGAGGCGCGACCGGCGC 3360
Db      3301  GACTGTGACACCGTGTCACTGACCTGAGGCTGTGAGTGTGAGGCGCGACCGGCGC 3360
Qy      3361  GCTGATTCGGAAGCTCCGCGGAGCAGAGCTGACTGCTGTGAGGCGCGACCGGCGC 3420
Db      3361  GCTGATTCGGAAGCTCCGCGGAGCAGAGCTGACTGCTGTGAGGCGCGACCGGCGC 3420
Qy      3421  ACTGCGCTCAGAGCTTCAAGACATCTGTGATGATGAGGCGCGACCGGCGCGAGCGG 3480
Db      3421  ACTGCGCTCAGAGCTTCAAGACATCTGTGATGATGAGGCGCGACCGGCGCGAGCGG 3480
Qy      3481  GAGCAGACACGAGCGCTGTCAAGCGCGGCTTCAAGTCCAGAGGAGGAGGCGGCGC 3540
Db      3481  GAGCAGACACGAGCGCTGTCAAGCGCGGCTTCAAGTCCAGAGGAGGAGGCGGCGC 3540

Db      3481  GAGCAGACACGAGCGCTGTCAAGCGCGGCTTCAAGTCCAGAGGAGGAGGCGGCGC 3540
Qy      3541  CACACCCAGGCGCGACCGCTGTGAGTGTGAGGCTTGTGAGGCTGTGAGGCGGCTGTG 3600
Db      3541  CACACCCAGGCGCGACCGCTGTGAGTGTGAGGCTTGTGAGGCTGTGAGGCGGCTGTG 3600
Qy      3601  CATGTCCGGGTGAAGGCTGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 3660
Db      3601  CATGTCCGGGTGAAGGCTGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 3660
Qy      3661  GAGTGTGACACACCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 3720
Db      3661  GAGTGTGACACACCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTG 3720
Qy      3721  GGGCGAGCTTTTCTTCAACAGAGGCGGCTTCACTCCCAATGAGTAATGTCATCC 3780
Db      3721  GGGCGAGCTTTTCTTCAACAGAGGCGGCTTCACTCCCAATGAGTAATGTCATCC 3780
Qy      3781  CCAGATTGCGCAATGTTTCACCGCTGCGCTGCTTGTGCTTCAACCGGCGGCGGCT 3840
Db      3781  CCAGATTGCGCAATGTTTCACCGCTGCGCTGCTTGTGCTTCAACCGGCGGCGGCT 3840
Qy      3841  AGGTGAGACCTGTGAAGAGACCTGTGAGTGTGAGGCTTGTGAGTGTGAGGCTGTG 3900
Db      3841  AGGTGAGACCTGTGAAGAGACCTGTGAGTGTGAGGCTTGTGAGTGTGAGGCTGTG 3900
Qy      3901  CCTGTGACACAGGCGAGGACCTGTGACCTGTGAGTGTGAGGCTTGTGAGTGTGAGG 3960
Db      3901  CCTGTGACACAGGCGAGGACCTGTGACCTGTGAGTGTGAGGCTTGTGAGTGTGAGG 3960
Qy      3961  GAGTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 4015
Db      3961  GAGTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 4015

RESULT 14
US-10-449-565-1
; Sequence 1, Application US/10449565
; Publication No. US20030225027A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Jun Jian
; APPLICANT: Huang, Cui-Fen
; APPLICANT: Lin, Maie
; APPLICANT: King, Hsiang-fu
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Fragments and Uses thereof
; FILE REFERENCE: 9661-037
; CURRENT APPLICATION NUMBER: US/10/449,565
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 60/384,806
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2702)..(3454)
US-10-449-565-1

Query Match      100.0%; Score 4015; DB 15; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAGCGCTGCTCTCTGTGCGGACAGTGTGAGGAGGCTTGGCCCGGCGGATGCC 60
Db      1  GCAGCGCTGCTCTCTGTGCGGACAGTGTGAGGAGGCTTGGCCCGGCGGATGCC 60
Qy      61  GCGCGCTCCCGCTGCGGAGCGGCTGCGCTGCGGAGCGAGCCATGACCGGAGGCT 120
Db      61  GCGCGCTCCCGCTGCGGAGCGGCTGCGCTGCGGAGCGAGCCATGACCGGAGGCT 120

```

OY	121	GC	CGCGTGGGCAACGTTGCGGCGCGCTGAGGGGCCCCAGGGGCTGAGCGGCTGATGACAGCGG	180
Db	121	GC	CGGTGGGCAACGTTGCGGCGCGCTTGAAGGCCCCAGGGGCTGAGCGGCTGATGACAGCGG	180
OY	181	GG	ACCAGGCGGCGCTTTCGCGCGGCTTGGTGGGCGACGTCGTGGTGTGTCGAGCCCTGAGAGC	240
Db	181	GG	ACCAGGCGGCGCTTTCGCGCGGCTTGGTGGGCGACGTCGTGGTGTGTCGAGCCCTGAGAGC	240
OY	241	AC	GGCGCGCCCCCGCGCGCCCCCTCTCTCCGCGCAGGATGTCCTTGAGAGAGCTGTGGC	300
Db	241	AC	GGCGCGCCCCCGCGCGCCCCCTCTCTCCGCGCAGGATGTCCTTGAGAGAGCTGTGGC	300
OY	301	CC	GAGTGTGCAAGAGGCTGTGCGAGAGCGGCGGAGAGAAAGTCGTGGCTTCGCGCTTCGC	360
Db	301	CC	GAGTGTGCAAGAGGCTGTGCGAGAGCGGCGGAGAGAAAGTCGTGGCTTCGCGCTTCGC	360
OY	361	GCT	GTGTGACGAGGGGCGCGCGGGGGGCCCCCGAGAGCCTTTCACACACAGCTGTGCGAGCTA	420
Db	361	GCT	GTGTGACGAGGGGCGCGCGGGGGGCCCCCGAGAGCCTTTCACACACAGCTGTGCGAGCTA	420
OY	421	CCT	GCACCAACAGGTGACCGACGCACTGCGGGGAGACGGGGCGTGGGGCTTCCTTCGC	480
Db	421	CCT	GCACCAACAGGTGACCGACGCACTGCGGGGAGACGGGGCGTGGGGCTTCCTTCGC	480
OY	481	CCG	CTGGGCGCACACAGTCGTGTGTTCACCTCTGTGGACAGCTGCGGCTCTTTGTGTGGT	540
Db	481	CCG	CTGGGCGCACACAGTCGTGTGTTCACCTCTGTGGACAGCTGCGGCTCTTTGTGTGGT	540
OY	541	GG	CTCCACAGCTGCGGCTACAGGATGTGGGGCGCGCGCTGTACACAGAGCTCGGCGGCGAC	600
Db	541	GG	CTCCACAGCTGCGGCTACAGGATGTGGGGCGCGCGCTGTACACAGAGCTCGGCGGCGAC	600
OY	601	TC	AGGCGCGGCGCGCGCGCACACAGCTAATGGAACCCCGAAGAGCGTCTGGAGTCGAGCGGC	660
Db	601	TC	AGGCGCGGCGCGCGCGCACACAGCTAATGGAACCCCGAAGAGCGTCTGGAGTCGAGCGGC	660
OY	661	CT	GGAACCAATAGCGTCAGAGAGGCGGGGGTCCCCCTGGGCGCTGCAGGCCCCGGGTGCAG	720
Db	661	CT	GGAACCAATAGCGTCAGAGAGGCGGGGGTCCCCCTGGGCGCTGCAGGCCCCGGGTGCAG	720
OY	721	GAG	GCGCGGGGGGCACTGTGCAGCGCAAGTCGCGCTGTGGCCCAAGAGGCGCAGCGTGGCG	780
Db	721	GAG	GCGCGGGGGGCACTGTGCAGCGCAAGTCGCGCTGTGGCCCAAGAGGCGCAGCGTGGCG	780
OY	781	TG	CCCCCTGAGCGGAGCGCGCGCTGTGGGAGGGGTCTGTGGCCACCCGGGCAAGCAC	840
Db	781	TG	CCCCCTGAGCGGAGCGCGCGCTGTGGGAGGGGTCTGTGGCCACCCGGGCAAGCAC	840
OY	841	GG	TGAGACCGAGTGAACCGTGGTTTTGTGTGTGTGCACCTGCGAGACCCGCGCAAGAAC	900
Db	841	GG	TGAGACCGAGTGAACCGTGGTTTTGTGTGTGTGCACCTGCGAGACCCGCGCAAGAAC	900
OY	901	CAC	CTCTTGGAGGGGTGCGCTCTCTGAGGACCGGCGACCTCCACCCATCGATGGGCGGCA	960
Db	901	CAC	CTCTTITGGAGGGGTGCGCTCTCTGAGGACCGGCGACCTCCACCCATCGATGGGCGGCA	960
OY	961	GC	ACCACGCGGGCGCCCCCATCCACATCGGGGCAACAGTCCCTGTGGGACAGGCTTGTCC	1020
Db	961	GC	ACCACGCGGGCGCCCCCATCCACATCGGGGCAACAGTCCCTGTGGGACAGGCTTGTCC	1020
OY	1021	CCG	GGTGTAGCGCGAGACCAAGCACTTCTCTACTCTTCAGGCGACAGAGACAGTGGC	1080
Db	1021	CCG	GGTGTGTAGCGCGAGACCAAGCACTTCTCTACTCTTCAGGCGACAGAGACAGTGGC	1080
OY	1081	GG	CCCTCTCTCTACTCACTCACTCTGTGAGGCGCAGCGCTGATGGCGCTCGAAGGCTGTGG	1140
Db	1081	GG	CCCTCTCTCTCTACTCACTCACTCTGTGAGGCGCAGCGCTGATGGCGCTCGAAGGCTGTGG	1140
OY	1141	GA	CACTCTTCTGAGGTTCCAGGCGCTGTAGTCAGAGGAGCTCCCGCAGAGTGTGCCCGGCT	1200
Db	1141	GA	CACTCTTCTTCTGAGGTTCCAGGCGCTGTAGTCAGAGGAGCTCCCGCAGAGTGTGCCCGGCT	1200
OY	1201	GC	CCGCGGCGCTAATGCGCAATGCGGCGCCCTGTTTCTGAGAGCTGCTTGGGAACACAGCGCA	1260

[illegible]

Db 2281 TCGGATGCGGATGTCAGAGAGCCGCCCATGAGCGATGCCAGAGGCTTTCAAGAGCA 2340
 Qy 2341 CGTCTTACTTGAAGAGCTCCAGCCGATATGAGAGAGTTCGTGGCTCACTGAGAGCA 2400
 Db 2341 GGTCTTACTTGAAGAGCTCCAGCCGATATGAGAGAGTTCGTGGCTCACTGAGAGCA 2400
 Qy 2401 GACCAAGCCGCTGAGAGAGTCCGCTGATATGAGAGAGTCTCTCCGTAATGAGAGCA 2460
 Db 2401 GACCAAGCCGCTGAGAGAGTCCGCTGATATGAGAGAGTCTCTCCGTAATGAGAGCA 2460
 Qy 2461 CAGTGGCTCTTTCAGAGCTCTTCTACGCTTATGAGAGCAAGCGCGTGGCATAGAGG 2520
 Db 2461 CAGTGGCTCTTTCAGAGCTCTTCTACGCTTATGAGAGCAAGCGCGTGGCATAGAGG 2520
 Qy 2521 CAGTGGCTCTTTCAGAGCTCTTCTACGCTTATGAGAGCAAGCGCGTGGCATAGAGG 2580
 Db 2521 CAGTGGCTCTTTCAGAGCTCTTCTACGCTTATGAGAGCAAGCGCGTGGCATAGAGG 2580
 Qy 2581 CAGCTTGTCTAGCGGCAATGAGAGCAAGCTGTTGCGGGGATTCGCGGGGCGGCT 2640
 Db 2581 CAGCTTGTCTAGCGGCAATGAGAGCAAGCTGTTGCGGGGATTCGCGGGGCGGCT 2640
 Qy 2641 GCTCTGCTGTTGTTGATGATATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2700
 Db 2641 GCTCTGCTGTTGTTGATGATATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2700
 Qy 2701 CTTCCTCAGAGACCTGATGAGAGTCTGAGTATGAGTGTGAGTGTGAGTGTGAGTGT 2760
 Db 2701 CTTCCTCAGAGACCTGATGAGAGTCTGAGTATGAGTGTGAGTGTGAGTGTGAGTGT 2760
 Qy 2761 GAGAGTGTGATATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2820
 Db 2761 GAGAGTGTGATATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2820
 Qy 2821 GCGGCGCCAGCGGCTATTTCCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2880
 Db 2821 GCGGCGCCAGCGGCTATTTCCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2880
 Qy 2881 GCGAGCGGCTATTTCCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940
 Db 2881 GCGAGCGGCTATTTCCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940
 Qy 2941 CCGCTTCAAGAGCTGAGAGCAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3000
 Db 2941 CCGCTTCAAGAGCTGAGAGCAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 3000
 Qy 3001 TCACAGCTGTTTCTGATTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3060
 Db 3001 TCACAGCTGTTTCTGATTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3060
 Qy 3061 CAGAGTCTTCTGCTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3120
 Db 3061 CAGAGTCTTCTGCTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3120
 Qy 3121 TCAGCAAGTGTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAG 3180
 Db 3121 TCAGCAAGTGTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAG 3180
 Qy 3181 CTGCTACTCATCTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3240
 Db 3181 CTGCTACTCATCTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3240
 Qy 3241 CCGGCTCTGAGGCTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3300
 Db 3241 CCGGCTCTGAGGCTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3300
 Qy 3301 GACTGAGACCGGTTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3360
 Db 3301 GACTGAGACCGGTTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3360
 Qy 3361 GGTGAGTGGAGGTTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3420
 Db 3361 GGTGAGTGGAGGTTGAGAGCAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 3420

Qy 3421 ACTGCCCTGAGACTTCAAGACCAATCTGAGATGATGAGGCAAGCCGAGCCAGAGCCG 3480
 Db 3421 ACTGCCCTGAGACTTCAAGACCAATCTGAGATGATGAGGCAAGCCGAGCCAGAGCCG 3480
 Qy 3481 GAGCAGACACAGAGAGCCCTGTTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3540
 Db 3481 GAGCAGACACAGAGAGCCCTGTTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3540
 Qy 3541 CACAGCAGAGCCGAGAGCCCTGTTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3600
 Db 3541 CACAGCAGAGCCGAGAGCCCTGTTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3600
 Qy 3601 CATGTCGAGTGAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 3660
 Db 3601 CATGTCGAGTGAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 3660
 Qy 3661 GAGTGTCCAGACACCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3720
 Db 3661 GAGTGTCCAGACACCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3720
 Qy 3721 GAGGCAAGCTTTCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3780
 Db 3721 GAGGCAAGCTTTCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3780
 Qy 3781 CAGAGTGTGAGTGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3840
 Db 3781 CAGAGTGTGAGTGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3840
 Qy 3841 AGGTGAGAGCCCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 3900
 Db 3841 AGGTGAGAGCCCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 3900
 Qy 3901 CCGTGTACAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3960
 Db 3901 CCGTGTACAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3960
 Qy 3961 GAGGTGTGAGGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4015
 Db 3961 GAGGTGTGAGGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4015

RESULT 15
 US-10-602-441-1
 ; Sequence 1, Application US/10602441
 ; Publication No. US20040106128A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genon Corporation
 ; APPLICANT: Majumdar, Anish Sen
 ; APPLICANT: Ferber, Iris
 ; APPLICANT: Frokies, Maria
 ; APPLICANT: Mang, Zhuo
 ; TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Revert
 ; FILE REFERENCE: 086/002
 ; CURRENT APPLICATION NUMBER: US/10/602,441
 ; CURRENT FILING DATE: 2003-06-24
 ; PRIOR APPLICATION NUMBER: 60/393,295
 ; PRIOR FILING DATE: 2002-06-27
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 4015
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-602-441-1

Query Match 100.0%; Score 4015; DB 17; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGCGTGGTCTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 60
 Db 1 GAGGCGTGGTCTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 60

QY 2221 GAGACAGCTCAAGAGTCAATCGCAGCATCATCAAAACCCAGAACACTGTCGTGGC 2280
 Db 2221 GAGACAGCTCAAGAGTCAATCGCAGCATCATCAAAACCCAGAACACTGTCGTGGC 2280
 QY 2281 TCGGATATCCGTGGTCCAGAAAGCCGCCATGAGCAGCTCCGCAAGGCTTCAAGAGCCA 2340
 Db 2281 TCGGATATCCGTGGTCCAGAAAGCCGCCATGAGCAGCTCCGCAAGGCTTCAAGAGCCA 2340
 QY 2341 CGTCTCACTGACAGACCTCCAGCCGCTATCATCGACAGTTCGTGGCTCACTGCGAGA 2400
 Db 2341 CGTCTCACTGACAGACCTCCAGCCGCTATCATCGACAGTTCGTGGCTCACTGCGAGA 2400
 QY 2401 GACCAAGCCGCTGAGAGATGCGCTGCTATCATGACAGAGCTCTCCCTGAATGAGGCGAG 2460
 Db 2401 GACCAAGCCGCTGAGAGATGCGCTGCTATCATGACAGAGCTCTCCCTGAATGAGGCGAG 2460
 QY 2461 CAGTGGCTCTTCAAGCTCTTCTCAAGCTTATGTCGCAACGCGCTGCGCATCAGGGG 2520
 Db 2461 CAGTGGCTCTTCAAGCTCTTCTCAAGCTTATGTCGCAACGCGCTGCGCATCAGGGG 2520
 QY 2521 CAAGTCTCACTGACAGAGTCCGAGGAGATCCGAGAGGCTCATCTCTCCAGCGCTCTG 2580
 Db 2521 CAAGTCTCACTGACAGAGTCCGAGGAGATCCGAGAGGCTCATCTCTCCAGCGCTCTG 2580
 QY 2581 CAGCTCTGCTACGCGCAATGAGAAACAAGCTGTTGCGGGATTCGGGGGAGCGGCT 2640
 Db 2581 CAGCTCTGCTACGCGCAATGAGAAACAAGCTGTTGCGGGATTCGGGGGAGCGGCT 2640
 QY 2641 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
 Db 2641 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
 QY 2701 CTTCCTCAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
 Db 2701 CTTCCTCAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
 QY 2761 GACAGTGTGAATCTTCCCTGTAAGAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
 Db 2761 GACAGTGTGAATCTTCCCTGTAAGAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
 QY 2821 GCGGCGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
 Db 2821 GCGGCGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
 QY 2881 GCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
 Db 2881 GCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
 QY 2941 CGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
 Db 2941 CGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
 QY 3001 TCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
 Db 3001 TCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
 QY 3061 CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
 Db 3061 CAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
 QY 3121 TCAGCAAGTTGGAAGAACCCCAATTTTCCGCGCGCTCATCTGAGACAGGCGCTCCCT 3180
 Db 3121 TCAGCAAGTTGGAAGAACCCCAATTTTCCGCGCGCTCATCTGAGACAGGCGCTCCCT 3180
 QY 3181 CTGCTACTCTCATCTGAAAGCCAGAGATGCTGCTGCGGGCCAGAGGCGCGC 3240
 Db 3181 CTGCTACTCTCATCTGAAAGCCAGAGATGCTGCTGCGGGCCAGAGGCGCGC 3240
 QY 3241 CGGCGCTCTGCGCTCGAGAGCCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
 Db 3241 CGGCGCTCTGCGCTCGAGAGCCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
 QY 3301 GACTGCAACCGTGTCACTAGTGCATCTCTGCGGGTCACTCAGAGACGCCAGACGCA 3360

Db 3301 GACTGCAACCGTGTCACTAGTGCATCTCTGCGGGTCACTCAGAGACGCCAGACGCA 3360
 QY 3361 GCTGAGTGGAGACTCCCGGGGAGCAGCGCTGACTGCTCGAGAGGCGCGAGCCAGCCGCGC 3420
 Db 3361 GCTGAGTGGAGACTCCCGGGGAGCAGCGCTGACTGCTCGAGAGGCGCGAGCCAGCCGCGC 3420
 QY 3421 ACTGCGCTGAGACTTCAAGACCACTCTGAGACTGATGAGCCAGCCGCGAGCCGCGC 3480
 Db 3421 ACTGCGCTGAGACTTCAAGACCACTCTGAGACTGATGAGCCAGCCGCGAGCCGCGC 3480
 QY 3481 GAGCAGACACAGCAGCCCTGCTGAGCGCGGCTCACTGCTGAGAGAGAGAGAGGCGCGC 3540
 Db 3481 GAGCAGACACAGCAGCCCTGCTGAGCGCGGCTCACTGCTGAGAGAGAGAGAGGCGCGC 3540
 QY 3541 CACACCCAGGCGCGAGCCGCTGAGAGTCTGAGAGCTGAGTGAAGTCTGAGAGGCTGAG 3600
 Db 3541 CACACCCAGGCGCGAGCCGCTGAGAGTCTGAGAGCTGAGTGAAGTCTGAGAGGCTGAG 3600
 QY 3601 CATGCTCGGCTGAGAGCTGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3660
 Db 3601 CATGCTCGGCTGAGAGCTGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3660
 QY 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCTGAG 3720
 Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCTGAG 3720
 QY 3721 GGGCGAGCTTCTTCTCAGCAGAGAGCCGCTTCACTTCCCAACAGGCTGAGGCTGAG 3780
 Db 3721 GGGCGAGCTTCTTCTCAGCAGAGAGCCGCTTCACTTCCCAACAGGCTGAGGCTGAG 3780
 QY 3781 CCAGATGCGCAATGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3840
 Db 3781 CCAGATGCGCAATGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3840
 QY 3841 AGTGTGAGACCTTGAAGAGACCTGAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGA 3900
 Db 3841 AGTGTGAGACCTTGAAGAGACCTGAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGA 3900
 QY 3901 CCTGTACACAGGCGAGAGACCTGAGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3960
 Db 3901 CCTGTACACAGGCGAGAGACCTGAGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3960
 QY 3961 GAGTGTGCTGAGAGTAAATAGATATAGATTTTCAAGTTTGAAGAAAAA 4015
 Db 3961 GAGTGTGCTGAGAGTAAATAGATATAGATTTTCAAGTTTGAAGAAAAA 4015

Search completed: October 30, 2004, 07:45:07
 Job time : 1774 secs